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Uncertainty analysis of SMART2-SUMO2-P2E-MOVE4

The Nature Planner soil and vegetation model chain

G.W.W. Wamelink, L.M.W. Akkermans, D.J. Brus, G.B.M. Heuvelink, J.P. Mol-Dijkstra & E.P.A.G. Schouwenberg

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WOt Wettelijke Onderzoekstaken Natuur & Milieu

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Uncertainty analysis of SMART2-SUMO2-P2E-MOVE4

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Abstract
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Models and model chains can provide a powerful tool to evaluate government policies regarding, e.g., nitrogen deposition or climate change. Since decisions based on model simulations can have a major impact on society, it is important to know the accuracy and uncertainty of the model simulations. This report offers an account of the uncertainty in the heart of the model chain of 'Nature Planner'. This chain consists of a soil model (SMART2), a vegetation succession model (SUMO2) and a plant species prediction model (MOVE4). Uncertainty was introduced in the most important model parameters, as well as two important input maps; a soil map and a groundwater map. We evaluated how the uncertainty propagates through the model chain and identified the major sources of the uncertainty in the end results, i.e. the predicted number of plant species. The main source of uncertainty are three regression functions that translate the soil model results for pH and nitrogen availability and the groundwater table into Ellenberg indicator values. Compared to these regression equations, other sources of uncertainty are almost negligible on average, although at some of the 1500 sites examined, the soil model parameters and the input maps also contribute significantly to the uncertainty. We recommend reducing the uncertainty by replacing the Ellenberg indicator values in the model chain by indicator values based on field measurements.

Keywords: model chain, soil, top marginal variance, uncertainty analysis, uncertainty propagation, vegetation

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Modellen en modelketens kunnen een krachtig instrument vormen om het overheidsbeleid op gebieden als stikstofdepositie of klimaatverandering te evalueren. Aangezien op modelsimulaties gebaseerde beslissingen grote maatschappelijke gevolgen kunnen hebben, is kennis van de nauwkeurigheid en de mate van onzekerheid van deze simulaties van groot belang. In dit rapport beschrijven wij de onzekerheid veroorzaakt door de belangrijkste modellen in de Natuurplanner. De Natuurplanner bestaat onder andere uit een bodemmodel (SMART2), een vegetatiesuccessiemodel (SUMO2) en een planten-soorten voorspellingsmodel (MOVE4). De voortplanting van onzekerheid is berekend op basis van de onzekerheid in modelparameters en de twee belangrijke invoerkaarten: bodemkaart en grondwaterkaart. De voornaamste bron van onzekerheid zijn de drie regressiefuncties die worden gebruikt om de modelresultaten (pH, stikstof-beschikbaarheid en voorjaarsgrondwaterstand) te vertalen in Ellenberg-indicatorwaarden. Op enkele van de 1500 bestudeerde sites geven ook de parameters van het bodemmodel en de invoerkaarten significante bijdragen aan de onzekerheid. Om de onzekerheid te beperken, bevelen we aan om de Ellenberg-indicatorwaarden te vervangen door indicatorwaarden die op veld-metingen zijn gebaseerd.

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Summary

Model chains are often used to investigate future developments of, e.g., conservation areas, as a result of changes in parameters like nitrogen deposition or climate. The model chain system used by the National Environmental Assessment Agency (PBL) is called Nature Planner. A major part of Nature Planner, i.e. the SMART2, SUMO2, P2E and MOVE4 models, was subjected to an uncertainty analysis.

The uncertainty in input sources like the soil map contributes to the uncertainty in all results further along the model chain, including the end result, which in this study was the number of plant species predicted for a site. We investigated the way the uncertainty propagates through the model chain by introducing uncertainty in the most important model parameters as well as two important input maps, the soil map and the groundwater table map. The parameters were combined into three groups:

1. Soil parameters from SMART2, including the soil and groundwater table maps;
2. Plant parameters from SUMO2;
3. Ellenberg parameters resulting from the translation of pH, groundwater table and nitrogen availability into Ellenberg indicator values (P2E module).

The uncertainty in the MOVE4 model was not included in the analysis, due to computational and runtime problems. The model output was examined as the number of plant species predicted by MOVE4 for different levels of soil pH, nitrogen availability, biomass and the Ellenberg indicator values for acidity (R), moisture (F) and nutrient availability (N).

The uncertainty analysis was carried out for three different vegetation types, viz. grassland, heathland and forest, at 500 sites each, resulting in a total of 1500 examined sites. We ran the models 15,000 times for each site. For each parameter and map included in the uncertainty analysis, we drew 3,000 different values. When the draws of the parameter values are combined in a particular way (e.g. Monte Carlo) it is possible to estimate the uncertainty in the model results, but also to attribute the variability of the results to particular parameters (groups). In addition to the effects of the input maps and the model parameters, we also included the effect of the uncertainty resulting from grazing of grasslands. The output variables of the model runs we examined were soil pH, nitrogen availability, biomass, Ellenberg R, Ellenberg F, Ellenberg N and the predicted number of plant species. The predicted number of plant species was calculated for a set of 30 species for grassland and for two different sets of 20 species each for heathland and forest. We looked at the uncertainty in the end result and the contribution of each parameter group to this uncertainty, but also at the contribution of each group, where applicable, to pH, nitrogen availability, biomass and the Ellenberg indicator values for acidity, moisture and nutrient availability.

The most important output of the model chain is the number of species predicted by MOVE4. The average predicted number of species was calculated for each vegetation type. For grassland, this was 1.58, with a standard deviation of 0.53, for heathland 4.87, with a standard deviation of 0.82 and for forest 4.33, with a standard deviation of 1.16. The average of the uncertainty estimates (i.e. the average of the estimated absolute variabilities over the 500 sites) ranged from 1.74 for grassland to 2.24 for heathland and 3.13 for forest.

The uncertainty in the predicted number of species was smaller than we had expected. The uncertainty in the MOVE4 output is mainly caused by the uncertainty in the Ellenberg parameters (Table A). The uncertainty in the model chain output is almost completely determined by the uncertainties in the parameters of the regression equations that translate the output of SMART2 and the groundwater table map into the Ellenberg indicator values. This is in line with the results of an earlier, simpler uncertainty analysis. Improving this relationship could reduce the uncertainty in the model chain. Alternatively, the Ellenberg indicator values could be replaced by parameters directly related to model output (e.g. pH). Note, however, that we also included the model uncertainty for P2E in the analysis, whereas the model uncertainty for SMART2 and SUMO2 was not included. The uncertainty of these two models is unknown and difficult to estimate, but excluding this uncertainty may well have led to underestimation of the uncertainty in the end result and the contributions of the two models to this uncertainty.

Table A. Percentage explained variance of the uncertainty of the MOVE4 output (predicted number of species) for each of the three parameter groups (the soil group includes the soil and groundwater table maps).

Type	**Explained variance (%)**		
	Soil	Plant	Ellenberg
Grassland	3	4	76
Heathland	6	0	71
Forest	5	2	68

The uncertainty in the biomass is mainly caused by the plant parameters (SUMO2) and the nitrogen availability. Thirty to fifty percent of the uncertainty in the nitrogen availability is determined by the soil parameters (the maps and SMART2), while 50-70% is determined by the plant parameters. The uncertainty in the soil pH is almost totally caused by the soil parameters.

The uncertainty calculated in this study is based on a limited number of parameters and two input maps. Since this set was derived from earlier studies, we expect that including other model parameters would not lead to much larger uncertainties. This may be different for the specific model uncertainty in SMART2 and SUMO2, which was not included in the analysis.

The uncertainty we obtained does not in itself give any information about the validity of the model predictions. This has to be tested against field measurements.

Samenvatting

Om de effecten van externe veranderingen op de natuur, zoals stikstofdepositie, klimaatverandering of versnippering te begrijpen en voor de toekomst te simuleren, maar ook om (toekomstig) beleid te evalueren, worden vaak modellen gebruikt. Het Planbureau voor de Leefomgeving gebruikt hiervoor de Natuurplanner, een interface waarin verschillende modellen op het gebied van natuur gekoppeld zijn. Een belangrijk onderdeel in de Natuurplanner is de modelketen SMART2-SUMO2-MOVE4. Hiermee kan op basis van simulaties van grondwater, bodem en vegetatieprocessen uitspraken gedaan worden over mogelijke gevolgen van beleid, vegetatiebeheer, klimaatverandering of depositie op het voorkomen van plantensoorten en duurzaam voorkomen van diersoorten. De resultaten worden gebruikt voor beleidsevaluatie en adviezen aan het beleid en politiek, vooral op landelijk niveau. Het is daarom van groot belang om te weten wat de onzekerheid is in de modeluitkomsten.

Onzekerheid in bijvoorbeeld de bodemkaart plant zich voort door de hele modelketen en draagt uiteindelijk bij aan de onzekerheid in het eindresultaat, in dit onderzoek het aantal plantensoorten dat ergens voor zou kunnen komen. Om te onderzoeken hoe groot de onzekerheid is in de modeluitkomsten, is een onzekerheidsanalyse uitgevoerd voor de belangrijkste kaarten en modellen van de Natuurplanner. De onzekerheid in de bodemkaart (bodemtype), grondwaterstandkaart en de modellen SMART2 (bodemprocessen) en SUMO2 (vegetatieprocessen) en de vertaalmodule P2E (van pH, gemiddelde voorjaarsgrondwaterstand gvg en stikstofbeschikbaarheid naar Ellenberggetallen) zijn meegenomen in de onzekerheidsanalyse. Onderzocht is hoe de onzekerheid doorwerkt in de MOVE4-berekeningen (het aantal soorten dat voor kan komen). De onzekerheid in MOVE4 zelf kon niet worden meegenomen door zowel modeltechnische problemen als problemen met de computertijd.

De hele modelketen is uitgevoerd voor 1500 random gekozen sites opgedeeld in drie vegetatietypen (grasland, heide en loofbos, 500 sites per type). Naast de effecten van de onzekerheden in de kaart en de modellen is voor grasland ook de onzekerheid veroorzaakt door beheer door middel van begrazen (door runderen) meegenomen. Per site zijn voor alle variabele parameterwaarden van de modellen en de bodem- en grondwaterkaart 3000 trekkingen gedaan. Er zijn dus bijvoorbeeld 3000 bodemkaarten getrokken. Om de statistische analyse te vereenvoudigen, zijn drie parametergroepen gemaakt waarvoor berekeningen zijn uitgevoerd: Groep 1: bodem, inclusief bodemkaart, grondwaterstandkaart en de SMART2-parameters,; Groep 2: plant, de SUMO2-parameters; Groep 3: Ellenberg, de regressieparameters van P2E. De kans op voorkomen van 30 plantensoorten voor grasland en 20 plantensoorten voor heide en bos is berekend en vervolgens is gekeken hoeveel soorten daadwerkelijk zouden kunnen voorkomen en vervolgens gesommeerd. De onzekerheid is bepaald voor bodem pH en stikstofbeschikbaarheid (beide uitvoer van SMART2), de biomassa (SUMO2), de Ellenberggetallen voor zuurgraad, vocht en stikstofbeschikbaarheid (P2E) en het aantal soorten. Behalve het vaststellen van de totale onzekerheid, is ook de bijdrage daaraan van de drie hiervoor genoemde parametergroepen geïdentificeerd. De trekkingen per groep zijn als groepen gecombineerd in een *Monte Carlo*-achtige setting, waardoor per groep de relatieve bijdrage aan de totale onzekerheid kan worden vastgesteld. In totaal zijn er 500 (sites) * 15.000 (combinaties van trekkingen) * 3 (aantal vegetatietypen) is 22.500.000 runs van de modelketen uitgevoerd. Voor MOVE4 is dit aantal groter, omdat runs per plantensoort worden uitgevoerd. Voor heide en bos is de kans op voorkomen voor 20 soorten berekend, voor grasland voor 30 soorten. Dit geeft 450.000.000 en 675.000.000 runs voor MOVE4.

De belangrijkste outputvariabele is het aantal soorten waarvan verwacht wordt dat ze voor kunnen komen, berekend door MOVE4. Voor 500 sites per vegetatietype is het

aantal soorten berekend. Voor heide wordt voor de spreiding over de 500 sites een gemiddeld aantal soorten van 4,87 berekend met een standaarddeviatie van 0,82, voor bos is dit respectievelijk 4,33 en 1,16 en voor grasland 1,58 en 0,53. De spreiding van de onzekerheid voor de 500 sites voor heide heeft een gemiddelde 2,24 met een standaarddeviatie van 1,29, voor bos respectievelijk 3,13 en 0,97 en voor grasland 1,74 en 0,75. Normaal wordt de onzekerheid gegeven als variantie, maar voor de toegankelijkheid is hier de wortel uit de variantie gegeven.

