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Monitoring scheme for biotic habitat quality of Natura 2000 habitat types in Flanders, Belgium

Revision of the monitoring design

Toon Westra, Patrik Oosterlynck, Leen Govaere, An Leyssen, Luc Denys, Jo Packet, Kevin Scheers, Floris Vanderhaeghe and Jeroen Vanden Borre

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MONITORING SCHEME FOR BIOTIC HABITAT QUALITY OF NATURA 2000 HABITAT TYPES IN FLANDERS, BELGIUM

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Contents

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Abstract

- The Monitoring scheme for biotic Habitat Quality (MHQ) aims at assessing the proportion of the habitat area in bad condition, for the habitat types and subtypes in Flanders. The habitat quality is favourable when this proportion is lower than 25%. This information is needed to evaluate the structure and functions criterion and the overall conservation status of habitat types, and is therefore crucial for the 6-yearly reporting in the framework of the Habitat Directive.

- MHQ was implemented in 2014. In this report we review the design of MHQ with a focus on the trend information that is provided by the monitoring scheme.

- We propose following changes in the monitoring design of the open terrestrial habitat types and the stream habitat type (3260):

  - Decrease the duration of the monitoring cycle[1] from 12 years to 6 years, making it possible to assess the habitat quality trend after 12 years of monitoring (= 2 monitoring cycles of 6 years) instead of 24 years (= 2 monitoring cycles of 12 years)
  - Decrease the sample size within Special Areas of Conservation (SAC) from 170 to 80 sampling units per habitat type, as a sample size of 80 is sufficient to differentiate between favourable and unfavourable habitat quality for most habitat types
  - Decrease the sample size for habitat subtypes from 80 to 40 sampling units per subtype, as information on the conservation status for habitat subtypes is of lower priority and is not required for the European reporting (Habitat Directive)

- In the original design for standing water habitat types, all water surfaces larger than 5 ha were selected and a sample was drawn from the water surfaces smaller than 5 ha. We propose to take a sample from the water surfaces with and area between 5 and 50 ha, as it is not feasible (and necessary) to measure all the water surfaces within this area class. We also propose to drop the oversampling within SAC as most water surfaces are situated within SAC and oversampling is not necessary.

- We do not modify the monitoring design for the forest habitat types, keeping a monitoring cycle of 12 years, as there is an important synergy with the Flemish Forest Inventory that has the same monitoring cycle of 12 years.

- The changes in the monitoring design are summarized in Table 1. The total sample size per year stays almost the same.

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[1] The monitoring cycle is the period in which all sampling units are measured. In a monitoring cycle of 6 years, sampling units are measured every 6 years. Decreasing the duration of the monitoring cycle results in increase of the number of sampling units that have to be measured per year.

Table 1: Changes in the design of MHQ: duraction of the monitoring cycle, sample size per habitat type (n Flanders), sample size per habitat type within SAC (n SAC), sample size per subtype (n subtype), total sample size over all types and subtypes per year (n total / year)

habitat category	design	cycle (years)	n Flanders	n SAC	n subtype	n total / year	sampling unit
terrestrial open habitat	original	12	80	170	80	247	36 m diameter circle plot
	new	6	80	80	40	258	
stream habitat	original	12	80	170		15	100 m river segment
	new	6	80	80		17	
standing water habitat	original	6	40 and all > 5 ha[*]	80	40	43.5	entire water surface
	new	6	80 and all > 50 ha[†]	0	40	42	

[*] A sample is taken for all watersurfaces < 5 ha and all watersurfaces > 5 ha are selected

[†] A sample is taken for all watersurfaces < 50 ha and all watersurfaces > 50 ha are selected

- Table 2 summarizes the Minimal Detectable Difference (MDD) for habitat quality status and trend.

Table 2: Summary of Minimal Detectable Differences (MDD) for habitat quality status and trend. The habitat proportion (prop.) in bad condition assumes that the habitat condition is eather good or bad (binary variable). The proportion of favourable indicators is the percentage of the quality indicators that are favourable at a certain location.

	habitat quality status	habitat quality trend	
sample size	habitat prop. in bad condition (MDD from 25%-threshold)	habitat prop. in bad condition (mdd between 2 periods)	prop. favourable indicators (MDD between 2 periods)
40	-16.1% and +21 %	19% - 37%	3.1% - 5%
80	-12.1% and +14.6 %	10% - 19%	2.2% - 3.5%
170	-8.7% and +9.8 %	5% - 9%	1.5% - 2.4%

Samenvatting

- Het meetnet voor biotische habitatkwaliteit (Monitoring scheme for biotic Habitat Quality of MHQ) heeft als doel om per habitattype en -subtype te bepalen welk aandeel zich in een slechte staat bevindt. De habitatkwaliteit is gunstig wanneer dit aandeel kleiner is dan 25%. Deze informatie is nodig om het criterium 'structuur en functies' te beoordelen en de globale staat van instandhouding te bepalen per habitattype, en is daarom van groot belang voor de 6-jaarlijkse rapportage in kader van de Habitatrichtlijn.

- MHQ is in 2014 van start gegaan. In dit rapport reviseren we het meetnetontwerp, met speciale aandacht voor de trendinformatie die het meetnet levert.

- We stellen volgende wijzigingen voor aan het meetnetontwerp voor de open terrestrische habitattypen en het aquatisch habitattype 3260:

  - halvering van de duur van de meetcyclus[2] van 12 jaar naar 6 jaar, zodat het mogelijk wordt om na 12 jaar (2 meetcycli van 6 jaar) de trend in habitatkwaliteit te bepalen i.p.v. na 24 jaar (2 meetcycli van 12 jaar)
  - vermindering van de steekproefgrootte binnen de Speciale Beschermingszones (SBZ) van 170 naar 80 steekproefeenheden per habitattype omdat een steekproefgrootte van 80 voor de meeste habitattypen volstaat om een onderscheid te maken tussen een gunstige en ongunstige kwaliteit
  - vermindering van de steekproefgrootte binnen de habitatsubtypen van 80 naar 40 steekproefeenheden per subtype gezien de informatie over de staat van instandhouding van habitatsubtypen een lagere prioriteit heeft en niet noodzakelijk is voor de EU rapportage

- In het originele meetnetontwerp voor habitattypen in stilstaande wateren werden alle plassen groter dan 5 ha geselecteerd en werd er een steekproef getrokken uit de set van plassen kleiner dan 5 ha. We stellen voor om ook een steekproef te nemen uit de set van plassen met een oppervlakte tussen 5 ha en 50 ha om de haalbaarheid en kostenefficiëntie te verhogen. We stellen ook voor om de overbemonstering in SBZ te laten vallen omdat de meeste plassen in SBZ gelegen zijn, en de steekproef dus al voldoende plassen binnen SBZ bevat.

- Het meetnetontwerp voor de boshabitattypen zal niet gewijzigd worden. We behouden een meetcyclus van 12 jaar om een optimale synergie met de Vlaamse bosinventarisatie te behouden.

- De veranderingen aan het meetnetontwerp vatten we samen in Tabel 3. De totale meetinspanning per jaar blijft nagenoeg gelijk.

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[2] De meetcyclus is de periode waarin alle meetpunten worden bemonsterd. In een meetcyclus van 6 jaar worden de meetpunten om de 6 jaar bemonsterd. Een vermindering van de duur van de meetcyclus resulteert in een toename van het aantal te bemonsteren meetpunten per jaar.

Table 3: Veranderingen in het meetnetontwerp van MHQ: duur meetcyclus, steekproefgrootte per habitattype in Vlaanderen (n Vl), steekproefgrootte per habitattype in SBZ (n SBZ), steekproefgrootte per habitatsubtype (n subtype) en totaal aantal te bemonsteren steekproefeenheden per jaar voor alle habitattypen en -subtypen (n totaal / jaar)

habitat categorie	design	meetcyclus (jaren)	n Vl	n SBZ	n subtype	n tot / jaar	steekproefeenheid
terrestrisch open	originel	12	80	170	80	247	36 m diameter cirkelplot
	nieuw	6	80	80	40	258	
rivier	origineel	12	80	170		15	100 m rivier segment
	nieuw	6	80	80		17	
stistaande wateren	origineel	6	40 en alle > 5 ha*	80	40	43.5	volledige plas
	nieuw	6	80 en alle > 50 ha†	0	40	42	

* Steekproeftrekking voor plassen < 5 ha en selectie van alle plassen > 5 ha

† Steekproeftrekking voor plassen < 50 ha en selectie van alle plassen > 50 ha

- Tabel 4 geeft een overzicht van het Minimaal Detecteerbaar Verschil (MDV) voor de toestand en de trend van de habitatkwaliteit bij verschillende steekproefgroottes.

Table 4: Overzicht van Minimaal Detecteerbaar Verschil (MDV) voor de toestand en trend van de habitatkwaliteit. Bij het habitataandeel in slechte staat gaan we er vanuit dat habitat op een bepaalde locatie zich in een goede of slechte staat bevindt (binaire variabele). De proportie gunstige indicatoren geeft aan welk percentage van de kwaliteitsindicatoren gunstig scoren op een bepaalde locatie.

	toestand habitatkwaliteit	trend habitatkwaliteit	
steekproefgrootte	habitataandeel in slechte staat (mdv t.o.v. 25%-threshold)	habitataandeel in slechte staat (MDV tussen 2 periodes)	proportie gunstige indicatoren (mdv tussen 2 periodes)
40	-16.1% and +21 %	19% - 37%	3.1% - 5%
80	-12.1% and +14.6 %	10% - 19%	2.2% - 3.5%
170	-8.7% and +9.8 %	5% - 9%	1.5% - 2.4%

1 INTRODUCTION

Every six years member states of the European Union report on the conservation status of species and habitat types listed in the Annexes to the Habitats and Birds Directive. The Research Institute Nature and Forest (INBO) is responsible for the monitoring of these species and habitat types in Flanders, the northern part of Belgium.

INBO implemented a monitoring programme for habitat types that consists of the following parts:

- a field based habitat mapping campaign to assess the distribution, area and range of all habitat types and subtypes in Flanders
- a monitoring scheme to assess the biotic habitat quality for most habitat types and subtypes

An additional part for monitoring the natural environment is currently under development. It aims to assess selected abiotic conditions of habitat types to evaluate the principal pressures and threats.

In this report, we focus on the Monitoring scheme for biotic Habitat Quality (MHQ) and evaluate the design of this scheme as described by Westra *et al.* (2014). First, we briefly summarize the information needs and provide an overview of some of the characteristics of MHQ. Next we evaluate the sample size. The original sample size of the monitoring scheme was based on sample size calculations for the status of the habitat quality (Westra *et al.*, 2014). In this report we also explore the sample size for the habitat quality trend, as trend information is key in the habitat reporting. Finally, we evaluate some alternative scenarios for the monitoring design and document the modifications of the monitoring design that will be implemented. We do this separately for terrestrial habitat types, standing water habitat types and stream habitat types.

2 INFORMATION NEEDS

2.1 EUROPEAN LEVEL

Every six years each EU member state needs to report on the conservation status of the European protected habitat types listed in Annex 1 of the Habitat Directive.

The conservation status of habitat types should be assessed per biogeographical region and is determined by four criteria (DG Environment, 2017):

- **Range**
- **Area**
- **Specific structure and functions (including typical species)**
- **Future prospects**

Each of these criteria is evaluated according to the evaluation matrix specified in the reporting guidelines in DG Environment (2017).

The conservation status of **specific structure and functions (including typical species)** is assessed as follows:

- **Favourable**: structures and functions (including typical species) in good condition and no significant deteriorations / pressures
- **Unfavourable – Bad**: more than 25% of the area is unfavourable as regards its specific structures and functions (including typical species)
- **Unfavourable – Inadequate**: any other combination
- **Unknown**: no or insufficient reliable information available

The guidelines (DG Environment, 2017) stress the importance of trend information, as trends are decisive for the assessment of conservation status since usually only stable or positive trends can result in an overall favourable conservation status (FCS) conclusion. It is advised that more attention should be paid to the methodology of monitoring schemes to improve the quality of trend information. A short-term trend is considered as the trend over two reporting cycles (12 years). The recommended period for assessing longer-term trends is four reporting cycles (24 years).