De onzekerheid in de MOVE4-uitvoer wordt voornamelijk veroorzaakt door het P2E-model. De onzekerheid in de vertaalfuncties van modeluitvoer uit SMART2 (stikstofbeschikbaarheid en pH) en de grondwaterkaart (gvg) bepaalt voor alle typen (bos heide en grasland) feitelijk in grote mate hoe groot de onzekerheid is in het eindresultaat (Tabel B).

Tabel B. Percentage variantie in de uitvoer van MOVE4 (aantal soorten dat verwacht wordt) voor elk van de drie vegetatietypen dat toe te schrijven is aan de onderscheiden parametergroepen. De bodemgroep is inclusief de bodem- en grondwaterkaart.

Type	**Verklaarde variantie (%)**		
	Bodem	Plant	Ellenberg
Grasland	3	4	76
Heide	6	0	71
Bos	5	2	68

De onzekerheid in het eindresultaat (‘het aantal soorten dat verwacht wordt’) is kleiner dan misschien mocht worden verwacht. Verontrustend is het dat de onzekerheid vrijwel geheel wordt bepaald door een ‘simpele’ vertaalmodule. Uit eerdere onderzoeken was echter ook al naar voren gekomen dat de vertaling van de pH, stikstofbeschikbaarheid en grondwaterstand naar de Ellenberg-indicatorwaarden erg onzeker is. Als we de onzekerheid in de modeluitkomst willen verkleinen, zou daar de aandacht naar uit moeten gaan. Dat kan bijvoorbeeld door het vervangen van de Ellenberggetallen door indicatoren gebaseerd op gemeten bodemparameters waardoor de P2E-module overbodig wordt. MOVE4 zou dan ook vervangen moeten worden door een model waar de kans op voorkomen is gebaseerd op gemeten parameters als pH, nitraatconcentratie en gvg. Hierbij dient te worden opgemerkt dat voor SMART2 en SUMO2 alleen de onzekerheid in de parameters is meegenomen, maar dat voor de P2E-module ook de modelonzekerheid is meegenomen. Het effect van de modelonzekerheid van SMART2 en SUMO2 is onbekend en heeft dus een onbekend effect op het de resultaten. De onzekerheid kan dus groter zijn dan hier aangegeven.

De onzekerheid in de biomassa wordt vooral veroorzaakt door de plantparameters (SUMO2 zelf) en door de stikstofbeschikbaarheid. Voor de stikstofbeschikbaarheid geldt dat die afhankelijk van het vegetatietype voor 30 tot 50% afhangt van de bodem-parameters (de beide kaarten en SMART2) en voor 50 tot 70% van de plant-parameters. De onzekerheid in de zuurgraad van de bodem (pH) hangt nagenoeg volledig af van de bodemparameters.

In dit onderzoek wordt de berekende onzekerheid veroorzaakt door een beperkt aantal modelparameters en twee invoerkaarten. Op basis van eerdere studies is gekozen voor deze beperkte set van invoerparameters. De buiten beschouwing gelaten parameters leiden waarschijnlijk niet tot een grotere onzekerheid, voor de niet meegenomen modelonzekerheid van SMART2 en SUMO2 is dit onzeker.

De berekende onzekerheid zegt niets over hoe goed het model het vergeleken met de werkelijkheid doet; het gaat hier alleen om interne modelonzekerheid en waar die vandaan komt. De relatie met veldmetingen moet worden onderzocht door middel van een validatie.

1 Introduction

The application of models or model chains, i.e. several models linked to each other and communicating with each other, gets more widespread in ecological research. Examples of such model chains are Century (Parton *et al.*, 1993; Kirschbaum & Paul, 2002), NUCOM (Van Oene *et al*., 1999a), FORGRA, (Jorritsma *et al.,* 1999), MASSIMO (Schmid *et al*., 2006), FORSPACE (Kramer *et al*., 2003), NICHE (Koerselman *et al.,* 1999) and ForSAFE (Wallman *et al*., 2005). Model chains are particularly useful to gain understanding of the effects of regional and global problems like acid and nitrogen deposition or global warming on species and populations dynamics. Policy makers often use model chain forecasts to evaluate the effect of different possible measures to (partly) undo the effect of human interference with the environment or to forecast possible effects of human interference for the future (Wamelink *et al.* 2005).

Since government policies may be partly based on model runs it is important to quantify the accuracy of the model predictions. Millions of corporations and tax payers' money may be involved in countermeasures (Wamelink *et al*. 2005). The uncertainty of model predictions may be large for just one model (Wamelink & Van Dobben, 2003, Kros *et al*. 2002, Wamelink 2008), let alone for a model chain (Schouwenberg *et al.* 2000). However, accumulating model uncertainties in model runs were often neglected in the past. To be able to determine uncertainties in outputs from model chains it is necessary to subject the whole chain to an uncertainty analysis and include uncertainty propagation analysis in the chain.

The major goal of this research was to estimate the uncertainty in the final model results, i.e. the number of species present at a site which is predicted by MOVE4. The second goal was to investigate the sources of uncertainty and the uncertainty propagation in the model chain. This will give information about the most uncertain part of the model chain and the possibility to improve the performance of the model chain.

Therefore, we subjected our model chain, SMART2-SUMO2-MOVE4, a major chain within the Nature Planner (Van der Hoek & Bakkenes 2007), to an uncertainty analysis. SMART2 is a soil model (Kros 2002), SUMO2 a vegetation model (Wamelink *et al*. 2009a) and MOVE4 a plant species model (Van Adrichem *et al*. 2010). The uncertainty in two input maps, a soil map and a groundwater table map, was also included. The uncertainty in intermediate results and the final result (the number of plant species predicted to be present) were estimated and the relative contribution of the uncertainty in the models and maps were separated. Model runs were carried out site specific for 500 randomly chosen sites for grassland, heathland and deciduous forest, and reported uncertainties are related to the site level.

This report was reviewed by two reviewers, Dr. P.W. Goedhart of Biometris Wageningen UR and Dr. P. Jansen of Environmental Assessment Agency (PBL). The reviews are included in the report in Appendix 13 including the reaction of the authors.

2 General explanation of the method

Parameters values used in models, as ours, but also input maps are almost per definition uncertain. This implies that the model outcome, e.g. the number of species present, is not a fixed value but an estimate of this value with an uncertainty. This uncertainty may be small but can also be that large that an estimated outcome becomes pointless. Since political decisions are based on the model chain investigated here the uncertainty of the model output is of high importance. To estimate the uncertainty and to locate the major sources of uncertainty we carried out an uncertainty analysis for the hart of our model chain the Nature Planner. To accomplish this we carried out a great number of model runs in which we varied the model parameters. For this we estimated the uncertainty in the model parameters and draw many alternative parameter values based on the distribution of the possible parameter values. With these draws the model chain was run and the outcome was compared. When the draws of the parameter values are combined in a certain way (e.g. Monte Carlo) it is possible to estimate the uncertainty in the model results, and also to appoint the variability of the results to certain parameters or groups of parameters

We conducted an uncertainty analysis in which uncertainty in the soil and, groundwater table map was propagated through the models SMART2, SUMO2, P2E and MOVE4. Uncertainties about model parameters were taken into account as well. The models considered are all part of the Nature Planner model chain (Van der Hoek & Bakkenes, 2007). The sensitivity of the output for variation in the input maps for soil and vegetation of the Nature Planner was investigated earlier by Van der Hoek *et al.* (2006).

In this study, uncertainty is defined as the variance in the model output that can be ascribed to uncertainty in the model input parameters and input maps.

The following model outputs are investigated:
- pH (SMART2);
- N-availability (SMART2);
- Total biomass (SUMO2);
- Ellenberg value for acidity, Rellen (P2E);
- Ellenberg value for moisture,Fellen (P2E);
- Ellenberg value for Nitrogen, Nellen (P2E);
- Biodiversity index, i.e. predicted number of occurring plant species (MOVE4).

These outputs are investigated one by one, so each time only a single output variable y_k is considered.

The model input parameters can be distinguished into four distinct independent parameter groups:
- Soil parameters (including soil map, groundwater table and SMART2 parameters);
- Vegetation parameters (SUMO2);
- Regression parameters and model error to calculate Ellenberg indicator values (P2E);
- Regression parameters used in MOVE4 (not included in this analysis.

The parameters in each of these four groups are assumed to be independent of the parameters in the other groups, e.g. the SUMO2 parameters are assumed to be independent of the soil and P2E parameters. We assume that the vegetation parameters are independent from the soil parameters, e.g. parameters as minimum and maximum N content of the vegetation and maximum growth rate are assumed independent from soil type. This must be confused with the fact that these in the field realized values for these parameters are partly depending on the soil type present. This independence assumption, which is needed in order to estimate the uncertainty due to a group of parameters, has the following consequences:

a. Soil type, groundwater table and soil parameters are all in the same group, so it will not be possible to assess the effect of Soil Type independently of the effect of other soil parameters.
b. As the MOVE4 parameters are not independent of soil and vegetation, it is not possible to include a parameter group 'Vegetation Type'. Instead, the calculations will be performed separately for three vegetation types grassland, deciduous forest and heathland.

The uncertainty analysis then consists in determining which portion of the output variability can in principle be ascribed to each of these four groups of input parameters (note that the fourth group, MOVE4 parameters, were left out this analysis).

The uncertainty analysis is conducted by means of a Monte Carlo study. To this end, 500 sites are selected from the Dutch nature map (EHS) for each of grassland, forest and heathland, respectively. So in total we have 1500 sites. The 500 sites is a compromise between the amount of sites necessary to estimate the uncertainties and the maximum number of model runs that are possible. Then, using literature and expert judgements, a distribution is assumed for each parameter, such that the location and width of this distribution reflect the expected value and uncertainty associated with the parameter in question.

For the models SMART2 and SUMO2, the selection of the parameters was based on previous uncertainty analyses performed for these models (Finke *et al*. 1999, Kros *et al.* 1999, Kros *et al*. 2002, Wamelink 2008). For the model P2E, the mean and standard error of the transfer functions for pH to Rellen and mean spring water table (MSW) to Fellen were based on Wamelink *et al.* (2002). The statistical distribution for the parameter governing the translation of nitrogen availability to Nellen was specially designed for this project (see 7.4).

In this process, the sites remain fixed, only their characteristics (soil type, groundwater table, vegetation) are considered uncertain. Spatial correlation is taken into account. Details about the distributions assumed are given in Chapter 5 and 6 and Appendices 1 and 2.

Once statistical distributions for the parameters have been defined, the Monte Carlo aspect of the study consists of sampling, for each site, 15,000 random draws for each parameter, from these distributions. Descriptive statistics of the samples drawn are given in Chapter 8.

For the uncertainty analysis the 15,000 random draws are divided into five sets of 3000, and parts of Sets 2 - 5 are replaced by values from Set 1. See Chapter 8 for a fuller description and explanation.

15,000 Model runs are then performed for each of the 500 sites per vegetation type. The model chain was run from 1990 until 2030 for all 1500 sites and 15,000 draws per site.

Finally, an uncertainty analysis is performed, that is, the variation in the model outputs thus obtained is studied. Because of the way in which parts of Set 2 – 5 were overwritten with value of Set 1, it will be possible to ascribe fractions of the output variation to the groups of input parameters.

One final remark: because of technical problems, it was not possible to include the uncertainty of the model MOVE4 in the analyses. The model itself should be reprogrammed to make it possible to include calculations of the chances with uncertainty in the model parameters. The uncertainty in MOVE4 itself was therefore not included in the analysis, but MOVE4 results were used to estimate the overall uncertainty in the results caused by all previous steps.

3 Model Chain description

3.1 The Nature Planner

The Nature Planner (Bakkenes *et al.* 2002; Van der Hoek & Bakkenes, 2007) is in fact an interface linking the models and input maps and providing output on a nation-wide scale. Common applications of the Nature Planner are the yearly national inventories of the environmental quality for the Dutch government. They make up the core of the model and are described briefly below, Figure 1 shows an overview of the models and maps that are investigated in this study.

3.1.1 Soil map and water table map

The soil map is derived from the national soil-mapping project (De Vries *et al.*, 2003). The map was simplified for the application of SMART2 to seven soil types; SP: Sand Poor, SR: sand rich, SC: Sand Calcareous, PN: Peat Non-calcareous, CN: Clay Non-calcareous, CC: Clay Calcareous, LN: loess Non-calcareous. The original soil map has a 1:50000 scale. It was rasterized (downscaled) to the 250*250m grid size, where each grid cell was assumed to have just one soil type, being the dominant soil type for the specific grid. The soil map is assumed to be independent of the used time scale (decades).

The water table map is based on a Dutch nationwide inventory (De Vries *et al.*, 2003). The groundwater tables from the inventory are simplified to five categories for application in SMART2 (Kros *et al.* 1995). The groundwater table map was also rasterized to the 250*250m grid size used in this project. The groundwater table map was also assumed to be constant in time, though this is less certain than the soil map, although many groundwater tables in the Netherlands are managed, they may change when land use changes.

3.1.2 SMART2

SMART2 (Kros *et al.*, 1995, Kros, 2002) is a simple one-compartment soil acidification and nutrient cycling model that includes the major hydrological and biogeochemical processes in the vegetation, litter and mineral soil. Apart from pH, the model also predicts changes in aluminium (Al^{3+}), base cation (BC), nitrate (NO_3^-), phosphate ($H_2PO_4^-$) and sulphate (SO_4^{2-}) concentrations in the soil solution and solid phase characteristics depicting the acidification status, i.e. carbonate content, base saturation and readily available Al content. SMART2 is an extension of the dynamic soil acidification model SMART (De Vries *et al.* 1989). The major extensions in SMART2 are the inclusion of a nutrient cycle and an improved modelling of hydrology. The SMART2 model consists of a set of mass balance equations, describing the soil input-output relationships, and a set of equations describing the rate-limited and equilibrium soil processes.

The soil solution chemistry in SMART2 (Fig. 2) depends solely on the net element input from the atmosphere (the product of deposition and filtering factor) and groundwater (seepage), canopy interactions (foliar uptake, foliar exudation), geochemical interactions in the soil (CO_2 equilibrium, weathering of carbonates, silicates and/or Al-hydroxides, SO_4^{2-} sorption and cation exchange) and a complete nutrient cycle (litterfall, mineralization, root uptake, nitrification and denitrification).

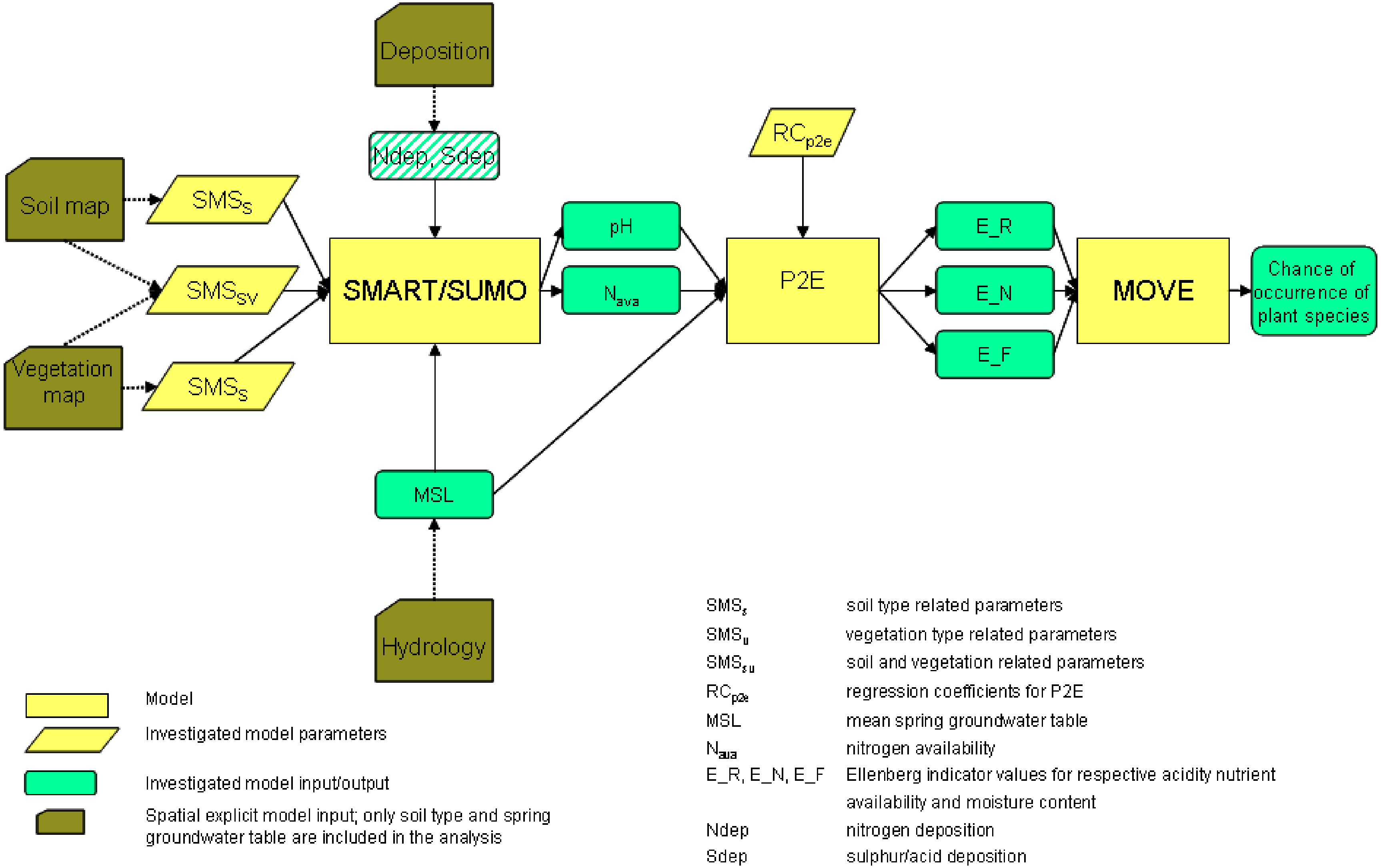
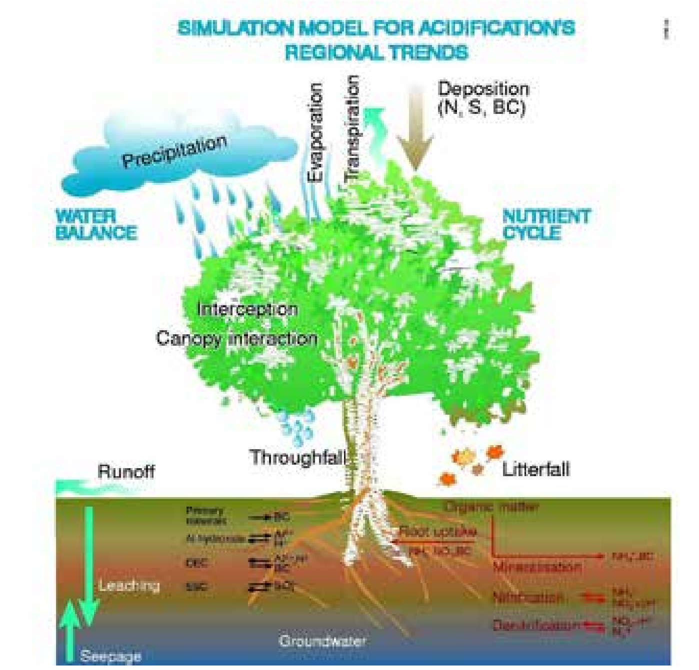


Fig. 1. Model chain investigated in this research. The models and maps make up part of the Nature Planner.

Fig. 2. The SMART2 model.



Processes that are not taken into account are: (i) N fixation and NH_4^+ adsorption, (ii) uptake, immobilization and reduction of SO_4^{2-}, (iii) complexation of Al^{3+} with OH^-, SO_4^{2-} and $RCOO^-$ and (iv) interaction between the soil solution and the vegetation. Growth of the vegetation and litterfall are modelled by a logistic growth function, which acts as a forcing function. Nutrient uptake is only limited when there is a shortage in the soil solution.

Soil interactions are either described by simple rate-limited (zero-order) reactions (e.g. uptake and silicate weathering) or by equilibrium reactions (e.g. carbonate and Al-hydroxide weathering and cation exchange). Influence of environmental factors such as pH on rate-limited reactions and rate-limitation of weathering and exchange reactions are ignored. Solute transport is described by assuming complete mixing of the element input within one homogeneous soil compartment with a constant density and a fixed depth (at least the root zone). Since SMART2 is a single layer soil model, neglecting vertical heterogeneity, it predicts the concentration of the soil water leaving the root zone. The annual water flux percolating from this layer is taken equal to the annual precipitation, which must be specified as model input. The time step of the model is one year, so seasonal variations are not considered. An uncertainty analysis of SMART2 was carried out by Kros *et al.* (2002).

Input data for the SMART2 application can be divided in system inputs and initial values of variables and parameters. System inputs are the atmospheric deposition, hydrology and vegetation development.

3.1.3 SUMO2

SUMO (Wamelink *et al.* 2009a,b) simulates biomass and nitrogen dynamics in five functional plant types: herbs and grasses, dwarf shrubs, shrubs, pioneer trees, and climax trees. Each functional type is assumed to consist of three organs: root, stem, and leaf. The time step of the model is one year. In each time step the biomass of the five functional types is computed, based on the biomass in the previous time step, biomass growth and death in the present time step, and removal of biomass by management. The growth is in turn calculated on the basis of an assumed maximum growth, which is reduced by nitrogen availability (provided by SMART2) and light interception. The dead biomass (litter with nitrogen content) is returned to the relevant pools in SMART2.

SUMO distinguishes six vegetation types (grassland, heathland, reedland, shrub vegetation, salt marsh and forest). In this research only the three main vegetation types in The Netherlands are included: grassland, heathland and forest. The model equations are parameterized for each combination of functional plant type and vegetation type. Much attention is given to the simulation of competition between the functional types. The competition for nutrients and light is assumed to be the driving force for succession. The initial vegetation type is given as input to the model.

For the functional types herbs/grasses, dwarf shrubs, and shrubs, SUMO simulates the total biomass of all species. For the functional types pioneer tree and climax tree the biomass of a specific tree species is simulated. Each species is given its own set of parameters. SUMO simulates the C and nutrient fluxes. The nutrients that become available through mineralization (simulated by SMART2) and atmospheric deposition is partitioned over the functional types and within each functional type over its organs, using fixed percentage distributions per functional type vegetation type combination. Nitrogen reallocation before litterfall is also simulated.

3.1.4 P2E

P2E is a conversion module, only consisting of three regression equations, which translates output from SMART2 and the groundwater table information to input for MOVE4. The nitrogen availability and pH, originating from SMART2 and the spring groundwater table are converted to Ellenberg indicator values for N, R and F, respectively. This conversion is regarded as the main source of uncertainty in the model chain (Schouwenberg *et al.* 2000; Wamelink & Van Dobben 2003). For the translation of N availability in Ellenberg N we used a new regression model based on expert knowledge (see Section 7.4). All three regression equations are simple linear regressions.

3.1.5 MOVE4

The MOVE4 statistical model is based on response curves for individual plant species (Van Adrichem *et al.* 2010). Curves have been estimated for over 900 plant species on the basis of about 100,000 vegetation relevés. The response values, expressed as the likelihood of a particular plant species to occur at a given combination of abiotic factors, are based on Ellenberg's indicator values (Ellenberg *et al.* 1991). The indicator values for moisture (F), acidity (R) are provided by the P2E module. The pH and nutrient availability are uncertain. They are based on the calculations of SMART2. MOVE4 also needs info on the salt content of the soil and the vegetation region and vegetation type (provided by SUMO2). A threshold value for the likelihood of a species being present is used to determine whether a species can actually occur. After this the number of species was summed. A response function per species is available for the different vegetation regions in The Netherlands. We applied the stand-alone version of MOVE4. This version was slightly changed to provide output necessary for the uncertainty analysis. The modifications do not influence the calculation or the scientific background of the model. MOVE4 calculates, besides the probability of occurrence of a species, also the standard error of the probability. This standard error cannot be used to estimate the uncertainty of the model MOVE4, since it is not based on the uncertainty of the model parameters themselves. For further explanation see Van Adrichem *et al.* (2010).

MOVE4 was run with three different species groups for the three different vegetation types, grassland, heathland and forest. The species list is given in Table 1. The species were selected to form a small but representative group for each vegetation type. It consists of common and rare species. The number of species for grassland is higher because the species richness is higher in grasslands compared to forests and dry heathlands in The Netherlands.