2.2 REGIONAL LEVEL

Flanders represents the northern part of Belgium and is almost entirely situated within the Atlantic biogeographical region, with the exception of Voeren in the easternmost part, which belongs to the Continental biogeographical region. INBO is responsible for the assessment of the conservation status (CS) of habitat types in Flanders. The results for Flanders are integrated with the results of the Walloon and Brussels Capital region to assess the CS of habitat types on the scale of Belgium per biogeographical region. This integrated assessment is reported to the European Commission.

The methodology used by INBO to evaluate the CS of the criterion specific structure and functions (including typical species) is based on the general guidelines by DG Environment (2017) and is described in more detail by Paelinckx *et al.* (2019). It requires information per habitat type on:

- the proportion of the habitat area in good condition (as assessed following the criteria and indicators by Oosterlynck *et al.* (2020)) and its trend
- the status of its habitat typical species (e.g. Red List status);
- landscape ecological coherence of the habitat;
- the existence of high pressures that cannot sufficiently be remediated by conservation measures.

MHQ supports the assessment of the habitat area that is in a good condition. We use the term 'biotic habitat quality' as the condition of a habitat is assessed based on biotic data. Further in this report we will only focus on this part of the information needs.

In Flanders 46 habitat types occur and several of these habitat types are subdivided into habitat subtypes (Appendix A). Nature policy in Flanders also requires information on the habitat quality for these habitat subtypes (Westra *et al.*, 2011). However, this information has a lower priority and therefore a lower precision (compared to the main habitat types) is acceptable. The report of Westra *et al.* (2011) also considered the need for assessing the habitat quality status within the network of Special Areas of Conservation (SAC) in Flanders with a higher precision. This is because most policy measures to improve the conservation status of habitat types are taken within SAC and we want to be able to evaluate these measures.

3 OVERVIEW OF MHQ

3.1 MONITORING TARGET

Based on the information needs we can summarize the main targets of MHQ as follows:

- the habitat quality **status** per habitat type and per habitat subtype for Flanders and for the network of SAC
  - What is the proportion of the habitat area that is in good/bad condition[1]?
  - Is the proportion of habitat in bad condition higher or lower than 25%?
- the habitat quality short-term (12 years) and long-term (24 years) **trend** per habitat type and per habitat subtype for Flanders and for the network of SAC
  - What is the trend of the proportion of the habitat area in good/bad condition?
  - Is the habitat quality stable, improving or deteriorating?

Figure 3.1 shows the different conclusions that can be drawn from the estimates (and the confidence interval) of the habitat quality status and trend. Note that the habitat quality status is unknown when the confidence interval includes the 25% threshold. Also note that we need to define an upper and a lower threshold for the habitat quality trend to differentiate between a stable and an unknown trend. When the confidence interval includes 0% change, the trend is stable in case of a small confidence interval or unknown in case of very wide confidence interval.

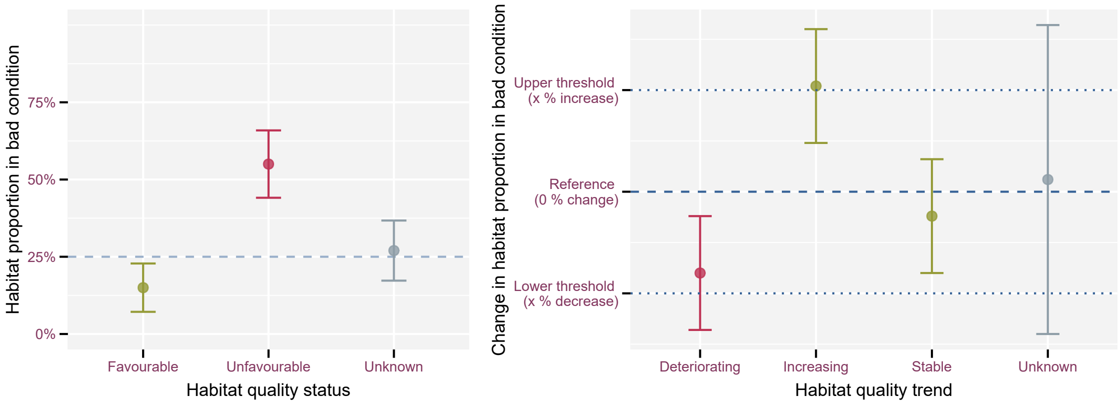

Figure 3.1: Possible coclusions for habitat quality status and habitat quality trend

We want to emphasize the difference between the *conservation status of structure and functions* and the *habitat quality status*. The *habitat quality status* is the estimated proportion of habitat area in good/bad condition for a certain period in time. As explained in section 2.2, the *conservation status of structure and functions* is an evaluation based on habitat quality status, habitat quality trend, habitat typical species, ecological coherence and pressures. MHQ only provide information on habitat quality status and trend and not on habitat typical species, ecological coherence and pressures.

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[1] In the Article 17 reporting forms 'not-good condition' is used instead of 'bad condition'.

The original design of MHQ (Westra *et al.*, 2014) was mainly based on the target for the habitat quality status. In this report we will evaluate how the design can be modified to better meet the monitoring target for the trend in habitat quality. We will evaluate different scenarios based on sample size calculations for status and trend in habitat quality. But first we summarize how habitat quality is defined and what needs to be measured in the field.

3.2 BIOTIC HABITAT QUALITY INDICATORS

The report of Oosterlynck *et al.* (2020) provides a series of criteria and indicators aimed at determining the local conservation status (= habitat condition) for 46 habitat types and 42 habitat subtypes. Different types of indicators are included that are related to:

- vegetation composition,
- vegetation structure,
- disturbances,
- spatial connectivity.

For each indicator a threshold value defines whether the indicator is favourable or unfavourable. Combining the results for the different indicators allows an overall assessment of the habitat quality at a habitat location. The selection of the indicators and their threshold values is based on their capacity to cover the habitat's functioning in an objective (i.e. based on national and international scientific literature), unambiguous, practical, measurable and comprehensive way (Oosterlynck *et al.*, 2020).

The R package LSVI (Lommelen *et al.*, 2022) enables calculation and evaluation of the indicators for habitat quality in a standardized and semi-automated way and makes use of (Oosterlynck *et al.*, 2020).

3.3 FIELD MEASUREMENTS

The field measurements for MHQ consist of two parts:

- vegetation composition: presence and cover of plant species per vegetation layer,
- structure variables: measurement of variables related to vegetation structure.

The spatial scale at which these variables are measured, depends on the habitat type and is shown in 3.1. Note that these measurements do not allow the evaluation of the indicators related to spatial connectivity.

Table 3.1: Spatial scale at which the vegetation composition and structure variables are measured

category	habitat type	vegetation composition	structure variables
terrestrial	forest	16 m x 16 m square plot	36 m diameter circle plot
	open	3 m x 3 m square plot	36 m diameter circle plot
aquatic	stream	100 m river segment	100 m river segment
	standing water	entire water body	entire water body

INBO developed standardized field protocols (sfp) for the MHQ field measurements that allow the evaluation of most of the indicators in (Oosterlynck *et al.*, 2020). The sfp for the aquatic habitat type 3260 has already been published (Leyssen, An, 2017), while publication of the protocols for the terrestrial and standing water habitat types is planned in the near future.

4 SAMPLE SIZE EVALUATION

Sample size calculations provide an insight in the relationship between sample size and the minimal detectable effect size for a given significance level α and power π. α is the probability of a type I error, i.e. the probability of concluding that there is an effect based on a sample, when in reality there is no effect in the population. π is the probability to detect an effect based on a sample, when the effect also exists in reality.

The original sample size of the monitoring scheme is based on sample size calculations for the status of the habitat quality Westra *et al.* (2014). We will first reproduce the sample size calculations by Onkelinx *et al.* (2007) Next we will also perform a sample size calculation for the trend in habitat quality.

As in Westra *et al.* (2014), we will choose a power π of 0.80 and a significance level α of 0.05.

4.1 HABITAT QUALITY STATUS

4.1.1 Minimal detectable difference between the proportion of habitat in bad condition and the 25%-threshold

The quality of a habitat type is unfavourable (on a regional scale) when more than 25% of the habitat area is in a bad condition. Here we want to determine the minimal detectable difference from the 25%-threshold.

For a straightforward sample size calculation for the minimal detectable difference from a threshold value, we can apply the *proportion test* (Cohen, J., 1988) using the function `pwr.p.test` of the pwr package (Champely, 2020).

Figure 4.1 and Table 4.1 show the results of the sample size calculations. The results can be interpreted as follows. When in reality less than 16.3 % of the habitat is in bad condition, we will be able to conclude that the habitat proportion in bad condition is significantly lower than the 25%-threshold when we have sample size of 170 (with $\pi = 0.80$ and $\alpha = 0.05$). Hence, the minimal detectable difference is 8,7 %. Similarly, when in reality more than 34,8 % of the habitat has a bad condition, we will be able to conclude that the habitat proportion with a bad quality is significantly higher than the 25%-threshold. When the habitat proportion with a bad quality is between 16,3 % and 34,8 %, a sample size of 170 will not allow us to detect a difference from the 25%-threshold with a probability of at least 0.80 (π) and a type I error of at most 0.05 (α).

Table 4.1: Minimal detectable difference (mdd) from 25% - threshold as a function of the sample size with $\alpha = 0.05$ and $\pi = 0.80$

			mdd from 25%	
sample size	favourable	unfavourable	lower	higher
40	< 8.9 %	> 46 %	-16.1%	+21 %
80	< 12.9 %	> 39.6 %	-12.1%	+14.6 %
170	< 16.3 %	> 34.8 %	-8.7%	+9.8 %
400	< 19.2 %	> 31.3 %	-5.8%	+6.3 %
1000	< 21.3 %	> 28.9 %	-3.7%	+3.9 %

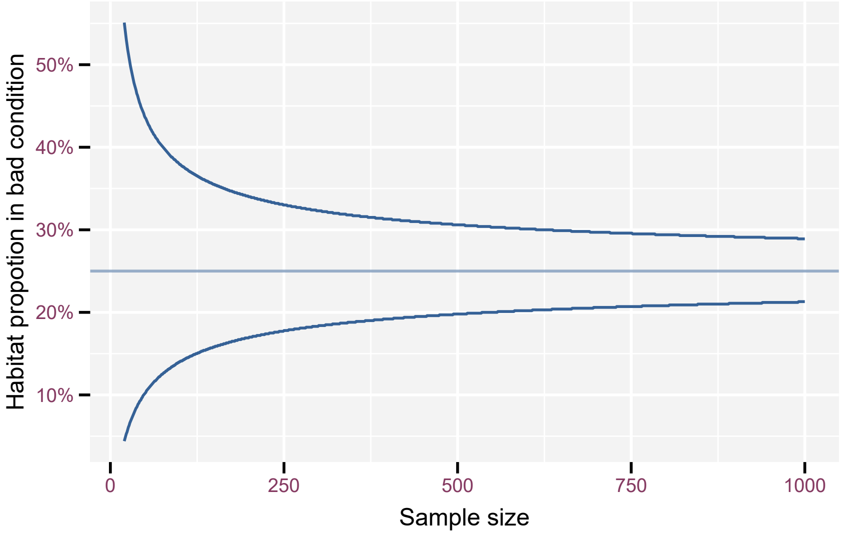

Figure 4.1: Relationship between sample size and minimal detectable difference

4.1.2 Comparison with results of the 2019 habitat reporting

In Figure 4.2 we show the estimated habitat proportions in bad condition for terrestrial habitats, as reported in 2019. The figure also shows the 95% - confidence interval of the estimate and the sample size on which the estimate is based (text above the confidence interval). The estimates are ordered in the x-axis from low to high sample size. Note the difference between Figure 4.2 and Figure 4.1. Figure 4.2 shows the *estimated* proportion based on one sample, while the *real* proportion (the population parameter) is unknown. In Figure 4.1 the y-axis corresponds with the (real) proportion in the population and we assume a large number of samples.

The 2019 report is based on the plots that were measured in the period 2014 - 2018. This means that only a subset of the total sample size was measured at that time, as the total monitoring cycle was 12 years. This subset is still representative for the sample as a whole due to the nature of the sampling design. Only for the more common forest habitat types we already reached the total sample size, as we could make use of the measurements of the Flemish Forest Inventory.