Table 1. Species used for the simulation in MOVE4 for grassland, heathland and forest. The given taxon number (TaxonNr) follows the MOVE4 code, The taxon code (TaxonCode) is according the CBS code, without p_.

Grassland			**Heathland**			**Forest**		
TaxonNr	Taxon Code	name	TaxonNr	Taxon Code	name	TaxonNr	Taxon Code	name
8	p_11	*Aegopodium podagraria*	42	p_61	*Antennaria dioica*	80	p_139	*Betula pubescens*
13	p_18	*Agrostis stolonifera*	81	p_140	*Betula pendula*	221	p_398	*Deschampsia flexuosa*
52	p_76	*Apium graveolens*	87	p_148	*Botrychium lunaria*	249	p_447	*Empetrum nigrum*
62	p_100	*Artemisia maritima*	107	p_186	*Calluna vulgaris*	284	p_513	*Fagus sylvatica*
77	p_135	*Bellis perennis*	154	p_266	*Carex trinervis*	293	p_530	*Rhamnus frangula*
100	p_174	*Calamagrostis epigejos*	213	p_379	*Cuscuta epithymum*	363	p_658	*Ilex aquifolium*
117	p_205	*Cardamine pratensis*	221	p_398	*Deschampsia flexuosa*	423	p_759	*Lonicera periclymenum*
156	p_269	*Carlina vulgaris*	265	p_473	*Erica tetralix*	428	p_766	*Luzula campestris*
171	p_298	*Cerastium semidecandrum*	293	p_530	*Rhamnus frangula*	464	p_832	*Molinia caerulea*
179	p_315	*Chenopodium polyspermum*	310	p_558	*Genista anglica*	503	p_909	*Oxalis acetosella*
188	p_330	*Cirsium acaule*	311	p_560	*Genista pilosa*	529	p_943	*Pinus sylvestris*
218	p_390	*Dactylis glomerata*	312	p_561	*Genista tinctoria*	590	p_1020	*Prunus serotina*
221	p_398	*Deschampsia flexuosa*	464	p_832	*Molinia caerulea*	598	p_1036	*Quercus petraea*
248	p_446	*Elymus repens*	515	p_924	*Pedicularis sylvatica*	599	p_1037	*Quercus robur*
279	p_492	*Euphorbia cyparissias*	544	p_963	*Polygala vulgaris*	651	p_1118	*Salix caprea*
299	p_542	*Galeopsis speciosa*	599	p_1037	*Quercus robur*	652	p_1119	*Salix cinerea*
305	p_549	*Galium saxatile*	662	p_1133	*Sambucus nigra*	662	p_1133	*Sambucus nigra*
313	p_562	*Gentianella amarella*	703	p_1199	*Danthonia decumbens*	836	p_1634	*Rubus fruticosus*
330	p_593	*Gymnadenia conopsea*	755	p_1284	*Thymus serpyllum*	778	p_1329	*Vaccinium myrtillus*
346	p_631	*Holcus lanatus*				779	p_1331	Vaccinium vitis-idaea
421	p_755	*Lolium multiflorum*						
422	p_756	*Lolium perenne*						
442	p_792	*Malva sylvestris*						
510	p_917	*Parapholis strigosa*						
518	p_928	*Peucedanum carvifolia*						
522	p_932	*Phleum pratense subsp. pratense*						
537	p_952	*Poa annua*						

Grassland			Heathland			Forest		
TaxonNr	Taxon Code	name	TaxonNr	Taxon Code	name	TaxonNr	Taxon Code	name
541	p_959	*Poa trivialis*						
584	p_1013	*Potentilla verna*						
612	p_1056	*Ranunculus repens*						
632	p_1093	*Rumex acetosa*						
670	p_1141	*Satureja acinos*						
703	p_1199	*Danthonia decumbens*						
725	p_1235	*Spergula morisonii*						
750	p_1268	*Teesdalia nudicaulis*						
775	p_1323	*Utricularia intermedia*						
786	p_1345	*Veronica agrestis*						
796	p_1358	*Veronica persica*						
824	p_1411	*Phleum pratense subsp. bertolonii*						
859	p_1921	*Festuca rubra*						

3.2 Deposition scenario and model runs

The model simulations were run for the period 1980 – 2030 with output in 2030.

The National Institute of Public Health and the Environment (RIVM) calculated deposition in response to different emission variants in the Netherlands in order to get insight into the coherence between emission, quality of the environmental quality and health risks to formulate new goals for deposition reduction (Beck *et al.*, 2001). We evaluated the base variant of the different deposition scenarios that were generated by RIVM with a period from 1980 to 2030. A strong deposition reduction is assumed in this scenario (Fig. 3). From 1980 till 1990, the N-deposition is almost constant, but SO_x-deposition decreases strongly. The NH_3-deposition decreases almost linearly from 1800 mol ha^{-1} y^{-1} to 300 mol ha^{-1} y^{-1} between 1990 and 2030. The NO_x-deposition decreases in the same period from 800 to 100 ha^{-1} y^{-1}. The SO_x-deposition decreases between 1990 and 1997 with 50% and in the latter period until 2030 with almost the remaining 50%, finally from 1500 mol ha^{-1} y^{-1} in 1980 to 70 mol ha^{-1} y^{-1} in 2030.

The whole model chain was run for all sites. For grassland the model was run with mowing once a year and grazing with a varying density of cows, depending on the available amount of food available for the cows. Model settings were kept constant during the runs. Model runs were performed with SMART2 version 3.6.1 (rev 32), SUMO2 version 3.2 (rev 30) and MOVE4. The version of P2E is described further on. Rainfall and temperature were kept constant, as was the CO_2 concentration. Although changes in these parameters may influence the model results itself tremendously, it is unknown how large the uncertainty in the model results will change. However, we expect that variation in the input itself will not affect the uncertainty itself to a great extent, including the uncertainty in these parameters may though.

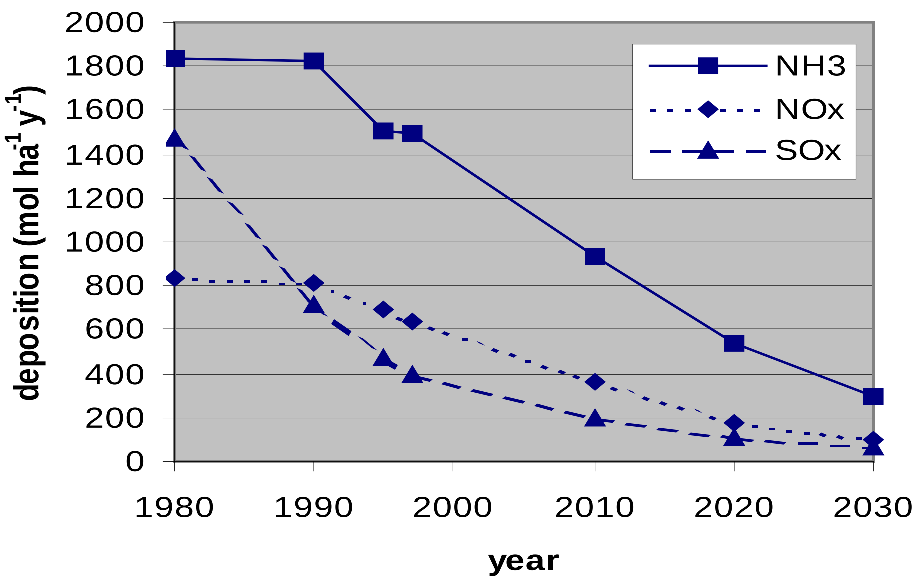


Fig. 3. Evaluated deposition scenario for ammonium, oxidized nitrogen compounds and oxidized sulphur compounds in the air.

4 Selection of sites and simulation of soil type and water table

4.1 Selection of simulation locations

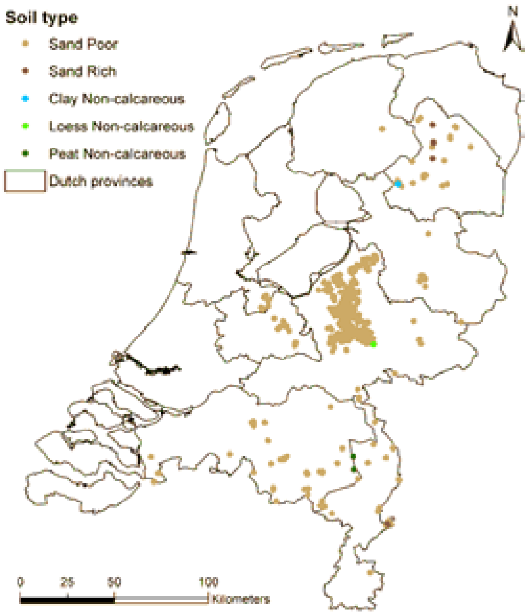
Locations for simulation of model output were selected from the sites of a 250 m x 250 m grid. The grid sites were stratified according to nature target types (for nature target types see Wamelink *et al.* 2005). The number of simulation sites was 500 for each of the three vegetation types grassland, heathland and forest. The number of simulation sites within a stratum was proportional to its area, with a minimum of two sites. The simulation sites within a stratum were selected by simple random sampling. Figure 4 shows the location of the simulation sites in grassland, heathland and forest.

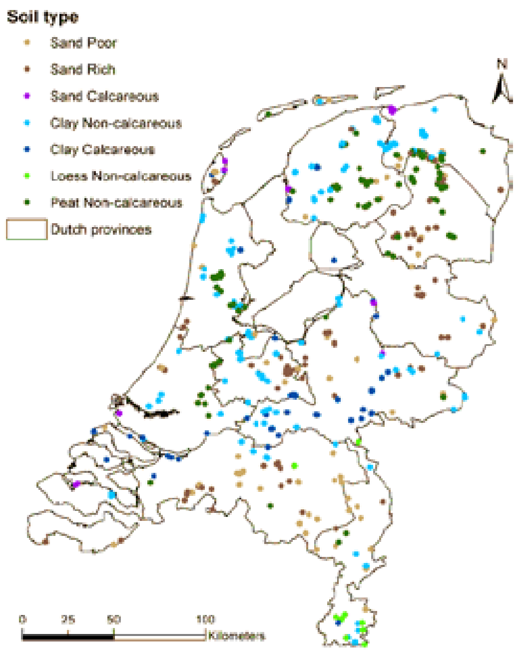
Fig. 4. Location of the 500 selected sites for grassland (left), heathland (right) and forest (bottom).

4.2 Simulation of soil type

The model SMART2 requires input maps of soil type and the Mean Spring Water Table. These two maps are regarded as uncertain and are used in the uncertainty analysis.

SMART distinguishes seven soil types. These soil types have been simulated by Bayesian Maximum Entropy as described by Brus *et al.* (2008). In total 8369 observations in the Soil Information System of Alterra were used as 'hard' observations of the seven soil types (De Vries *et al.* 2003). The soil type at the simulation sites as depicted on the soil map of the Netherlands 1:50.000 was used as 'soft' information. Figure 5 shows three simulations of soil types at the 500 sites.





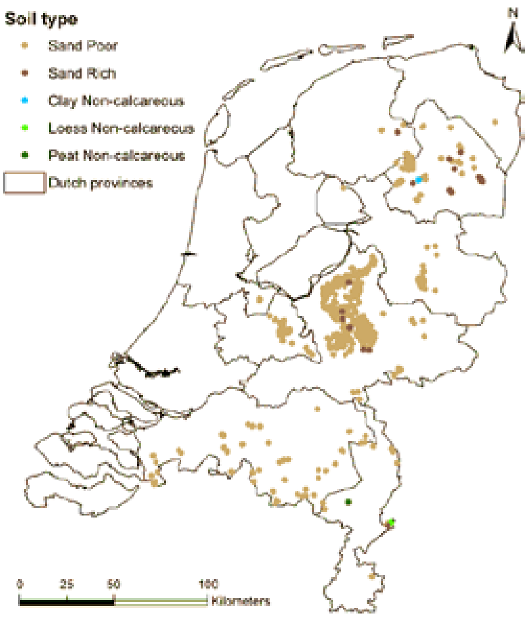


Figure 5. Three of the 15,000 simulations of the soil types at 500 sites for grassland (left), heathland (right) and forest (bottom).

The simulation of the most frequent soil type for grassland is given in Figure 6. All seven soil types occur as the most frequent one, on different locations. As may be expected Loess occurs in the south of The Netherlands. Peat is mostly frequently present in the western and northern part (former lowland peat, now mostly mixed with clay). Clay soils can mostly frequently be found in the West and North, but also in the river estuaries. Sandy soils are frequently simulated for the eastern higher part of the Netherlands and in the dunes. All this is as expected. However, for some of the sites also different soil types are simulated. The variation in soil type is expressed as the entropy for the sites, as a measure for the uncertainty (see Brus *et al.* 2008, Fig. 6). For many sites only one soil type is drawn; the entropy is almost zero, so it is for these sites clear what the dominant soil type is, where for other sites the uncertainty is bigger. The blue dots indicate that in some of the 15,000 drawings another soil type is drawn than the one according to the soil map. The entropy is given on a scale from 0 to 1. A simple example with two probabilities (i.e. two soil types) for for instance with probabilities (0.05, 0.95) the entropy is 0.20, for (0.10, 0.90) it is 0.33 and for (0.50, 0.50) the entropy is 0.69. Only for very few sites the entropy value is very high indicating that the soil type is very uncertain, with an entropy higher than 0.8. The average entropy for the soil type for the 500 sites is 0.25, which is relatively small. This indicates that on average the uncertainty in the soil type is not very high.

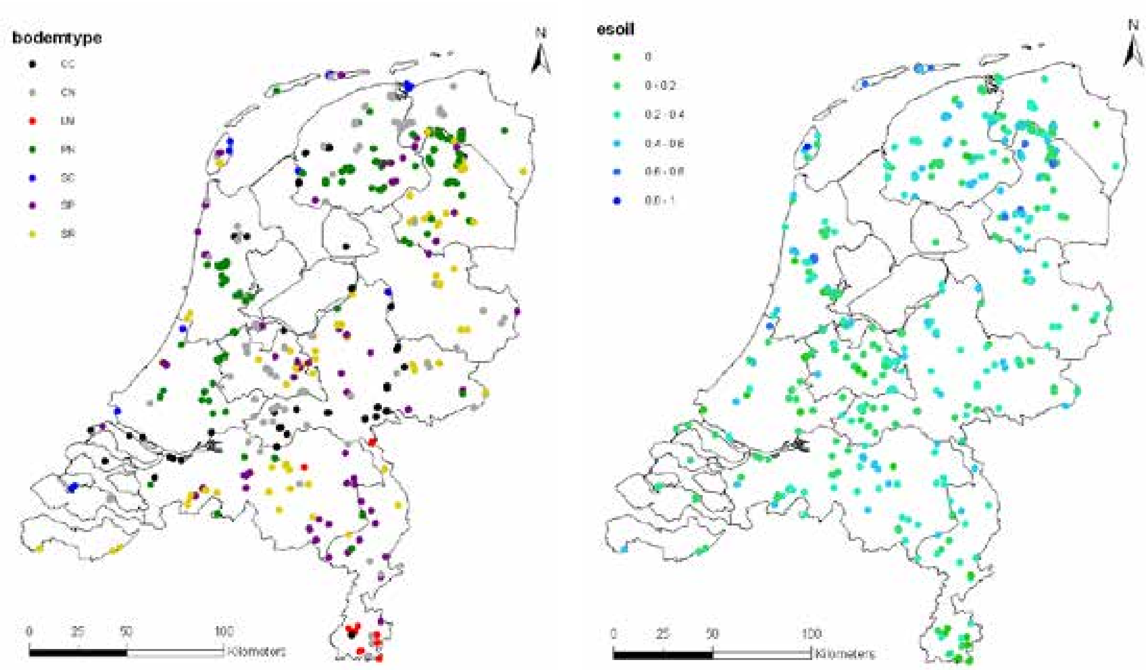


Fig.6. Most frequently drawn soil type (left) and the average entropy (right) per site for grassland soils. The most frequent type and average entropy are based on 3000 simulations of the soil type for each site. The higher the entropy, the higher the variation and thus the uncertainty in the soil type is.

The main soil type simulated for heathland sites is poor sand (Fig. 7). For some sites this is rich sand while the other soil types are almost nowhere dominant. This is as could be expected since in The Netherlands most heathlands are situated on sandy soils with nutrient poor circumstances. For many sites the entropy (the uncertainty) in the soil type is rather low, for most sites it is almost absent and only for a few sites it is substantial (Fig. 7). This implies that the soil type for (inland) heathland is not a large source of uncertainty.

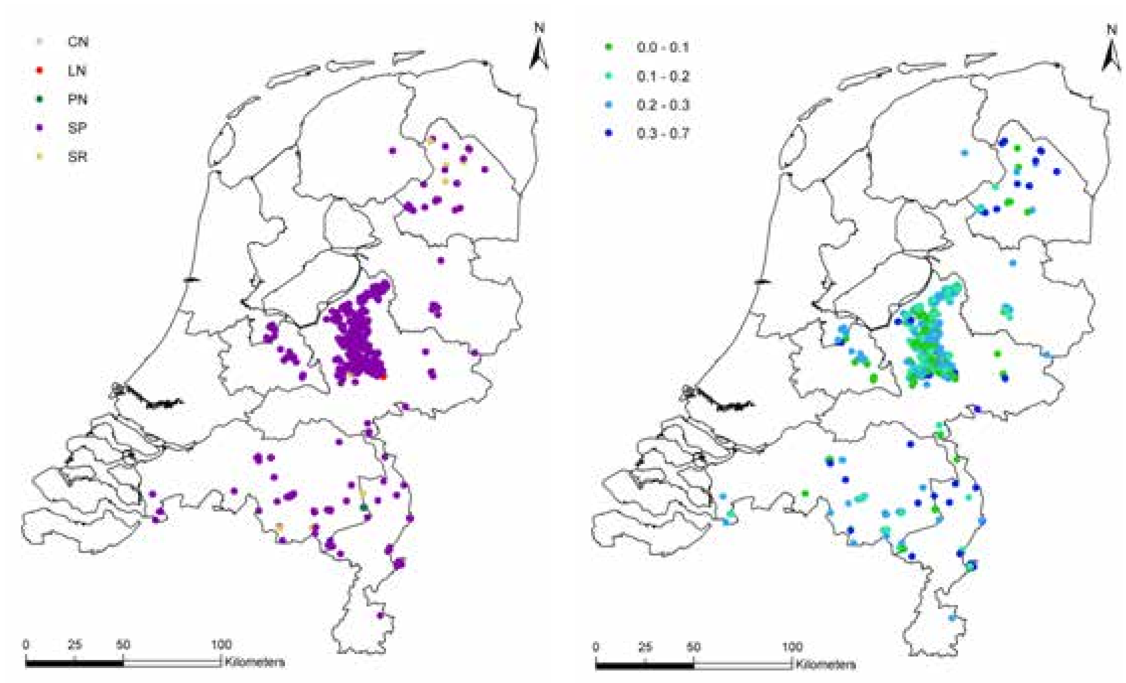


Fig.7. Most frequently drawn soil type (left) and the average entropy (right) per site for heathland soils. The most frequent type and average entropy are based on 3000 simulations of the soil type for each site. The higher the entropy, the higher the variation and thus the uncertainty in the soil type is.

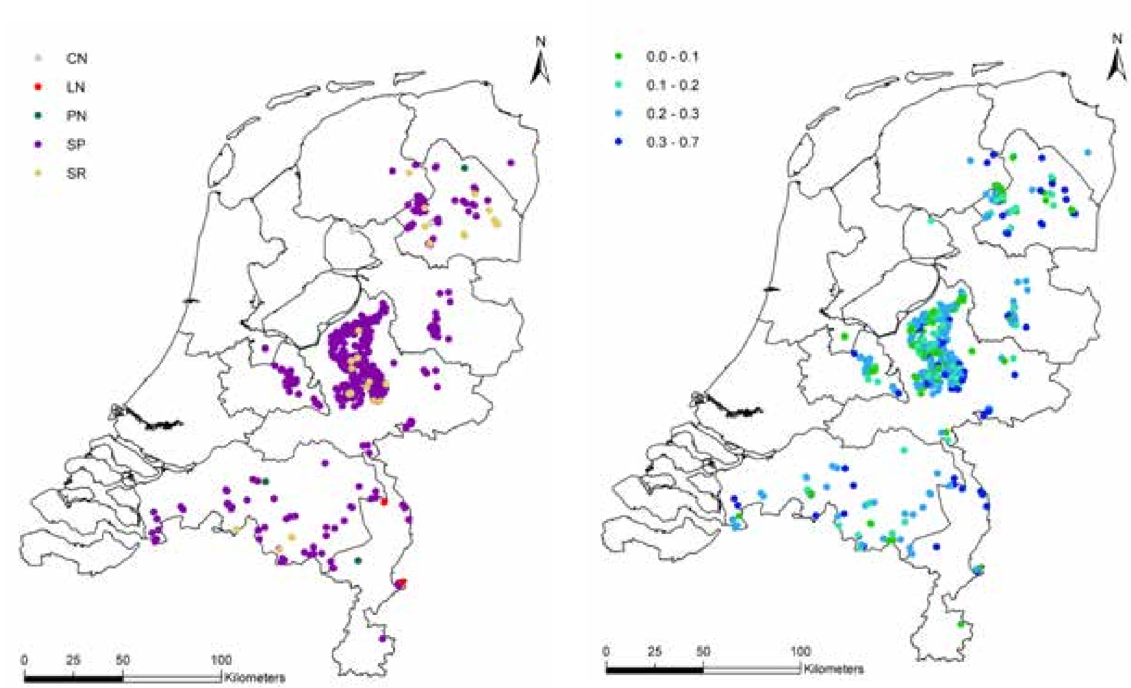


Fig.8. Most frequently drawn soil type (left) and the average entropy (right) per site for forest soils. The most frequent type and average entropy are based on 3000 simulations of the soil type for each site. The higher the entropy, the higher the variation and thus the uncertainty in the soil type is.

For most of the forest sites poor sand is on average the dominant simulated soil type followed by rich sand. As for heathland the other soil types are almost absent (Fig. 8). The entropy (uncertainty) in the simulated soil type is relative low with most of the values smaller than 0.3. Large uncertainties occur all over The Netherlands and do not seem to be correlated with a soil type.

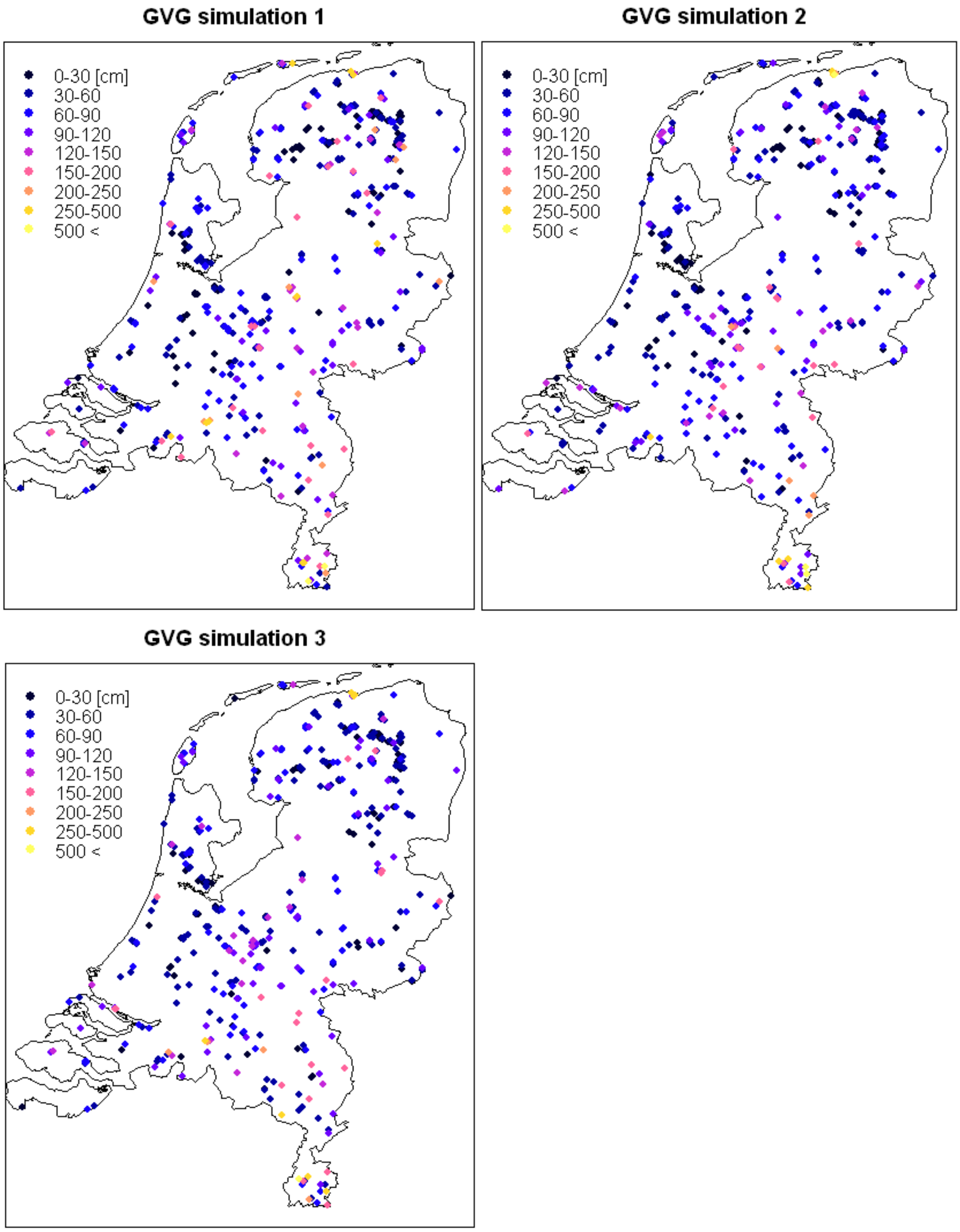


Fig. 9. Three simulations of the spring groundwater table (GVG) for the 500 grassland sites