The habitat types are represented by the habitat code and the colour corresponds with the habitat quality evaluation: favourable, unknown or unfavourable. For many habitat types we can already conclude that the quality is unfavourable, even with a sample size much smaller than 170. This is because in many cases the habitat proportion in bad condition is much higher than the 25%-threshold and such large differences can be detected with sufficient power based on smaller sample sizes, as can be seen in Figure 4.1 and Table 4.1. Only for two habitat types (2160 and 2190) we need a higher precision in order to conclude if the proportion with bad quality is higher or lower than the 25%-threshold.

In the coming years, it will be more relevant for nature policy to have information on the trend of habitat quality (does the quality of the unfavourable habitat types improve?) than to invest in a higher precision of the status of habitat quality. In other words, it will probably be better to shorten the original monitoring cycle and to start revisiting the measured plots sooner than originally planned. This requires an adjustment of the monitoring design. Therefore we will also perform sample size calculations for trends in habitat quality. This way we can find a good balance between the precision of the habitat quality status and the precision of the trend.

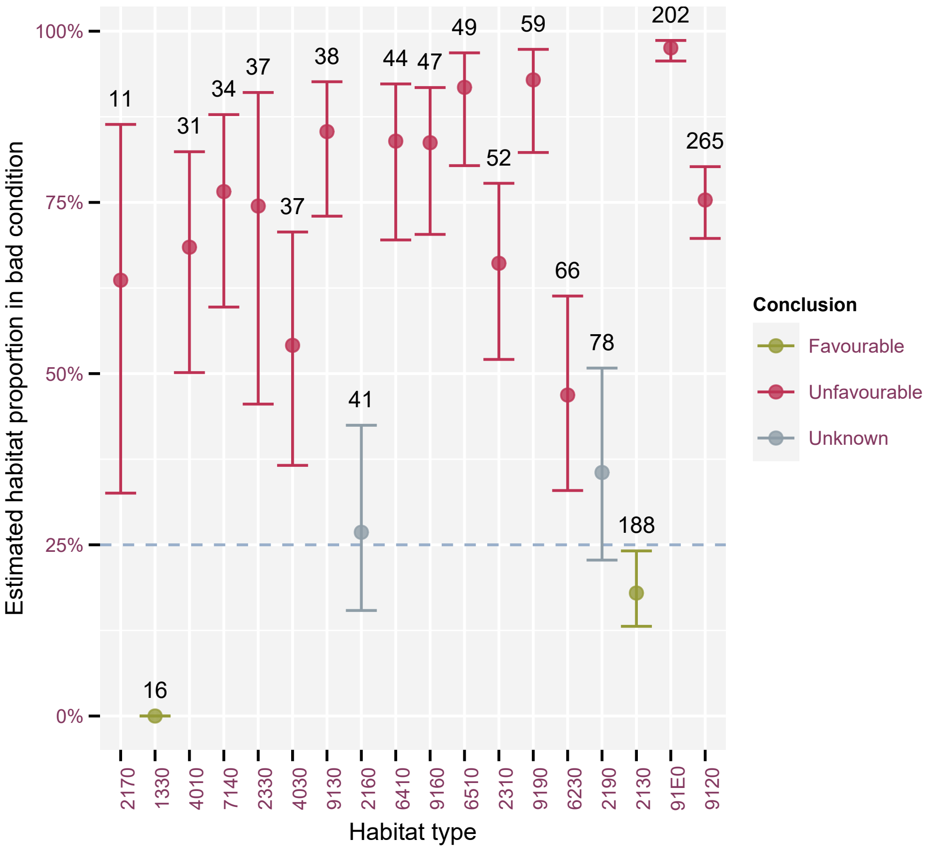

Figure 4.2: Results of the habitat reporting for terrestrial habitat types

4.2 TRENDS IN HABITAT QUALITY

We will first assume that the habitat condition is a binary variable (good or bad) and analyse which difference between proportions of habitat in bad condition we can detect.

Next, we will evaluate which differences we can detect when a continuous variable is used to express the habitat condition.

4.2.1 Difference between proportions

To determine the detectable difference in habitat proportions in bad condition between two points in time, we apply the *McNemar test* (Chow, S. C. and Shao, J. and Wang H., 2003) using the function `McNemar.Test` in the R package TrialSize (Zhang *et al.*, 2020).

The habitat monitoring scheme consists of permanent plots resulting in paired observations. When the habitat quality in a plot is measured at two time points t_1 and t_2, we can have one of the following combinations.

	t_2	
t_1	bad	good
bad	no change	bad -> good
good	good -> bad	no change

The difference in the habitat proportion in bad condition between t_1 and t_2 corresponds with the difference in the habitat area that evolves from bad to good (hab_{01}) and the area that evolves from good to bad (hab_{10}). Figure 4.3 shows the minimal detectable increase/decrease in the habitat proportion in bad condition as a function of the sample size and the *dynamics* of the habitat type. We define the dynamics as a measure for the amount of habitat for which the condition changes given a total net change in habitat condition:

$$\frac{hab_{01} + hab_{10}}{|hab_{01} - hab_{10}|}$$

Suppose that the net habitat proportion in bad condition decreases with 10 %, then the dynamics are equal to 2 when 15% of the habitat area changes from good to bad and 5% of the habitat area from bad to good. The higher the dynamics, the higher the minimal detectable difference.

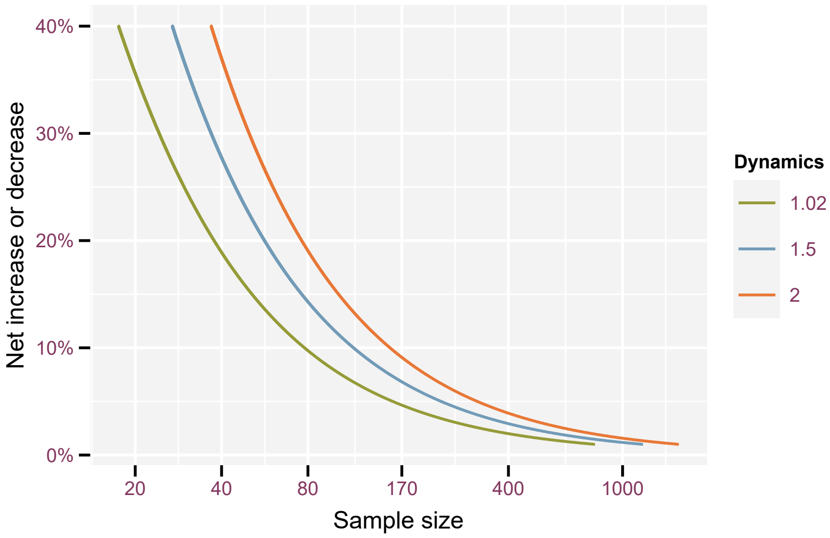

Figure 4.3: Minimal detectable effect as a function of sample size and the dynamics with α = 0.05 and π = 0.80

Table 4.2 gives an overview of the results for different values for the dynamics. With a sample size of 170 we can detect a difference in the habitat proportion in bad condition of about 5 % when dynamics are low (with α = 0.05 and β = 0.8) and a difference of 9 % when dynamics are high.

Table 4.2: Minimal detectable difference as a function of sample size and dynamics (low dynamics = 1.02, medium dynamics = 1.5 and high dynamics = 2) with α = 0.05 and π = 0.80

	net decrease or increase (%)		
sample size	low dynamics	medium dynamics	high dynamics
40	18.9	27.7	36.9
80	9.7	14.3	19.1
170	4.7	6.8	9.1
400	2.0	2.9	3.9

It is hard to predict which values for the dynamics can be expected for the different habitat types. However, data from the Flemish Forest Inventory might give us an idea for the forest habitat types. Table 4.3 shows the number of paired observations and the number of plots that evolve from bad to good quality (n_{01}) and from good to bad quality (n_{10}). For habitat type 9120 the dynamics are equal to 2.2. For the other forest habitat types we can not get a reliable estimate of the dynamics as the sample size is too low or there is no net difference. Anyway, assuming high dynamics in sample size calculation does not seem exaggerated.

Table 4.3: Observed dynamics for forest habitat types based on data from the Flemish Forest Inventory

habitat type	n_{paired}	n_{01}	n_{10}	dynamics
9120	115	3	8	2.2
9130	13	1	0	1.0
9160	19	1	0	1.0
9190	17	0	0	
91E0	43	3	3	

4.2.2 Differences between habitat quality indicators

Continuous, discrete or categorical variables that measure habitat quality are more sensitive to changes than a binary variable (good or bad habitat condition). Examples of such variables are:

- values of habitat quality indicators as listed in (Oosterlynck *et al.*, 2020)
- the proportion of habitat quality indicators for a certain habitat type that are favourable
- a continuous habitat quality index based on the distance to the threshold values for the different habitat quality indicators of a habitat type

For the exploration of the detectable effect size as a function of the sample size, we assume continuous variables with a normal distribution. This enables a straightforward power analysis based on the paired t-test using the `pwr.t.test` of the pwr package (Champely, 2020). Although not all habitat quality indicators will have normally distributed paired differences, we believe that this method will give us a general idea on the relationship between detectable effect size and sample size.

We will verify some of the results of the paired t-test, by applying a more advanced method to calculate the power using the R package `simr` (Green & MacLeod, 2016). The advantage of this method is that we can make use of other distributions, such as the poisson distribution and the binomial distribution. More details are provided in Appendix B .

4.2.2.1 Sample size calculation for continuous variables based on the paired t-test

When applying the paired t-test, the detectable effect size (d) equals the mean of the differences between paired observations divided by the standard deviation of the differences. Figure 4.4 and Table 4.4 show the detectable effect size as a function of the sample size.

Table 4.4: Detectable effect as a function of sample size and significance level with $\pi = 0.80$

Sample size	Detectable effect
40	0.454
80	0.317
170	0.216
400	0.140

The detectable effect is a quite abstract measure and not so easy to interpret. To make things more comprehensible, in Figure 4.5 and Table 4.5 we show a variable expressed as a percentage with values between 0 and 100. This could be for example the proportion of habitat indicators that are favourable on a certain location or the vegetation cover of a certain species group. With a sample size of 170 we can detect a mean difference of approximately 1 to 3 % depending on the standard deviation of the difference. With a sample size of 80 this is approximately 1.5 to 5 %.

We will further explore the data of the Flemish Forest Inventory (Wouters *et al.*, 2008) to get a rough idea of the standard deviation of differences we can expect for habitat quality indicators.

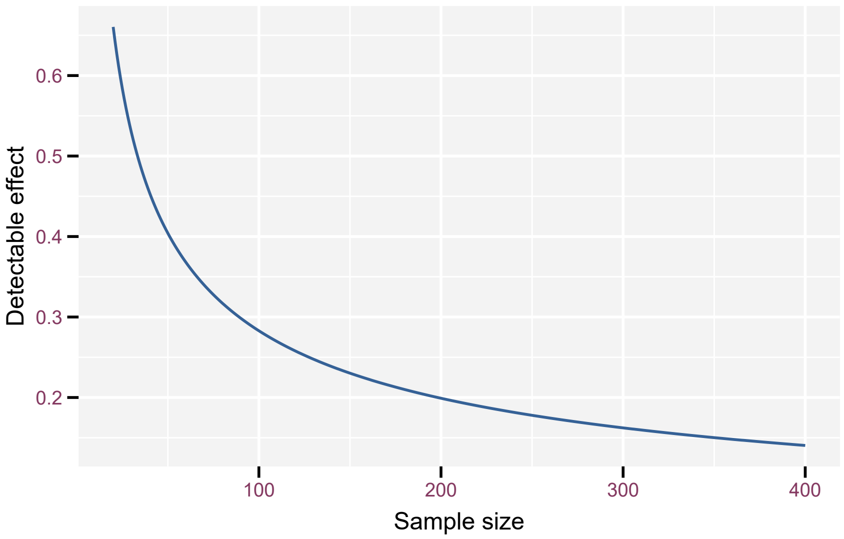

Figure 4.4: Detectable effect size (d) as a function of the sample size with $\pi = 0.8$