4.3 Simulation of Mean Spring Water table

To simulate Mean Spring Water table (MSW) and the distribution of the uncertainty, first MSW at the 8369 locations with hard observations of soil type was computed from the observed Mean Highest Water table (MHW) and Mean Lowest Water table (MLW) at these locations (De Vries *et al.* 2003):

$$MSW = 5.4 + 0.38 * MHW + 0.19 * MLW$$

The histogram of MSW showed strong positive skewness, and therefore MSW was transformed by taking natural logs. Boxplots of MSW per soil type showed differences in mean and variances between soil types. Therefore, log-transformed values were standardized, i.e., the soil-type average was subtracted and the result divided by the soil-type standard deviation. Standardized, log-transformed MSW-values were simulated by (conditional) sequential simulation using a simple kriging model (Goovaerts *et al*., 1997), and the simulated values at the selected sites were back transformed. Figure 9 shows three simulations of MSW at the 500 sites.

5 Distributions of SMART2 inputs

As well as soil and water maps, SMART2 also needs many soil parameters as input. Default values are given for the seven soil types. Nine of the most sensitive and uncertain parameters in SMART2, based on expert judgement, were considered uncertain in this study: initial C/N, content of aluminium in secondary Al compounds in the soil (Alox), dissolution constant for Al-hydroxide (KAlox), selectivity constant for H/BC2 exchange (KHBc), selectivity constant for Al/BC2 exchange (KAlBc), initial base saturation (bsat_0), cation exchange capacity (CEC) and weathering flux of base cation X (Na, BC2, as Na_we and BC2_we). Summary statistics for these nine soil characteristics, derived from a Dutch forest inventory (De Vries *et al.* 1989), are given in Fig 10. For two of the nine soil parameters no observations were available so that parameters of the marginal probability distributions were chosen using expert judgment. The used distributions are given in Appendix 1. Minima and maxima do not refer to the observations but are absolute minima and maxima that each soil parameter must satisfy to be physically plausible.

The nine soil parameters vary in space and may thus take on different values at different locations, even when locations have the same soil type. Their values depend on soil type and are spatially correlated, because the values of the soil parameters at two locations tend to be similar when the locations have the same soil type and/or when the distance between the locations is small. Moreover, the soil parameters are also cross-correlated. The uncertainty model of the nine spatially distributed soil parameters must take all this into account and hence the geostatistical model to be used and the associated stochastic simulation method are not straightforward.

The geostatistical model used for each of the nine soil parameters is given by

$$Z(x) = m(x) + s(x) * e(x)$$

where Z(x) is the soil parameter at location x, m(x) the mean and s(x) the standard deviation, which both depend on soil type and whose values are given in Appendix 1. The stochastic residual e(x) was taken as a zero-mean, unit-variance, second-order stationary normally distributed random field, which is fully characterized by a semivariogram. Note that it was assumed that e(x) is independent of soil type. The variograms of the first seven soil parameters were fitted using the same data that were used to compute the summary statistics. Cross-correlations were modelled using cross-variograms. To ensure positive-definiteness, the linear model of coregionalization was employed (Goovaerts *et al.* 1997).

The semi- and cross-variograms are presented in Fig. 11. The semivariograms and cross-variogram of the standardized BC2_we and Na_we were defined using expert judgement. The nugget to sill ratio was taken as 0.30 for BC2_we and 0.55 for Na_we, whereas the variogram range was taken as 100 km in both cases. The cross-correlation of the two variables was taken as - 0.2, whereas the correlations with the other seven soil parameters were assigned a zero value, based on expert judgement.

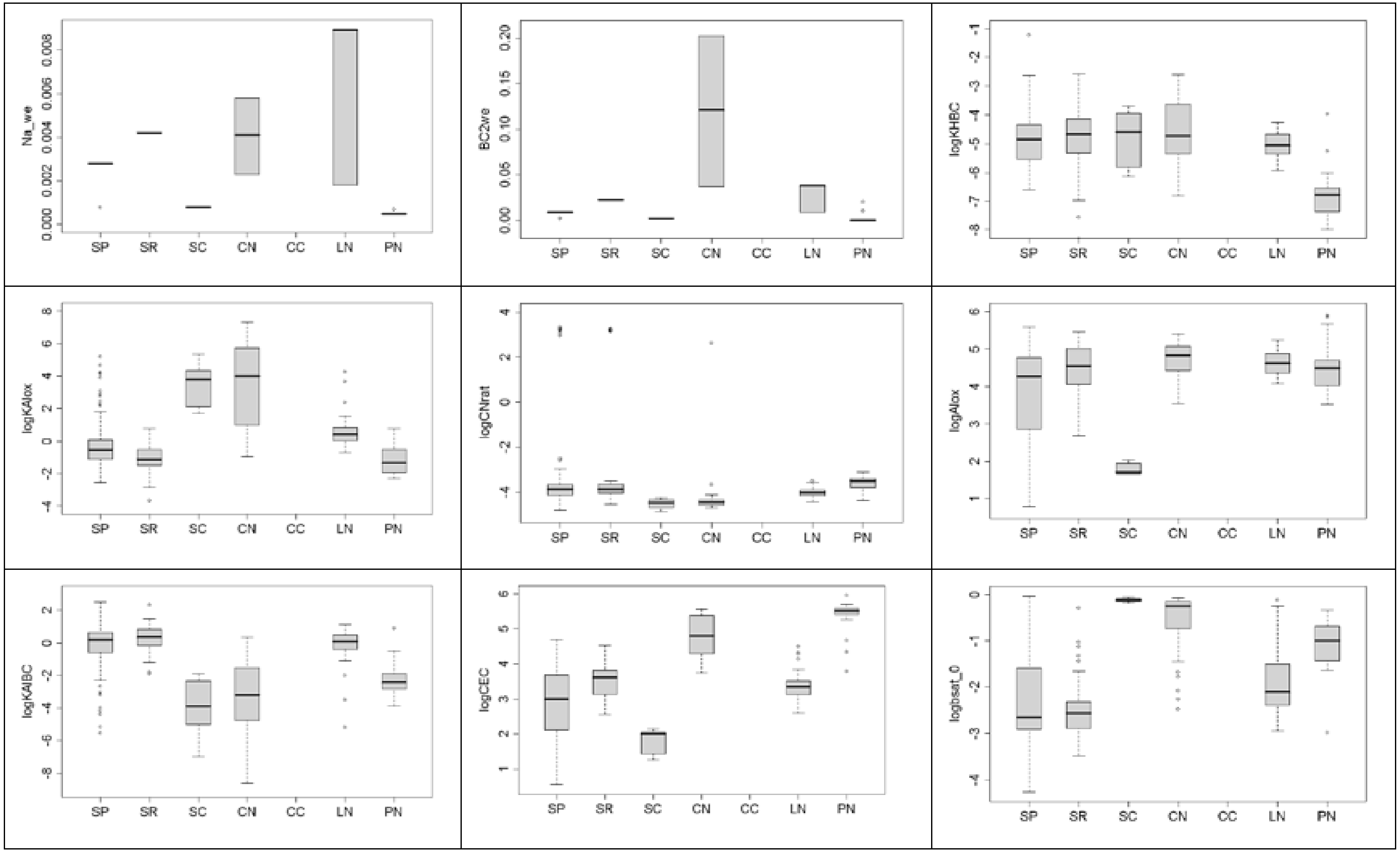


Fig 10. Box plots for the 300 forest plots of the nine SMART2 parameters used for the parameter estimation. The nation-wide values based on these are given in Appendix 1. With SP: sand poor, SR: sand rich, SC: sand calcareous, CN, clay neutral, CC: clay calcareous, LN: loss neutral, PN: peat neutral. The box plots present the median (bold horizontal line), the first and third quartiles (bottom and top of grey box), and the sample minimum and maximum. The dots represent samples that are considered outliers.

Geostatistical stochastic co-simulation was used to generate realizations from the nine soil parameters at the 500 sampling locations per vegetation type. Conditional simulation was used to exploit the information contained in the available data. Since soil type has an important effect on the probability distribution of the soil parameters and is uncertain as well, a hierarchical approach was used. Each of the soil type realizations simulated using Bayesian Maximum Entropy (see above) was used as input to simulate the additional soil parameters. Thus, the differences between simulated soil parameters both include differences in soil type as well as differences in soil parameters given soil type. In total, 15,000 simulations were generated.

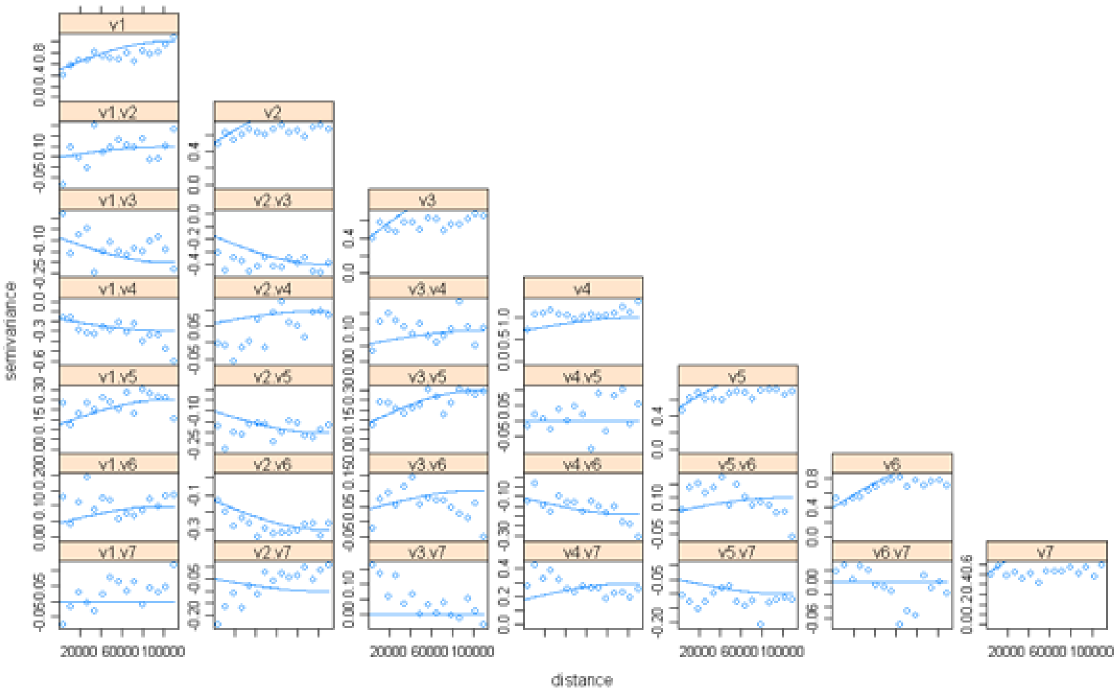


Figure 11. Semivariograms and cross-variograms of the first seven standardised soil parameters.