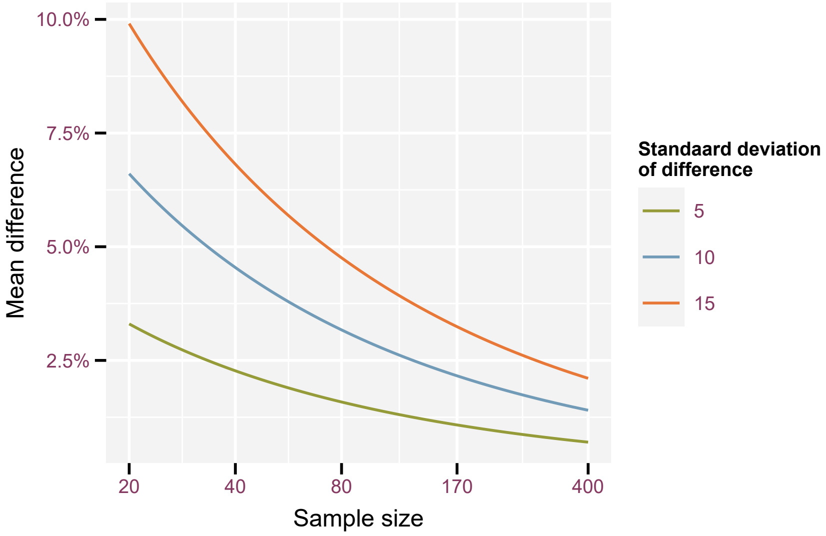

Figure 4.5: Detectable mean difference as a function of sample size and standard deviation of the difference for a variable that is expressed as a percentage with $\alpha = 0.05$ and $\pi = 0.80$

Table 4.5: Detectable mean difference as a function of sample size and standard deviation of the difference with $\alpha = 0.05$ and $\pi = 0.80$

	sd difference		
sample size	5	10	15
40	2.3	4.5	6.8
80	1.6	3.2	4.8
170	1.1	2.2	3.2
400	0.7	1.4	2.1

4.2.2.2 Example 1: trend in proportion of favourable indicators for forest habitat types

The Forest Inventory data allows the calculation and evaluation of most habitat quality indicators defined in (Oosterlynck *et al.*, 2020) for plots that are located in a forest habitat types. Based on this, we can determine the proportion of the total number of indicators that are favourable per plot. Figure 4.6 shows this proportion for plots that were measured in both the first period (1997-1998) and the second period (2009-2018) of the Flemish Forest Inventory.

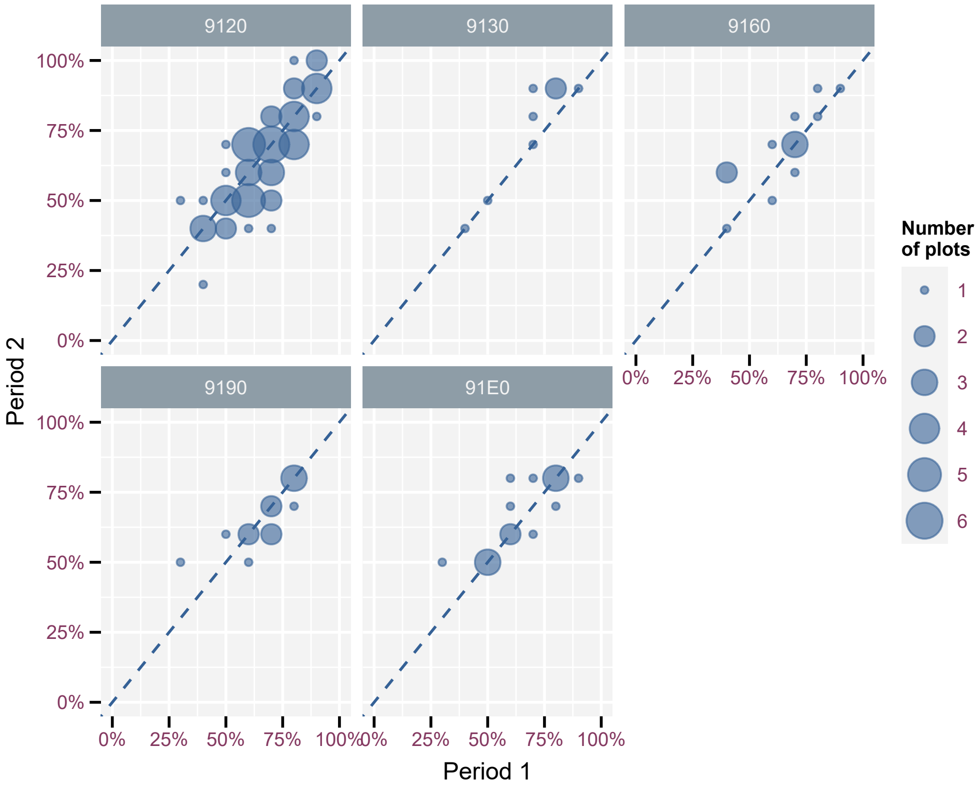

Figure 4.6: Proportion of habitat quality indicators that are favourable per plot, for both periods of the Flemish Forest Inventory

Table 4.6 gives the mean difference of the proportion of favourable indicators between period 2 and period 1, the standard deviation of the difference and the detectable effect size (d). The table also shows the p-value of the paired t-test and the conclusion that can be drawn per type and for all types together ('91xx'). The standard deviation of the differences ranges approximately from 7% to 11%.

Table 4.6: Observed difference of the proportion of favourable indicators for forest habitat types

habitat type	sample size	mean difference	sd difference	d	p-value	conclusion
9120	60	-1.17	10.43	-0.112	0.390	unknown
9130	8	6.25	7.44	0.840	0.049	increase
9160	13	3.85	9.61	0.401	0.175	unknown
9190	13	-0.77	8.62	-0.089	0.753	unknown
91E0	15	2.00	9.41	0.213	0.424	unknown
91xx	109	0.46	9.94	0.046	0.631	unknown

When the estimated effect size (d) would correspond with the true effect size, a sample size of 80 would be sufficient to detect the effect for 9130 and 9160 as can be seen in Figure 4.4 and Table 4.4. For the other habitat types we would need a higher sample size, but these are quite small effect sizes.

Table 4.7 shows the range of the minimum detectable difference in proportion of favourable indicators that can be expected for different sample sizes with a power π of 0.80. This is based on the range of values for the standard deviation of differences as shown in Table 4.6.

Table 4.7: Minimum detectable differencev(mdd) in proportion of favourable indicators that can be expected for different sample sizes with a power pi of 0.80

sd difference	sample size	d	mdd
7 - 11	40	0.45	3.1% - 5%
	80	0.32	2.2% - 3.5%
	170	0.22	1.5% - 2.4%

To verify the results we calculated the power for habitat type 9120 using the `simr` package. The power is close to 0.8 for all combinations of sample size and effect size, confirming the results in Table 4.7. The estimated power using `simr` is shown in Table B.1 in Appendix B.

4.2.2.3 Example 2: trend in indicator values for forest habitat types

Here we use the Forest Inventory data to get a rough idea on the detectable effect size for individual habitat quality indicators. We analyse four indicators:

- number of key species in the herb layer
- proportion of key species in the herb layer
- total cover of encroachment species
- total cover of invasive alien species in the shrub and tree layer

Figure 4.7 shows the indicator values for both periods of the Flemish Forest Inventory.

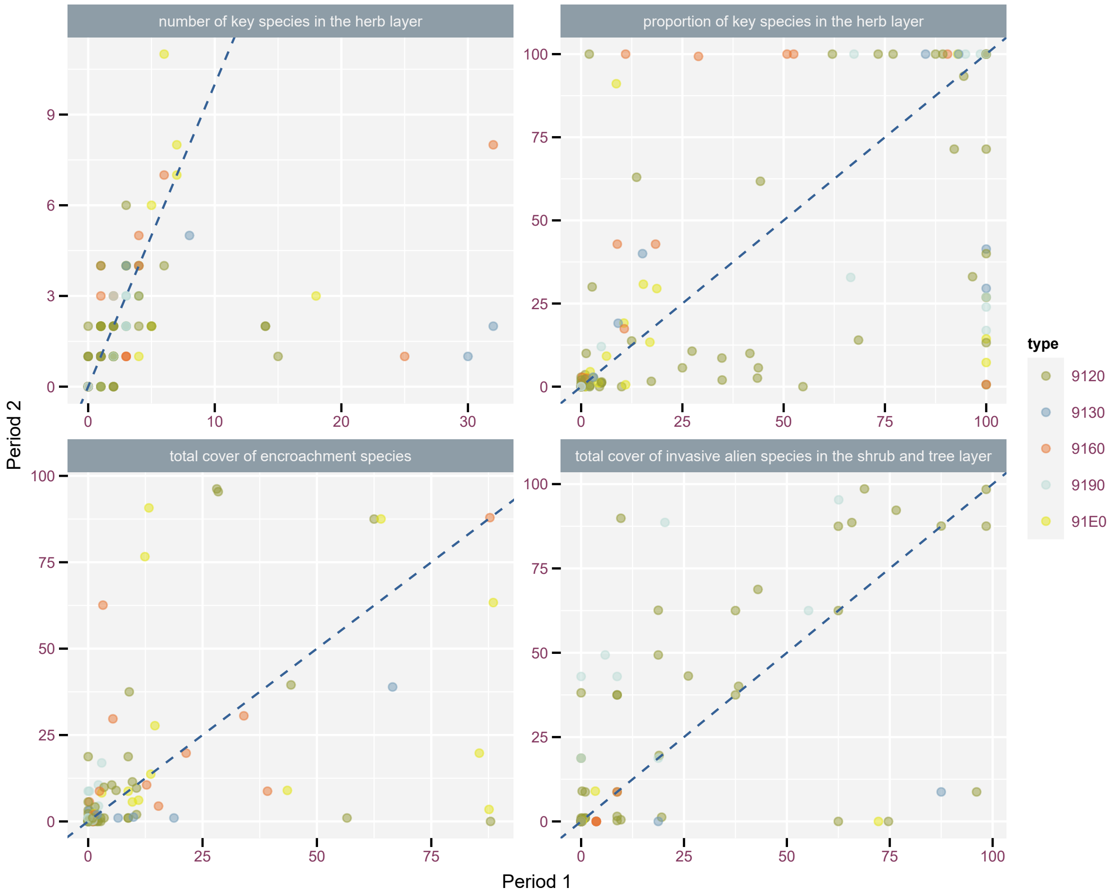

Figure 4.7: Indicator values for both periods of the Flemish Forest Inventory

Table 4.8 gives the observed effect size d for the habitat quality indicators. The table also shows the p-value of the paired t-test and the conclusion that can be drawn per type and for all types together ('91xx'). We can also compare d with the values in Table 4.4 to evaluate which differences can be detected for different sample sizes (assuming that the observed d values are the true values).

Table 4.8: Observed effect size (d) for four habitat quality indicators

habitat type	sample size	indicator	mean diff	sd diff	d	p-value	conclusion
9120	60	number of key species in the herb layer	-0.78	2.99	-0.261	0.047	decrease
		proportion of key species in the herb layer	-7.86	31.08	-0.253	0.055	unknown
		total cover of encroachment species	1.06	19.38	0.055	0.673	unknown
		total cover of invasive alien species in the shrub and tree layer	2.88	24.01	0.120	0.356	unknown
91E0	15	number of key species in the herb layer	-0.93	4.33	-0.215	0.418	unknown
		proportion of key species in the herb layer	-4.44	40.58	-0.109	0.678	unknown
		total cover of encroachment species	-2.28	41.47	-0.055	0.835	unknown
		total cover of invasive alien species in the shrub and tree layer	-4.45	18.81	-0.237	0.375	unknown
91xx	109	number of key species in the herb layer	-1.58	5.70	-0.277	0.005	decrease
		proportion of key species in the herb layer	-5.48	35.98	-0.152	0.115	unknown
		total cover of encroachment species	0.59	22.20	0.027	0.782	unknown
		total cover of invasive alien species in the shrub and tree layer	2.19	22.96	0.095	0.322	unknown

Table 4.9 shows the range of the detectable mean difference for the habitat quality indicators that can be expected for different sample sizes. It is based on the range of observed values for the standard deviation of the indicators as shown in Table 4.8.

Table 4.9: Expected range for minimum detectable difference (mdd) for habitat quality indicators

indicator	sd difference	sample size	mdd
number of key species in the herb layer	2 - 6	40	0.9 - 2.7
		80	0.6 - 1.9
		170	0.4 - 1.3
proportion (%) of key species in the herb layer	31 - 41	40	14 - 18.4
		80	9.9 - 13.1
		170	6.8 - 9
total cover (%) of encroachment species	19 - 42	40	8.6 - 18.9
		80	6.1 - 13.4
		170	4.2 - 9.2
total cover (%) of invasive alien species in the shrub and tree layer	18 - 25	40	8.1 - 11.2
		80	5.8 - 8
		170	4 - 5.5

We used the `simr` package to verify the results in Table 4.9. The estimated power based on `simr` was higher than 0.80 for the number of key species and similar to 0.80 for the total cover of encroachment species for habitat type 9120 (Table B.2 and Table B.3. This indicates that the minimal detectable differences in 4.9 are valid or even slightly smaller in case of the number of key species.

5 SAMPLE DESIGN FOR TERRESTRIAL HABITAT TYPES

5.1 HABITAT TYPES AND SUBTYPES INCLUDED IN MHQ

As mentioned in Westra *et al.* (2014), MHQ does not contain a monitoring scheme for all terrestrial habitat types or habitat subtypes that occur in Flanders. For several habitat types a habitat quality monitoring scheme is not considered as a feasible or appropriate approach. This is the case for:

- very rare terrestrial habitat types (defined as habitat types with an area lower than 10 ha or occurring on less than 15 locations): a monitoring scheme would result in a very high density of plots which might impact the vulnerable vegetation;
- estuaries (type 1130): the habitat quality has to be evaluated on a landscape scale;
- mudflats (type 1140): this habitat type is not included in Oosterlynck *et al.* (2020);
- very dynamic habitat types (type 1130, 2110 and 7150): a basic habitat quality assessment combined with habitat area mapping is considered a more appropriate approach;
- habitat type 6430: a very patchy habitat type for which an accurate sampling frame is not yet available;
- habitat type 9110: habitat type only occurring in the continental biogeographical region of Flanders and covering only a small area compared to the total area of 9110 in Belgium. Therefore a separate estimate for Flanders is not considered very relevant.

An oversampling is considered for all habitat subtypes except for the very rare terrestrial subtypes (defined as habitat subtypes with an area lower than 10 ha or occurring on less than 15 locations). For very rare terrestrial habitat types and subtypes we intend to perform a basic habitat quality assessment on the whole of the habitat surface in combination with the habitat area mapping. An exception is Calcareous dune slacks (2190_mp) for which we do perform an oversampling although the total area of this habitat subtype is 8 ha. This is because the subtype was already selected for oversampling in the original design (Westra *et al.*, 2014) as the area at that time was estimated to be 30 ha, and we would like to continue the monitoring scheme to detect trends.

Appendix C shows for which habitat types a monitoring scheme was developed and for which subtypes oversampling is considered. The area and the number of locations for the terrestrial habitat types (to determine the very rare habitat types and subtypes) is derived from the terrestrial part of the standardized map of habitat types in Flanders (Wouters *et al.*, 2021). This data source is a processed and interpreted version of the Natura 2000 habitat map (De Saeger *et al.*, 2020). The standardized map is processed in a way it can be easily imported and analysed in R. It can be imported in R by using the function `read_habitatmap_terr()` of the n2khab package (Vanderhaeghe *et al.*, 2022).

In the original design of Westra *et al.* (2014) a monitoring scheme was also planned for habitat type 5130 and 6430. However these monitoring schemes were not implemented. Habitat type 5130 is considered a very rare habitat type (see Appendix C) and for habitat type 6430 a sampling frame is currently missing as mentioned above.

5.2 SCENARIOS FOR THE SAMPLE DESIGN

We will calculate the total number of sampling units that have to be measured per year for different scenarios. The scenarios are characterised by following parameters:

- monitoring cycle: the number of years in which all sampling units have to measured
- n_{fl}: the sample size per habitat type for the whole of Flanders
- n_{sac}: the sample size per habitat type within the Special Areas of Conservation (SAC)
- $n_{subtype}$: the (minimum) sample size per habitat subtype for the whole of Flanders

The method for the calculation of the total sample size per habitat type is explained in Westra *et al.* (2014). In a first step a finite population corrections is applied on n_{fl}, n_{sac} and $n_{subtype}$. This is because the calculated sample sizes in section 4 are valid for infinite populations. Yet, most habitat types or subtypes cover a relatively small area and can therefore be considered as a finite population. The finite sample size n_{finite} is calculated as follows:

$$n_{finite} = \frac{N n_{infinite}}{n_{infinite} + (N - 1)}$$

with:

$$n_{infinite} = \text{infinite sample size}$$

$$N = \text{total population size}$$

For the terrestrial habitat types a population unit corresponds with a 32m x 32m grid cell and the total population size is calculated by dividing the total area of the population by the area of a grid cell (approximately 0.1 ha). Next we distribute $n_{fl_{finite}}$ over the strata *inside SAC* and *outside SAC* proportional to the area of both strata, and we calculate the extra number of sampling units to reach $n_{SAC_{finite}}$ inside sac. Then the total number of sampling units inside and outside SAC are distributed over the subtypes proportional to their area to obtain the expected sample size for each stratum. The required sample size per subtype $n_{subtype_{finite}}$ is also distributed over the strata inside SAC and outside SAC proportional to the area. Finally the extra number of sampling units to reach the required sample size per stratum is calculated.

Table 5.1 compares the original design of Westra *et al.* (2014) with four alternative scenarios for open terrestrial habitats. For forest habitat types no alternative scenarios are considered since the monitoring scheme was designed to make it compatible with the Flemish Forest Inventory. The table shows the total sample size for the monitoring cycle and the total sample size per year after applying the finite population correction. The table also gives information on the total number of sampling units initially selected in Flanders (tot_{fl}) and the total number of extra sampling units selected in the SAC ($extra_{SAC}$) and in the habitat subtypes ($extra_{subtype}$).

Table 5.1: Comparison between original design and four alternative scenarios. The selected scenarios are shown in bold.

scenario	cycle (years)	n_{fl}	n_{sac}	$n_{subtype}$	tot_{fl}	$extra_{sac}$	$extra_{subtype}$	total per cycle	total per year
Open habitat type									
original	12	80	170	80	1174	1388	392	2954	247
alternative 1	6	80	80	80	1174	181	611	1966	328
alternative 2	6	40	80	40	605	667	222	1494	249
alternative 3	**6**	**80**	**80**	**40**	**1174**	**181**	**189**	**1544**	**258**
alternative 4	6	40	80	80	605	667	672	1944	324
Forest type									
original	**12**	**80**	**0**	**80**	**405**	**0**	**545**	**950**	**80**

5.3 SELECTION OF OPTIMAL SCENARIO

In order to choose an optimal scenario, we summarize the results from chapter 4 in Table 5.2, showing the minimal detectable differences for habitat quality status and trend for the different sample sizes.

Table 5.2: Summary of minimal detectable differences (mdd) for habitat quality status and trend

	habitat quality status	habitat quality trend	
sample size	habitat prop. in bad condition (mdd from 25%-threshold)	habitat prop. in bad condition (mdd between 2 periods)	prop. favourable indicators (mdd between 2 periods)
40	-16.1% and +21 %	19% - 37%	3.1% - 5%
80	-12.1% and +14.6 %	10% - 19%	2.2% - 3.5%
170	-8.7% and +9.8 %	5% - 9%	1.5% - 2.4%

By comparing the costs (the number of sampling units that have to be measured per year as shown in Table 5.1) and the benefits (the minimal differences for status and trend that can be detected, Table 5.2), we decide to implement alternative 3 for the open habitat types. It allows the estimation of short-term trends (2 monitoring cycles of 6 years = 12 years) in habitat quality based on paired observations, as the monitoring cycle is lowered to 6 years. It also allows the estimation of the status of habitat quality on the scale of Flanders every six years with (approximately) the same precision as the original design, as the sample size per habitat type is kept to 80. The cost of alternative 3 is only slightly higher (11 extra sampling units per year) compared to the original design.

Appendix D gives an overview of the sample size per habitat type and subtype for the selected scenario.

The new design will be implemented once the required sample size in Appendix D is reached. In 2022 we have already started with the implementation of the second monitoring cycle for grassland, heath and marsh habitat types. The dune habitat types will follow in 2023.

5.4 SAMPLING PROCESS

As in Westra *et al.* (2014), the sampling process relies on the so-called grts-master sample for Flanders (Onkelinx *et al.*, 2019). This is a spatially balanced sample for the whole of Flanders based on the Generalized Random-Tessellation Stratified (GRTS) method (Stevens & Olsen, 2004). The sample consists of a grid of 32 meter x 32 meter cells, each having a unique ranking number. It can be imported in R using the function `read_GRTSmh` from the n2khab package (Vanderhaeghe *et al.*, 2022) A sample with sample size n for a certain habitat type is selected as follows: (1) select all grid cells of the master sample that overlap with the sampling frame of the target habitat type and (2) select the n grid cells with the lowest ranking number.

An important thing to take into account in the sampling process is that the sampling frame (based on the Natura 2000 habitat map of De Saeger *et al.* (2020)) often consists of polygons that are only partially covered by the target habitat type. This means that selected sampling units are often not located in the target habitat type. In the Natura 2000 habitat map (De Saeger *et al.*, 2020) the variable $phab$ gives the proportion of a polygon covered by a habitat type.

In the original design by Westra *et al.* (2014) this was tackled by first estimating the average detection rate for each habitat type, within each stratum:

$$\text{detection rate} = \frac{\sum phab * area_{polygon}}{\sum area_{polygon}}$$

Next, based on the detection rate, we selected the expected number of sampling units that have to be visited to reach the required sample size for the target habitat type (within each stratum). However, it appeared that for some habitat types the detection rates were lower than estimated from the habitat map and below 50 %. To increase the efficiency of the field work, we created a protocol to randomly select an alternative sampling unit in the field, in order to replace an initially selected sampling unit that did not contain the target habitat type. This protocol was only applied when the detection rate was very low.

The replacement method described above increases the efficiency of the field work, but can also potentially result in biased estimates of habitat quality. The method causes a higher selection probability for sampling units in polygons with a low $phab$. Biased estimates can be avoided by using proper weights in the data analysis. However, this makes analysis more complex.

In the updated design we introduce an alternative method that results in an equal probability sample. This method consists of an extra step in which population units of the target habitat type are selected with a probability equal to $phab$. For example, population units that are located in a habitat map polygon that is covered by a habitat type for 30% ($phab = 30$), all have a selection probability of 30%. In the next step, sampling units are selected (from the selected population units in the previous step) based on the grts-ranking until the required sample size is obtained. In this method, when a sampling unit does not contain the target habitat type, it is always replaced with another sampling unit (that does contain the habitat type) within the same habitat polygon. Therefore, no additional sampling units have to be selected as in the original design, making field work more efficient. Replacing a sampling unit is also based on the grts-ranking: the sampling unit that contains the target habitat type, with the lowest grts-ranking within the same habitat polygon is selected.

When habitat polygons are very large, the replacement method gets very time consuming as sampling units might lay far apart. Therefore we limit the search area to a window of 7 X 7 grid cells around the initial sampling unit.

To make the sampling process reproducible we make use of the data source `raster_runif` (Westra & Vanderhaeghe, 2021). This is a grid with the same dimensions and resolution as the grts-master sample for Flanders in which every raster cell has a random value between 0 and 1 according to the uniform distribution. A population unit is selected when the `raster_runif` value is lower than the $phab$ value.

In the original sampling process the extra selection step was not used. However, we can set $phab$ value to 1, for all the original sampling units that are located in the target habitat (and that were measured in the first monitoring cycle). Therefore they will be selected in the updated sample, independent of the `raster_runif` value.

In the second step we will use the grts-ranking to select the sampling units until the required sample size is reached. In this second step sampling units that were measured in the first monitoring cycle might not get reselected. This happens when the area of a habitat type increases resulting in new population units. Some of these new population units will have a lower grts-ranking than previously selected sampling units and will therefore be included in the sample replacing sampling units with a higher grts-ranking. This is an important benefit of grts-type sampling designs which thus allow accommodating changes in the sampling frame over time.

6 SAMPLE DESIGN FOR STANDING WATER HABITAT TYPES

6.1 STANDING WATER HABITAT TYPES INCLUDED IN MHQ

A monitoring scheme for all standing water habitat types and subtypes are included in MHQ. These are all the habitat types for which the code in Appendix A starts with 31 and habitat subtype 2190_a (Dune slack ponds). Habitat subtype 2190_a was not included in Westra *et al.* (2014) as it was not yet designated at that time. However a monitoring scheme was designed and implemented in 2016.