6 Distributions for SUMO2 inputs

From the model SUMO2 the nine most important parameters were selected: initial biomass, maximum growth rate, minimum and maximum nitrogen content, biomass distribution over the organs, light interception, organ death, number of grazers (cows) and the biomass eaten by cows (see Appendix 2 for the values and conditions; the correlation matrices are given in Appendix 3, see also Wamelink 2008). These were selected based on an earlier uncertainty analysis (Wamelink 2008) and expert knowledge. For two of the selected parameters much data are available and the average values and uncertainties can be calculated (minimum and maximum N content), all others are almost totally based on expert knowledge (e.g. maximum growth speed and light interception by leaves) and consequently the uncertainty was estimated based on expert knowledge too. Since SUMO2 simulates the vegetation processes for five functional types and three organs, parameter values are given per functional type or functional type organ combination. The number of grazers and the amount of biomass they eat in a year has a one to one relation. For each parameter the correlations between the values per functional type or functional type organ combination are used for the drawing of the 15,000 parameter values. The used procedure was similar to the procedure used for the simulation of the soil parameters.

7 Distributions for P2E regression parameters

7.1 Ellenberg equations: general

P2E consists of three linear equations for the conversion of the acidity (pH of the top soil, 0-30cm), groundwater table (MSG) and nitrogen availability (of the top soil) parameters to Ellenberg numbers (E_R; acidity, E_F; moisture and E_N; nutrient availability):

$$1: \quad E_R = a_R + b_R * \mathrm{pH} + e_R \,.$$

$$2: \quad E_F = a_F + b_F * \mathrm{MSG} + e_F \,.$$

$$3: \quad E_N = a_N + b_N * \mathrm{Nav} + e_N \,.$$

This chapter explains how the uncertainty in the regression coefficients and the variance of the error term are modeled.

Each equation will be dealt with in a separate subsection. All subsections contain the following:

- The first part describes how the parameters of the pertaining linear equation are estimated. These parameters are: the coefficients a and b, their standard errors and correlations, and the variance of the error term e.

The values thus obtained will be used as the parameters of a multivariate normal distribution. From this distribution a sample of 15,000 'observations' was drawn.

- The last part of each section gives some results showing the extent to which the moments of the generated sample match the corresponding characteristics of the distribution that was used to generate them.

For the P2E parameters the spatial correlation is assumed to be perfect, i.e. the same set of 15,000 simulated P2E values will be used for all 500 locations per vegetation type, i.e. for grassland, heathland and forest. We assume that the P2E regression equations are nationwide the same and that the uncertainty in them is also the same everywhere. Unpublished research for both The Netherlands and Europe seems to confirm this assumption. However, this was not further investigated and we did not do any test what the consequences would be if the spatial correlation would be imperfect.

7.2 Ellenberg R

7.2.1 Grassland

The coefficients for the Ellenberg R equation were estimated from a sample of 2762 observations on pH and E_R (Fig. 12). The values for E_R were estimated based on the vegetation composition at the location where pH was measured (see Wamelink *et al.* 2002). The regression is only based on data obtained from grassland sites.

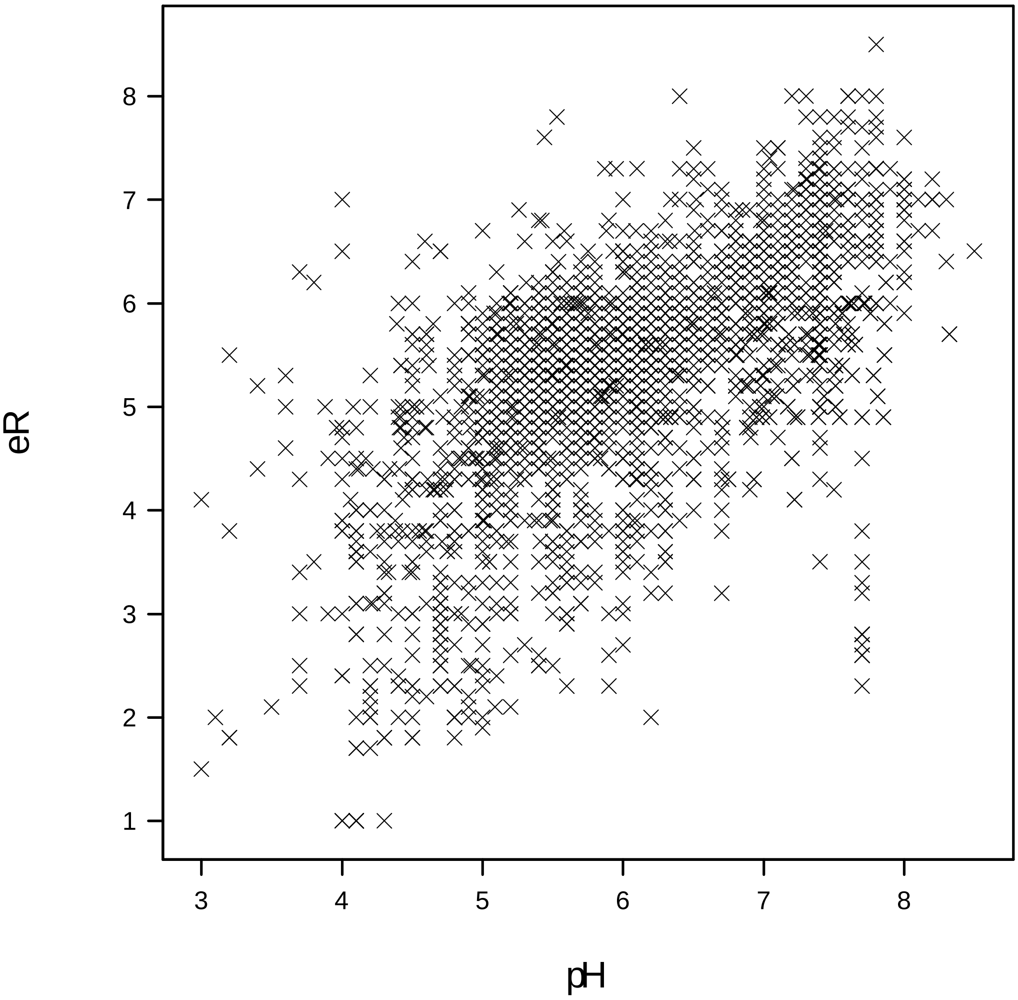


Fig. 12. Scatter plot of measured soil pH against estimated Ellenberg indicator value for acidity (eR) for grassland.

From these data, the following coefficients were estimated for the conversion of pH into an Ellenberg R number:

$$E_R = a_R + b_R \text{*pH} + e_R = 1.2669 + 0.6732 * \text{pH} + e_R \,.$$

The standard errors for a_R and b_R are 0.105 and 0.017 respectively; the residual standard error is 0.858; and the correlation between a_R and b_R is -0.988. Hence, the parameters of the assumed multivariate distribution assumed for the coefficients $[a_R, b_R, e_R]$ are given by:

```
VARCOV MATRIX Ellenberg R
                    aR          bR          eR
        aR    0.011010
        bR   -0.001788    0.000298
        eR    0.000000    0.000000    0.736164
     MEANS    1.266900    0.673200    0.000000
       SDS    0.104930    0.017250    0.858000
```

The covariance between a_R and b_R is obtained from the correlation and the variances.

The parameter values for the uncertainty analysis were generated in batches of 3000. Generating the first 3000 samples from this distribution resulted in the following sample values for the mean, variance and correlation:

```
  Means and variances of samples
  ------------------------------
Mean[aR]    Mean[bR]    Mean[eR]
  1.269      0.6729    0.002692

 Var[aR]     Var[bR]     Var[eR]
0.01134   0.0003060      0.7150

  Correlations between sampled values
  -----------------------------------
      aR    1.000
      bR   -0.989    1.000
      eR   -0.016    0.019    1.000
               aR       bR       eR
```

These values agree nicely to the parameters that were used to generate the sample. Values in the other batches were similar.

7.2.2 Heathland

The coefficients for the Ellenberg R equation were estimated from a sample of 317 observations on pH and E_R (Fig. 13). The values for E_R were estimated based on the vegetation composition at the site/point where the pH was measured (see Wamelink *et al.* 2002). The regression is only based on data obtained from heathland sites.

From these data, the following coefficients were estimated for the conversion of pH into an Ellenberg R number:

$$E_R = - 0.0424 + 0.5492 * \text{pH} + e_R.$$

The standard errors for a_R and b_R are 0.2691 and 0.0583 respectively; the residual standard error is 0.658 and the correlation between a_R and b_R is -0.988. Hence, the parameters of the assumed multivariate distribution assumed for the coefficients $[a_R, b_R, e_R]$ are given by:

```
VARCOV MATRIX Ellenberg R
              aR         bR          eR
      aR      0.07243
      bR      - 0.01549 0.00340
      eR      0.000000  0.00000     0.811
   MEANS      -0.424    0.5492      0.000
     SDS      0.2691    0.0583      0.658
```

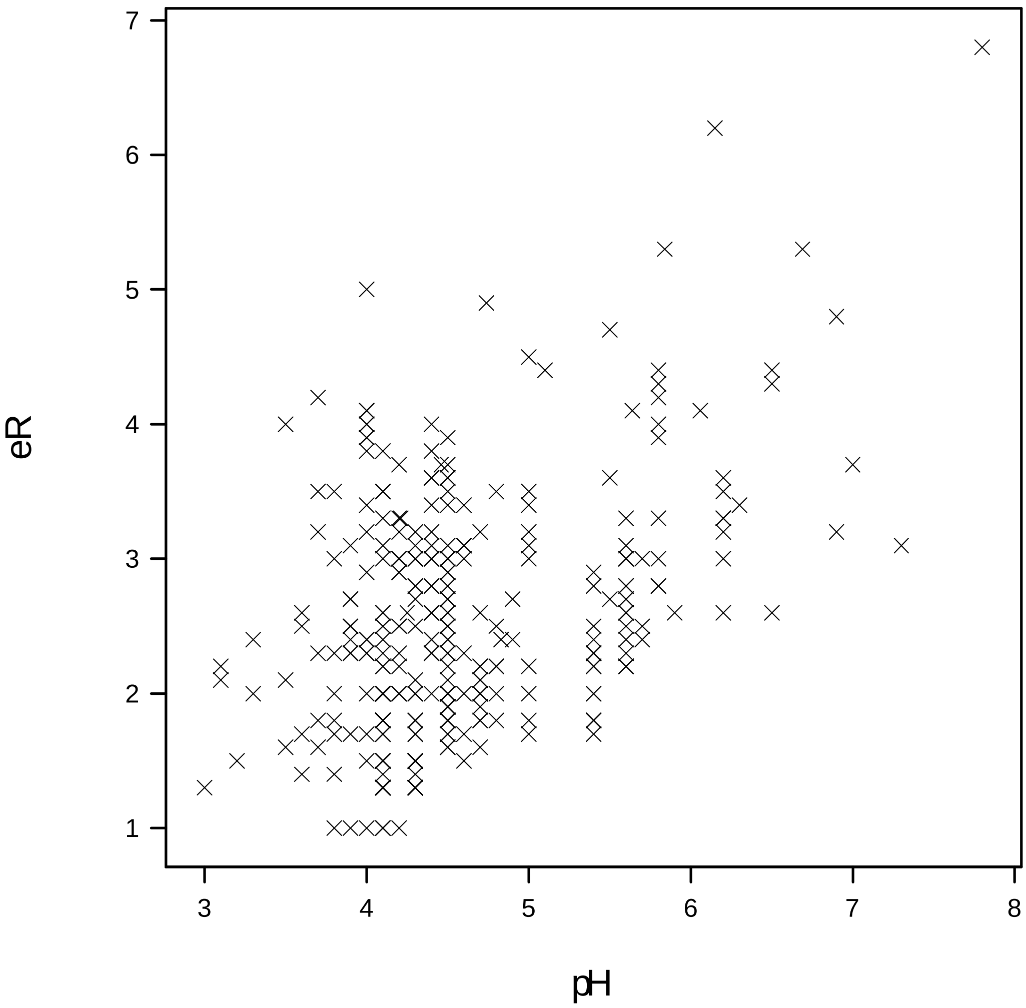


Fig. 13. Scatter plot of measured soil pH against estimated Ellenberg indicator value for acidity (eR) for heathland.

7.2.3 Forest

The coefficients for the Ellenberg R equation were estimated from a sample of 416 observations on pH and E_R (Fig. 14). The values for E_R were estimated based on the vegetation composition at the point the pH was measured (see Wamelink *et al.* 2002). The regression is only based on data obtained from forest sites.

From these data, the following coefficients were estimated for the conversion of pH into an Ellenberg R number:

E_R = - 0.0424 + 0.5492 * pH + e_R.