6.2 ORIGINAL DESIGN

The population unit for the standing water monitoring scheme is an entire water body. The original design for the standing water habitat types in Westra *et al.* (2014) consists of a stratified sample with a combination of following strata:

- area class of the water body
    - `area <= 1 ha`
    - `1 ha < area <= 5 ha`
    - `5 ha < area < 50 ha`
    - `area >= 50 ha`
- inside or outside a special area of conservation (SAC)

The original design can be summarized as follows:

- draw a sample for 3130_aom, 3150, 3160 in area classes `area <= 1 ha` and `1 ha < area <= 5 ha`
    - with an initial sample size of 40 sampling units for Flanders (n_{fl})
    - select extra sampling units within SAC until 80 sampling units are selected
    - apply the finite population correction (see paragraph 5)
    - divide sample size equally over both area classes
- selection of all water bodies for other area classes and other habitat types and habitat subtypes

Although a monitoring cycle of 12 years was proposed in Westra *et al.* (2014), the monitoring schemes for standing water habitat types were implemented with a monitoring cycle of 6 years. This is because the field work could be combined with other surveys. To be able to detect short-term trends (12 years) in habitat quality we will keep this monitoring cycle of 6 years.

6.3 IMPACT OF THE SAMPLING FRAME ON THE SAMPLE SIZE IN THE ORIGINAL DESIGN

The number of water bodies within each stratum will have an impact on the number of selected sampling units. The main impact is that all water bodies in the area classes `5 ha < area < 50 ha` and `area >= 50 ha` are selected in the original design. Furthermore, the number of population units also has an impact on the finite population correction.

Therefore, we want to compare the sampling frame that was originally used for designing the monitoring schemes with the latest available sampling frame.

The original sampling frame consists of the polygons with standing water habitat types in the 2014 version of the Natura 2000 habitat map.

Since 2014 new data sources became available:

- the map of the water surfaces in Flanders (Leyssen *et al.*, 2020)
- updated information on the presence of aquatic habitat types, made available through the 2020 version of the Natura 2000 habitat map (De Saeger *et al.*, 2020)

Both data sources are combined in the map of standing water habitat types (Westra *et al.*, 2021), which is used as the current sampling frame. It can be imported in R by using the function `read_watersurfaces_hab()` of the n2khab package (Vanderhaeghe *et al.*, 2022).

Table 6.1 shows the total sample size and the total number of sampling units in the sampling frame, for both the original sampling frame (habitatmap_2014) and the current sampling frame (watersurfaces_hab_2021). It is clear that the watersurfaces_hab_2021 sampling frame contains a lot more sampling units than the original sampling frame (habitatmap_2014), which results in a much higher sample size. In Table 6.2 the comparison is shown per habitat type and subtype. The current sampling frame also contains the 2190_a habitat subtype resulting in the selection of sampling units for this subtype. This is not the case for the original sampling frame.

Note that some watersurfaces contain more than one habitat type. Therefore, the total number of watersurfaces in Table 6.1 is smaller than the sum of the number of watersurfaces per type in Table 6.2.

Table 6.1: Total sample size per area class for standing water habitat types based on the original design and the total number of sampling units for both the original sampling frame (habitatmap_2014) and the current sampling frame (watersurfaces_hab_2021)

version sampling frame	area <= 1 ha	1 ha < area <= 5 ha	5 ha < area < 50 ha	area >= 50 ha
habitatmap_2014	107 of 562	92 of 160	58 of 58	4 of 4
watersurfaces_hab_2021	179 of 2135	145 of 333	83 of 83	7 of 7

Table 6.2: Total sample size and the total number of sampling units per standing water habitat type and per area class based on the original design for both the original sampling frame (habitatmap_2014) and the current sampling frame (watersurfaces_hab_2021)

type	version sampling frame	area <= 1 ha	1 ha < area <= 5 ha	5 ha < area < 50 ha	area >= 50 ha
2190_a	watersurfaces_hab_2021	32 of 292	5 of 5	0	0
3110	habitatmap_2014	4 of 4	1 of 1	0	0
	watersurfaces_hab_2021	0	5 of 5	1 of 1	0
3130_aom	habitatmap_2014	37 of 369	37 of 101	31 of 31	0
	watersurfaces_hab_2021	42 of 1100	42 of 135	36 of 36	1 of 1
3130_na	habitatmap_2014	12 of 12	14 of 14	7 of 7	0
	watersurfaces_hab_2021	34 of 159	34 of 152	48 of 48	2 of 2
3140	habitatmap_2014	9 of 9	4 of 4	11 of 11	1 of 1
	watersurfaces_hab_2021	21 of 60	21 of 22	20 of 20	4 of 4
3150	habitatmap_2014	28 of 126	25 of 29	11 of 11	3 of 3
	watersurfaces_hab_2021	36 of 371	36 of 56	25 of 25	4 of 4
3160	habitatmap_2014	18 of 53	12 of 13	1 of 1	0
	watersurfaces_hab_2021	34 of 313	34 of 61	6 of 6	0

The total sample size that results from the current sampling frame is much higher than in the original design. Therefore we will explore two alternative scenarios that are better adapted to the current sampling frame.

6.4 ALTERNATIVE SCENARIOS

We propose the following alternative scenarios:

- draw a sample for all types with more than 30 water surfaces in the area classes `area <= 1 ha`, `1 ha < area <= 5 ha` and `5 ha < area <= 50 ha`
    - select an initial sample size of 80 for Flanders
    - select extra sampling units within SAC
        - **alternative 1: until 80 sampling units are selected**
        - **alternative 2: no extra sampling units**
    - select minimum 40 sampling units for each subtype (select extra sampling units if needed)
    - finite population correction
    - distribute sample size over different area classes dividing the sample size equally over the three area classes
- selection of all water surfaces for other area classes (`area > 50 ha`) and other habitat types (type 3110)

Table 6.3 shows the total sample sizes per area class for the different alternative scenarios.

Sample sizes of the alternative scenarios are comparable to the original sample size (except for 3130_aom).

We choose alternative 2 (no extra sampling units within SAC) as most of the water bodies with habitat are located within SAC, and therefore a sample on the scale of Flanders already contains sufficient sampling units within SAC. Table 6.4 shows the sample sizes per type, per area class and inside/outside SAC for the selected scenario.

Table 6.3: Alternative sample size scenarios compared to the original design: total number of sampling units and total number of water surfaces

scenario	n_{fl}	n_{sac}	$n_{subtype}$	area <= 1 ha	1 ha < area <= 5 ha	5 ha < area < 50 ha	area >= 50 ha
alternative 1	80	80	40	121 of 2135	90 of 333	59 of 83	7 of 7
alternative 2	80	0	40	107 of 2135	83 of 333	55 of 83	7 of 7
original				107 of 562	92 of 160	58 of 58	4 of 4

Table 6.4: Number of sampling units per type and total number of water surfaces per type for the selected scenario

type	sac	area <= 1 ha	1 ha < area <= 5 ha	5 ha < area < 50 ha	area >= 50 ha
2190_a	outside	1 of 8	0	0	0
	inside	20 of 284	5 of 5	0	0
3110	inside	0	5 of 5	1 of 1	0
3130_aom	outside	6 of 293	1 of 15	2 of 5	1 of 1
	inside	16 of 807	11 of 120	11 of 31	0
3130_na	outside	2 of 31	3 of 34	4 of 12	1 of 1
	inside	10 of 128	10 of 118	11 of 36	1 of 1
3140	outside	6 of 23	4 of 6	9 of 12	3 of 3
	inside	9 of 37	11 of 16	6 of 8	1 of 1
3150	outside	5 of 79	3 of 8	5 of 6	3 of 3
	inside	18 of 292	19 of 48	17 of 19	1 of 1
3160	outside	1 of 15	1 of 2	0	0
	inside	21 of 298	21 of 59	6 of 6	0

In Table 6.5 we compare the number of water bodies that have to be measured per year in the original design and the updated design. Since measuring large water bodies requires more effort, we show the numbers per area class. We see that in the updated design a slightly higher number of water bodies with an area larger than 50 ha have to be measured. However, the number of water bodies smaller than 50 ha is lower.

Table 6.5: Number of sampling unit per year for the different area classes in both the original design and the updated design

scenario	area <= 1 ha	1 ha < area <= 5 ha	5 ha < area < 50 ha	area >= 50 ha
original design	17.8	15.3	9.7	0.7
updated design	17.8	13.8	9.2	1.2

6.5 SAMPLING PROCESS

As for the terrestrial habitat types, the sampling process relies on the grts-master sample for Flanders (Onkelinx *et al.*, 2019). To assign a grts-ranking to a water body (the population unit) we select a reference point in the water body using the function `st_point_on_surface` of the sf package (Pebesma, 2018). Next, the water body gets the grts-ranking of the grts-master grid cell in which the reference point is located. Once a grts-ranking is assigned to all water bodies, a sample can be drawn in a similar way as the terrestrial habitat types.

7 SAMPLE DESIGN FOR STREAM HABITAT TYPES

7.1 STREAM HABITAT TYPES INCLUDED IN MHQ

Only one stream habitat type is included in MHQ: habitat type 3260 (Water courses of plain to montane levels with the *Ranunculion fluitantis* and Callitricho-Batrachion vegetation). Habitat type 3270 also occurs in Flanders, yet its habitat quality is assessed based on the characteristics of the river bank vegetation. Furthermore it is considered a very dynamic habitat type for which a monitoring scheme is not feasible.

7.2 ORIGINAL DESIGN

The sampling frame of the original design is based on version 1.4 of the 3260 habitat map (Leyssen *et al.*, 2012). A sampling unit corresponds with a river segment of 100 meter.

In the original design the following strata were used:

- the position relative to SAC:
    - intersects with SAC or downstream of SAC
    - outside of SAC (and not downstream of SAC)
- size of catchment area
    - smaller than 10 km²
    - larger than 10 km²

An initial sample size of 80 in Flanders (n_{fl}) was chosen. Next, extra sampling units were selected within the stratum `intersects with SAC and downstream of SAC` until a sample size of 170 (n_{SAC}) was reached. This is because most policy measures to improve the habitat quality are taken within SAC. Therefore, we expect that differences in habitat quality will most likely occur in river segments that intersect with SAC or are situated downstream of SAC (and we want to be able to detect those differences).

In a next step, the sample size is distributed over catchment area classes `< 10 km²` and `> 10 km²` proportional to the length of habitat type 3260 in each class. The reason to include these strata in the original design, is that Westra *et al.* (2014) expected to be able to make use of the data collected by the Flemish Environmental Agency (VMM). The VMM makes use of the same field protocol as INBO, but only measures sampling units in catchment areas larger than 10 km². By dividing the sample size over the strata `< 10 km²` and `> 10 km²` and subtracting the number of sampling units measured by VMM in the stratum `> 10 km²`, we get the remaining number of sampling units per stratum that have to be measured by INBO to get a representative sample. However, VMM could not make a long term commitment for measuring sufficient sampling units in 3260 habitat. Therefore INBO decided to measure all sampling units in the monitoring scheme. As a consequence the stratum `catchment area` is no longer useful and will be removed from the design to reduce its complexity (see further).

Finally, the sample size for a finite population was calculated using the finite population correction. The total population size is the number of 100 meter segments with habitat type 3260. In the original design, the selected sampling units are measured in a monitoring cycle of 12 years.

Table 7.1 shows the original sample size (per monitoring cycle) for habitat 3260 per stratum.

Note: in Westra *et al.* (2014) an error was made when distributing the sample size over the different strata. So the sample size for each stratum is different here, but correct.

Table 7.1: Original sample size for habitat 3260

sac	catchment area	length 3260 (km)	n
intersecting or downstream	< 10 km²	16.8	20
	> 10 km²	109.6	130
outside	< 10 km²	31.6	13
	> 10 km²	31.2	13

7.3 UPDATE OF THE SAMPLE DESIGN FOR 3260

In the updated design we use version 1.7 of the habitat map of 3260 (Leyssen *et al.*, 2020) as the sampling frame. It can be imported in R by using the function `read_habitatstreams()` of the n2khab package (Vanderhaeghe *et al.*, 2022). Another change in the sample design is that we will no longer make use of the stratum `catchment area` as explained above. Finally, we will use the same design parameters as the terrestrial habitat types in order to get better information on trends in habitat quality:

- monitoring cycle = 6 years
- $n_{fl} = 80$
- $n_{SAC} = 80$

The result for the updated monitoring design can be found in Table 7.2.

Table 7.2: Sample size for updated monitoring design

sac	length 3260 (km)	n
intersecting or downstream	135.6	76
outside	72.7	27

In Table 7.3 the sample size for both versions are compared. The updated design results in a slightly higher sample size per year.

Table 7.3: Sample size for the monitoring cycle and per year for the original and the updated design

version	monitoring cycle	n per cycle	n per year
original design	12	176	15
updated design	6	103	17

7.4 SAMPLING PROCESS

As for the terrestrial and standing water habitat types, the sampling process relies on the grts-master sample for Flanders (Onkelinx *et al.*, 2019). The starting point of a 100 meter stream segment (the most downstream point) is used as the reference point to assign a grts-ranking to the stream segment (the population unit). The 100 meter segments were created by selecting points on the line segments of the 1.4 version of the 3260 map every 100 meter using the function `spsample` of the sp package (Bivand *et al.*, 2013). Each created point corresponds with the most downstream point of the 100 meter segment. This method was also applied to create additional population units based on the updated map of 3260 (Leyssen *et al.*, 2020) to update the sampling frame. However, it appeared that updating the sampling frame using this way could result in overlapping population units and manual correction was needed. To avoid this in the future, we will make use of the actual 100 meter line segments instead of points (representing the start of the segment). We will make use of the data source `watercourse_100mseg` (Vanderhaeghe & Westra, 2021). This data source represents all officially known watercourses of the Flemish Region (status 2020-08-07) as line segments of 100 m (or < 100 m, for the most upstream segment of a watercourse).

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A HABITAT TYPES AND SUBTYPES IN FLANDERS

Table A.1: Habitat types and subtypes in Flanders

	habitat type	habitat subtype
Coastal and halophytic habitats		
	Estuaries (1130)	
	Mudflats and sandflats not covered by seawater at low tide (1140)	
	Salicornia and other annuals colonizing mud and sand (1310)	Salicornia habitats dike inward (1310_pol)
		Low saltmarshes Salicornia habitats dike outward (1310_zk)
		High saltmarshes Saginion habitats dike outward (1310_zv)
	Spartina swards (Spartinion maritimae) (1320)	
	Atlantic salt meadows (Glauco-Puccinellietalia maritimae) (1330)	Saltmarshes dike outward (1330_da)
		Halophytic grasslands dike inward (1330_hpr)
Coastal sand dunes		
	Embryonic shifting dunes (2110)	
	Shifting dunes along the shoreline with Ammophila arenaria ('white dunes') (2120)	
	Fixed coastal dunes with herbaceous vegetation ('grey dunes') (2130)	Decalcified dune grasslands (2130_had)
		Calcareous dune grasslands (2130_hd)
	Atlantic decalcified fixed dunes (Calluno-Ulicetea) (2150)	
	Dunes with Hippophaë rhamnoides (2160)	
	Dunes with Salix repens ssp. argentea (Salicion arenariae) (2170)	
	Wooded dunes of the Atlantic, Continental and Boreal region (2180)	
	Humid dune slacks (2190)	Dune slack ponds (2190_a)
		Calcareous dune slacks (2190_mp)
		Other dune slacks (2190_overig)
Inland dunes		
	Dry sand heaths with Calluna and Genista (2310)	
	Inland dunes with open Corynephorus and Agrostis grasslands (2330)	Inland dunes with Corynephorus (2330_bu)
		Inland dunes with Aira (2330_dw)
Fresh and brackish water		
	Oligotrophic waters containing very few minerals of sandy plains (Littorelletalia uniflorae) (3110)	
	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea (3130)	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae (3130_aom)

		Oligotrophic to mesotrophic standing waters with vegetation of the Isoëto-Nanojuncetea (3130_na)
	Hard oligo-mesotrophic waters with benthic vegetation of Chara spp. (3140)	
	Natural eutrophic lakes with Magnopotamion or Hydrocharition - type vegetation (3150)	
	Natural dystrophic lakes and ponds (3160)	
	Water courses of plain to montane levels with the Ranunculion fluitantis and Callitricho-Batrachion vegetation (3260)	
	Rivers with muddy banks with Chenopodion rubri p.p. and Bidention p.p. vegetation (3270)	
Temperate heath and scrub	Northern Atlantic wet heaths with Erica tetralix (4010)	
	European dry heaths (4030)	
Sclerophyllous scrub	Juniperus communis formations on heaths or calcareous grasslands (5130)	Juniperus communis formations on heaths (5130_hei)
		Juniperus communis formations on calcareous grasslands (5130_kalk)
Natural and semi-natural grassland	Xeric sand calcareous grasslands (6120)	
	Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites) (6210)	Calcareous grasslands (Gentiano-Koelerietum) (6210_hk)
		Calcareous grassland fringes and scrubs (6210_sk)
	Species-rich Nardus grasslands, on silicious substrates in mountain areas (and submountain areas in Continental Europe) (6230)	Species-rich Agrostis grasslands (6230_ha)
		Wet Nardus grasslands (6230_hmo)
		Dry Nardus grasslands (6230_hn)
		Lime-rich dry Nardus grasslands (Betonico-Brachypodietum) (6230_hnk)
	Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae) (6410)	Junco-Molinion grasslands (6410_mo)
		Juncus acutiflorus grasslands with Scutellaria minor (6410_ve)
	Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels (6430)	Nitrophilous forest fringes with less common plant species (6430_bz)
		Filipendula tall herb communities (6430_hf)
		Epilobium hirsutum tall herb fringe communities (6430_hw)
		Brackish reed beds with Althaea officinalis (6430_mr)
	Lowland hay meadows (Alopecurus pratensis, Sanguisorba officinalis) (6510)	Arrhenatherion grasslands (6510_hu)
		Alopecurion grasslands with Silaum silaus and Oenanthe silaifolia (6510_hua)
		Lime-rich Cynosurion grasslands (Galio-Trifolietum) (6510_huk)
		Arrhenatherion grasslands with Sanguisorba officinalis (6510_hus)

Bogs, mires and fens	
Active raised bogs (7110)	
Transition mires and quaking bogs (7140)	Base rich quaking mires with Carex diandra (7140_base)
	Base poor, circum-neutral transition mires (7140_meso)
	Fern- and Sphagnum-rich reed beds on quaking bogs (7140_mrd)
	Oligotrophic and acidic transition mires and quaking bogs (7140_oli)
Depressions on peat substrates of the Rhynchosporion (7150)	
Calcareous fens with Cladium mariscus and species of the Caricion davallianae (7210)	
Petrifying springs with tufa formation (Cratoneurion) (7220)	
Alkaline fens (7230)	
Rocky habitats and caves	
Caves not open to the public (8310)	
Forest and scrub	
Luzulo-Fagetum beech forests (9110)	
Atlantic acidophilous beech forests with Ilex and sometimes also Taxus in the shrublayer (Quercion robori-petraeae or Ilici-Fagenion) (9120)	Oak-birch forests as acidic oak-beech sere (9120_qb)
Asperulo-Fagetum beech forests (9130)	Typical Atlantic neutrophilic beech forests (Endymio-Fagetum) (9130_end)
	Middle-European neutrophilic beech forests with Melica uniflora and Galium odoratum (Melico-Fagetum) (9130_fm)
Medio-European limestone beech forests of the Cephalanthero-Fagion (9150)	
Sub-Atlantic and medio-European oak or oak-hornbeam forests of the Carpinion betuli (9160)	
Old acidophilous oak woods with Quercus robur on sandy plains (9190)	
Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae) (91E0)	Riverine Salix forests (Salicetum albae) (91E0_sf)
	Ash-alder forests of slow-flowing rivers (91E0_va)
	Ash-alder spring forests (Carici remotae-Fraxinetum) (91E0_vc)
	Mesotrophic alder carrs (Carici elongatae-Alnetum) (91E0_vm)
	Eutrophic alder carrs (Filipendulo-Alnetum, Macrophorbio-Alnetum, Cirsio-Alnetum) (91E0_vn)
	Oligotrophic (alder-)birch carrs (Carici laevigatae-Alnetum) (91E0_vo)
Riparian mixed forests of Quercus robur, Ulmus laevis and Ulmus minor, Fraxinus excelsior or Fraxinus angustifolia, along the great rivers (Ulmenion minoris) (91F0)	

B POWER CALCULATIONS USING THE SIMR PACKAGE

B.1 METHDODOLGY

- In a first step we use existing data from the Flemish Forest Inventory to fit a generalized linear mixed models, with plot as random effect to specify that the observations are paired.
- Model assumptions can be verified using the function `plotQQunif` of the `DHARMa` package (Hartig, 2022).
- Next, we can use `simr` to modify the model by changing the sample size and effect size. For example, we can use the sample size and minimal detectable effect based on the paired t-test.
- Finally `simr` estimates the power for the specified sample size and effect size based on a number of simulations.

B.2 TREND IN PROPORTIONS OF FAVOURABLE INDICATORS OF HABITAT TYPE 9120

The following R code models the proportion of favourable indicators (prop_favourable) of habitat type 9120 for the different Forest Inventory periods using plot as a random effect:

```
model_prop_favourable_9120 <- lmer(formula = prop_favourable ~ period + (1|plot), data
= data_forest_paired)
```

Proportions have values between 0 and 1 and in theory follow a zero- and one-inflated beta distribution. However, here we assume a normal distribution to avoid complexity. These model assumptions are quite OK, as can be seen in the figure below (generated by the function `plotQQunif`).

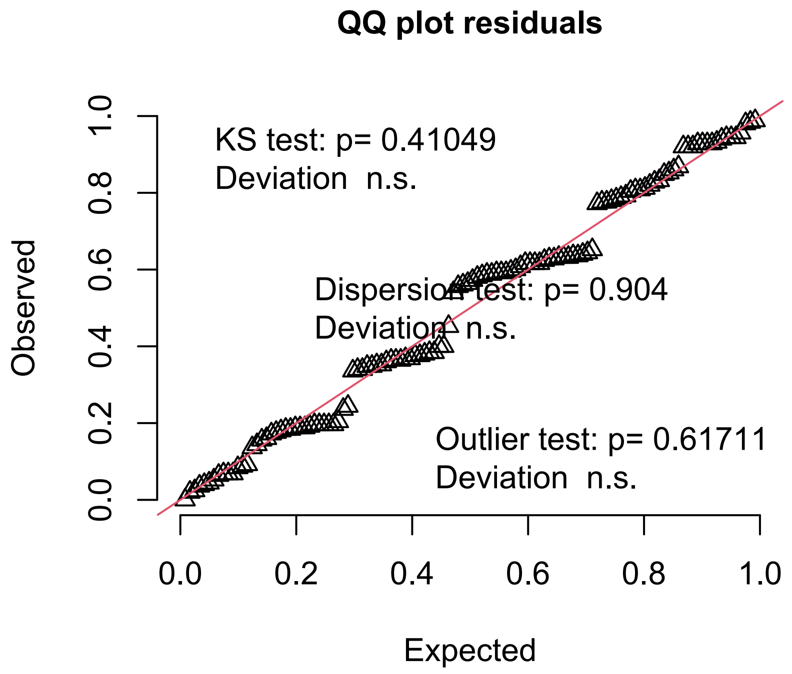

Table B.1 shows the minimal difference in proportions of favourable indicators of habitat type 9120 that can be detected with a power of 0.80 according to the paired t-test, for different sample sizes. Table B.1 also shows the estimated power based on `simr`. The power based on `simr` is close to 0.80 for all combinations of sample size and detectable difference, confirming the results from the paired t-test in Table 4.7.

Table B.1: Power (π) based on paired t-test and estimated power using simr for the detectable difference in proportions of favourable indicators (habitat type 9120)

sample size	detectable difference (%)	power paired t-test	power simr
40	4.69	0.8	0.784 [0.73 - 0.83]
80	3.34	0.8	0.792 [0.74 - 0.84]
170	2.29	0.8	0.812 [0.76 - 0.86]

B.3 TREND IN NUMBER OF KEY SPECIES OF HABITAT TYPE 9120

The following R code models the number of key species (n_keyspecies) of habitat type 9120 for the different Forest Inventory periods using plot as a random effect:

```
model_keyspecies_9120 <- lmer(formula = n_keyspecies ~ period + (1|plot), data = data_forest_paired)
```

The model assumptions are quite OK as can be seen in the figure below (generated by the function `plotQQunif`).

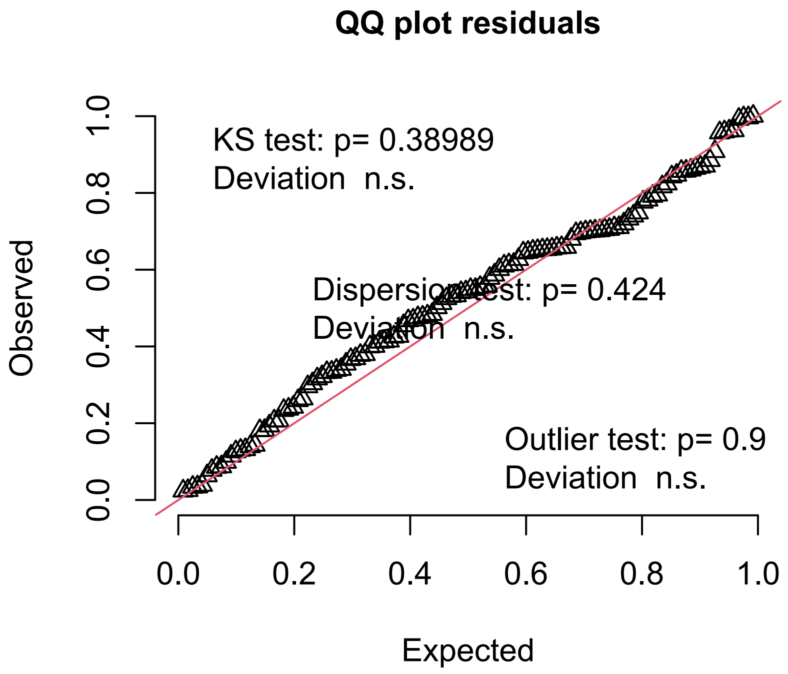

Table B.2 shows the minimal difference in the number of key species of habitat type 9120 that can be detected with a power of 0.80 according to the paired t-test, for different sample sizes. Table B.2 also shows the estimated power based on `simr`. The power based on `simr` is significantly higher than 0.80 for all combinations of sample size and detectable difference. This indicates that slightly smaller differences in the number of key species can be detected with a power of 0.80 (for habitat type 9120) with the same sample size. The results from the paired t-test in Table 4.9 can therefore be regarded as a conservative indication of the minimal detectable difference.

Table B.2: Power (π) based on paired t-test and estimated power and 95% confidence interval using simr for the detectable difference in the number of key species (habitat type 9120)

sample size	detectable difference (%)	power paired t-test	power simr
40	1.35	0.8	0.944 [0.91 - 0.97]
80	0.96	0.8	0.972 [0.94 - 0.99]
170	0.66	0.8	0.972 [0.94 - 0.99]

B.4 TREND IN TOTAL COVER OF ENCROACHMENT SPECIES OF HABITAT TYPE 9120

The following R code models the total cover of encroachment species (encroachment) of habitat type 9120 for the different Forest Inventory periods using plot as a random effect:

```
model_encroachment_9120 <- lmer(formula = logit_encroachment ~ period + (1|plot), data
= data_forest_paired)
```

Like proportions, plant cover follows a zero- and one-inflated beta distribution. Modelling such distributions is quite complex and the 'simr' package can not handle such models. However, assuming a normal distribution did not give good results. Therefore we first applied a logit transformation on the cover data:

$$\text{logit}(p) = \log\left(\frac{p}{1-p}\right)$$

The logit transformation of 0 and 1 is -Inf and +Inf. To avoid this we increased the zeroes with a small value of 0.001 and decreased the ones with 0.001 (0.999).

The model assumptions are still far from perfect but just pass the test.

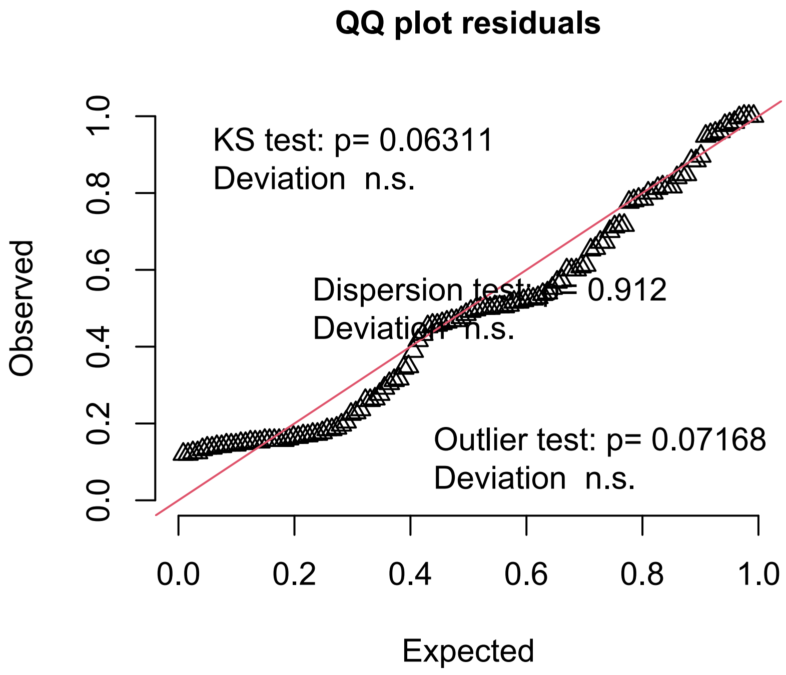

Table B.3 shows the minimal difference in the total cover of encroachment species of habitat type 9120, that can be detected with a power of 0.80 according to the paired t-test, for different sample sizes. Table B.2 also shows the estimated power based on `simr`. The power based on `simr` is slightly lower for a sample size of 40 and slightly higher for a sample size of 170, but overall the results are comparable to those of the paired t-test.

Table B.3: Power (π) based on paired t-test and estimated power and 95% confidence interval using simr for the detectable difference in total cover of encroachment species (habitat type 9120)

sample size	detectable difference (%)	power paired t-test	power simr
40	8.72	0.8	0.74 [0.68 - 0.79]
80	6.20	0.8	0.82 [0.77 - 0.87]
170	4.26	0.8	0.888 [0.84 - 0.92]

C HABITAT TYPES AND SUBTYPES INCLUDED IN MHQ

Table C.1 gives an overview of the habitat types for which a habitat quality monitoring scheme was developed. The table also provides the reason why a monitoring scheme was not considered the most appropriate approach for several habitat types. Terrestrial habitat types are considered very rare when the area is lower than 10 ha or when the habitat type occurs on less than 15 locations. The area and the number of locations was derived from the 2020 version of the Natura 2000 Habitat map (De Saeger *et al.*, 2020).

Table C.1: Selection of the habitat types for which a monitoring scheme is implemented

code type	area (ha)	# locations	monitoring scheme	reason
1130	759	2609	no	habitat quality evaluation on landsacpe scale
1140	2096	46	no	no habitat quality indicators available
1310	57	238	no	very dynamic habitat type
1320	2	49	no	very rare terrestrial type
1330	251	1264	yes	
2110	27	290	no	very dynamic habitat type
2120	446	415	yes	
2130	802	1236	yes	
2160	645	1041	yes	
2170	63	196	yes	
2180	245	195	yes	
2190	48	195	yes	
2310	2422	2078	yes	
2330	1077	1201	yes	
3110	1	1	yes	
3130	173	421	yes	
3140	8	18	yes	
3150	64	146	yes	
3160	31	91	yes	
3260	3	12	yes	
3270	27	51	no	very dynamic habitat type
4010	1851	2841	yes	
4030	4355	4203	yes	
5130	25	13	no	very rare terrestrial type
6120	13	18	no	
6210	4	18	no	very rare terrestrial type
6230	718	1755	yes	
6410	72	256	yes	
6430	991	2187	no	no accurate sample frame
6510	1783	2845	yes	
7110	2	1	no	very rare terrestrial type

Table C.1: Selection of the habitat types for which a monitoring scheme is implemented *(continued)*

code type	area (ha)	# locations	monitoring scheme	reason
7140	299	779	yes	
7150	41	205	no	very dynamic habitat type
7210	2	15	no	very rare terrestrial type
7230	10	24	no	very rare terrestrial type
9110	360	241	no	low priority
9120	17423	11160	yes	
9130	3350	2788	yes	
9150	3	11	no	very rare terrestrial type
9160	3600	4124	yes	
9190	3895	3092	yes	
91E0	11159	14783	yes	
91F0	1	1	no	very rare terrestrial type

Table C.2 gives an overview of which habitat subtypes are considered for oversampling.

Table C.2: Oversampling habitat subtypes

code type	code subtype	area (ha)	# locations	oversampling	reason
1330	1330_da	117	637	yes	
	1330_hpr	134	627	yes	
2130	2130_had	125	41	yes	
	2130_hd	678	1195	yes	
2190	2190_mp	8	50	yes	oversampling applied in 1st monitoring cycle
	2190_overig	40	145	yes	
2330	2330_bu	925	862	yes	
	2330_dw	116	262	yes	
3130	3130_aom	69	194	yes	
	3130_na	58	69	yes	
6230	6230_ha	239	611	yes	
	6230_hmo	146	412	yes	
	6230_hn	277	602	yes	
	6230_hnk	4	20	no	very rare terrestrtial subtype
6410	6410_mo	69	249	yes	
	6410_ve	2	7	no	very rare terrestrtial subtype
6510	6510_hu	1598	2543	yes	
	6510_hua	111	69	yes	
	6510_huk	60	199	yes	
	6510_hus	15	34	yes	
7140	7140_base	1	6	no	very rare terrestrtial subtype
	7140_meso	196	603	yes	
	7140_mrd	8	21	no	very rare terrestrtial subtype
	7140_oli	94	149	yes	
9120	9120_qb	673	623	yes	
9130	9130_end	3301	2738	yes	
	9130_fm	49	50	yes	
91E0	91E0_sf	346	610	yes	
	91E0_va	3960	5540	yes	
	91E0_vc	341	767	yes	
	91E0_vm	2955	3461	yes	
	91E0_vn	2776	3287	yes	
	91E0_vo	523	856	yes	

D SAMPLE SIZE PER HABITAT TYPE AND SUBTYPE

Table D.1 provides an overview per habitat type of:

- total initial sample size for Flanders (tot_{fl})
- number of extra sampling units selected within the SAC ($extra_{sac}$)
- number of extra sampling units selected per subtype ($extra_{subtype}$)
- total overall sample size for the monitoring cycle
- total overall sample size per year

Table D.1: Sample size per habitat type

habitat type	cycle (years)	tot fl	extra sac	extra subtype	total per cycle	total per year
1330	6	79	14	1	94	15.7
2120	6	79	5	0	84	14.0
2130	6	80	5	26	111	18.5
2160	6	80	4	0	84	14.0
2170	6	71	0	0	71	11.8
2180	6	78	3	0	81	13.5
2190	6	70	2	0	72	12.0
2310	6	80	12	0	92	15.3
2330	6	81	19	28	128	21.3
4010	6	80	3	0	83	13.8
4030	6	80	12	0	92	15.3
6230	6	82	25	27	134	22.3
6410	6	73	15	0	88	14.7
6510	6	81	54	95	230	38.3
7140	6	80	8	12	100	16.7
9120	12	81	0	76	157	13.1
9130	12	81	0	70	151	12.6
9160	12	80	0	0	80	6.7
9190	12	80	0	0	80	6.7
91E0	12	83	0	399	482	40.2

Table D.2 shows the number of extra sampling units per habitat subtype.

Table D.2: number of extra sampling units per habitat subtype

habitat type	subtype	extra subtype
1330	1330_da	1
	1330_hpr	0
2130	2130_had	26
	2130_hd	0
2190	2190_mp	0
	2190_overig	0
2330	2330_bu	0
	2330_dw	28
6230	6230_ha	6
	6230_hmo	18
	6230_hn	3
	6230_hnk	0
6410	6410_mo	0
	6410_ve	0
6510	6510_hu	0
	6510_hua	34
	6510_huk	31
	6510_hus	30
7140	7140_base	0
	7140_meso	0
	7140_mrd	0
	7140_oli	12
9120	9120_qb	76
9130	9130_end	2
	9130_fm	68
91E0	91E0_sf	76
	91E0_va	52
	91E0_vc	76
	91E0_vm	59
	91E0_vn	60
	91E0_vo	76