The standard errors for a_R and b_R are 0.211 and 0.042 respectively; the residual standard error is 1.145; and the correlation between a_R and b_R is -0.968. Hence, the parameters of the assumed multivariate distribution assumed for the coefficients $[a_R, b_R, e_R]$ are given by:

	aR	bR	eR
aR	0.04464		
bR	- 0.00861	0.00177	
eR	0.00000	0.0000	1.07
MEANS	1.757	0.2113	0.000
SDS	0.2113	0.0421	1.145

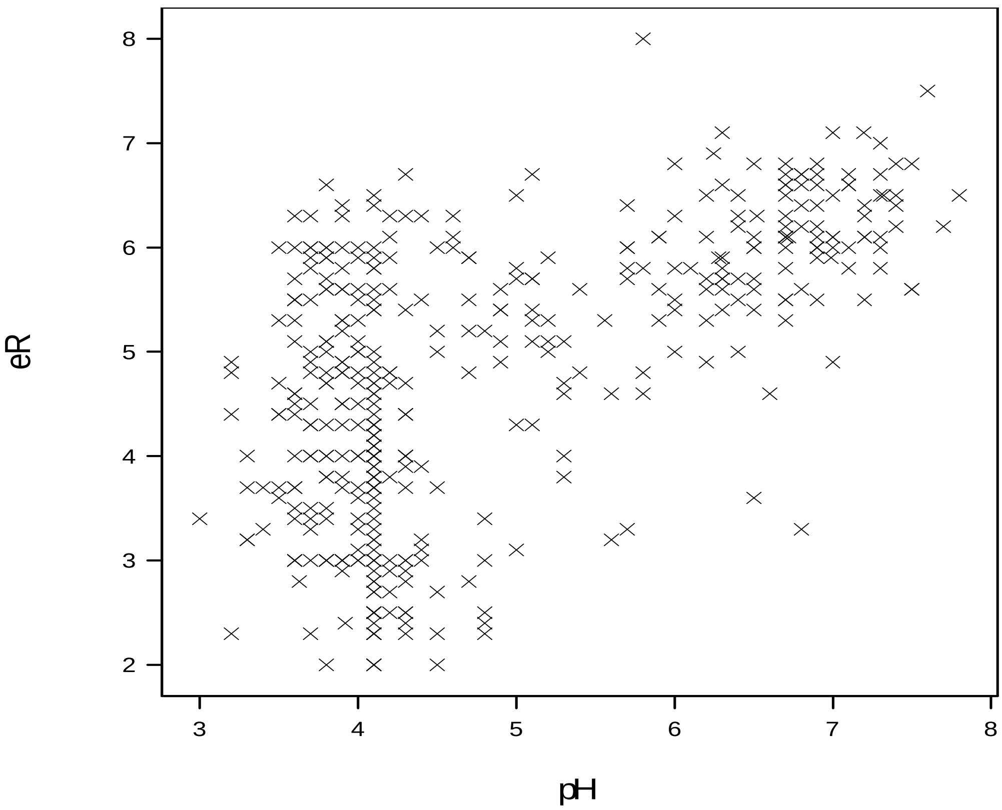


Fig. 14. Relation between measured soil pH and estimated Ellenberg indicator value for acidity (eR) for forest.

7.3 Ellenberg F, Grassland, heathland and forest

The coefficients for the Ellenberg F equation were estimated from a sample of 1536 observations on mean spring groundwater level and EF (Fig. 15). The regression is based on data obtained from grassland, heathland and forest sites. No separate regression equations for the three vegetation types were used, because of lack of data. Another problem is that for heathland there is no strong significant relation present. The regressions for forest and grassland are more or less the same.

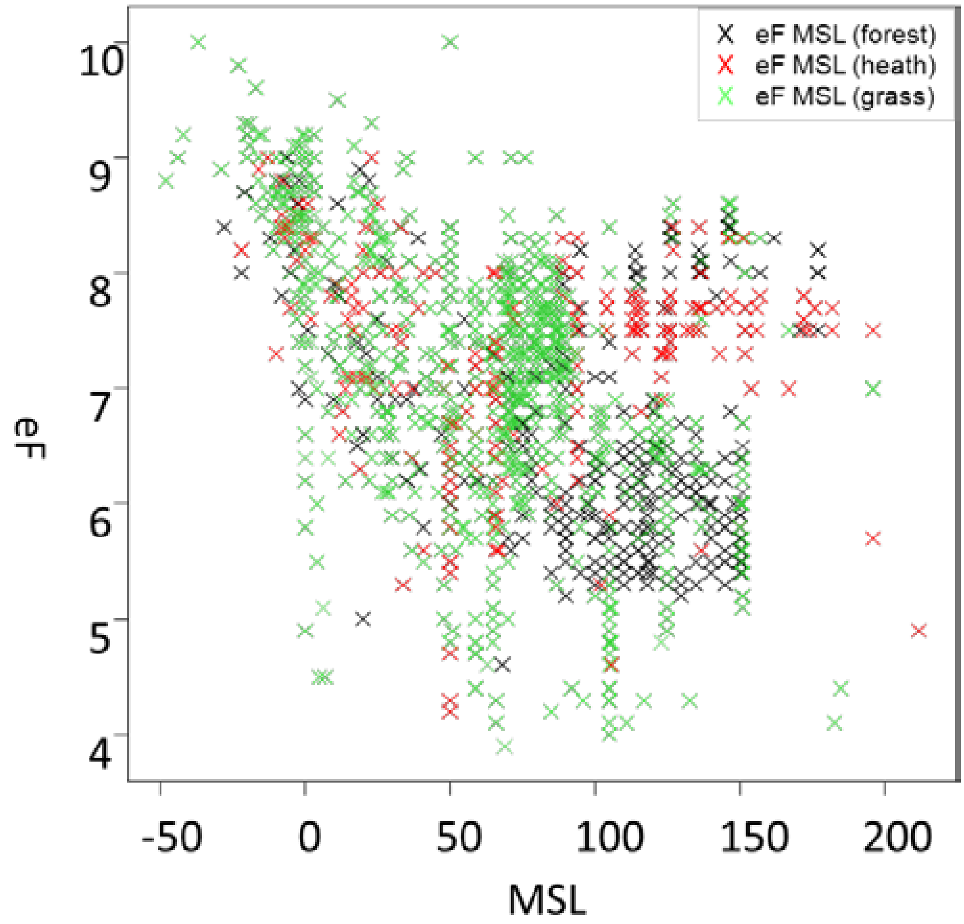


Fig.15. Scatter plot of the mean spring groundwater table (MSL) against the Ellenberg indicator value for moisture (eF), with in green grassland data, in red heathland data and in black forest data.

The relation between E_F and MSW was assumed to be linear. From the data, the following coefficients were estimated for the conversion of MSW into an Ellenberg F number (E_F):

$$E_F = a_F + b_F * MSW + e_F = 7.671 - 0.009 * MSW + e_F$$

The standard errors for a_F and b_F are 0.03792 and 0.00042 respectively; the residual standard error is 1.02; and the correlation between a_F and b_F is -0.848. As, for the uncertainty analysis for pH, the coefficients $[a_F, b_F, e_F]$ are again assumed to follow a multivariate normal distribution, the parameters of this distribution are now given by:

```
          VARCOV MATRIX Ellenberg F
                 aF           bF           eF
     aF    0.0014379
     bF   -0.0000135    0.0000002
     eF    0.0000000    0.0000000    1.0200000

  MEANS    7.671000    -0.009000     0.000000
    SDS    0.037920     0.000420     1.020000
```

Generating the first 3000 samples from this distribution resulted in the following sample values for the mean, variance and correlation:

```
Means and variances of samples
------------------------------
     Mean[aF]    Mean[bF]    Mean[eF]
       7.898    -0.01200    -0.03347

      Var[aF]      Var[bF]     Var[eF]
    0.002197 0.0000003626       1.077

Correlations between sampled values
-----------------------------------
          aF    1.000
          bF   -0.830    1.000
          eF    0.006   -0.004    1.000
                   aF       bF       eF
```

As in the case of Ellenberg R, these values agree with the parameters that were used to generate the sample.

7.4 Ellenberg N

For the regression of N-availability with Ellenberg N no distinction was made between vegetation types. Insufficient data are available to base three different regressions for the separate vegetation types on. That is why we decided to use just one translation function.

A priori, an expert judgment was made for the standard errors of a_N and b_N : these were thought to be 0.4 and 0.2, respectively. The residual variance was thought to be 0.8^2 = 0.64.

SMART2 was used to predict nitrogen availability for 145 sites for which also an Ellenberg N indicator value was available. Figure 16 shows the relationship between the thus obtained nitrogen availability and Ellenberg N. These data were considered inadequate for fitting a regression line.

Instead, the 145 pairs of values on N availability and Ellenberg-N values were taken, and the minimum and maximum value for both Ellenberg-N and N-availability were obtained for the whole set, where both values are not obtained from the same pair. The minimum nitrogen availability was then combined with the minimum Ellenberg indicator value and the maximum nitrogen availability was combined with the maximum Ellenberg value. We assumed that there is a linear relationship between the simulated nitrogen availability and Ellenberg-N. Furthermore, we assumed that a low nitrogen availability corresponds with a low Ellenberg-N score and a high nitrogen availability with a high Ellenberg-N score. Thus, a straight line was calculated as to go through the two points mentioned above.

Using the coefficients of this line, predicted Ellenberg-N values were sampled for the N-availabilities in the sample. The difference between these predictions and the observed N-availabilities were considered as residuals, and the sum of squared residuals was used to establish standard errors and covariances for a_N and b_N . The results were compared to the expert judgments to see if the expert judgments were tenable.

The red (diagonal) line in Fig. 16 shows the predictions obtained in the manner described above. The green (horizontal) line shows the predictions that would be obtained with ordinary least squares regression.

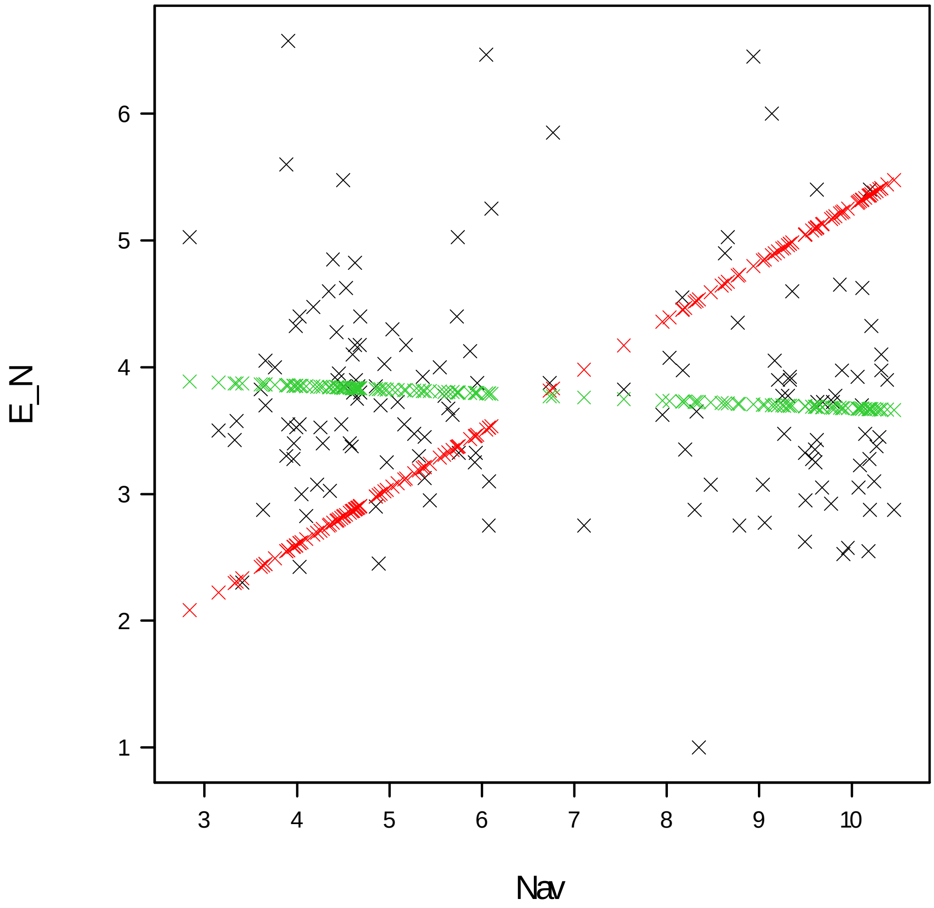


Fig. 16. Relation between modelled nitrogen availability (Nav, by SMART2) and calculated Ellenberg indicator value for Nutrients (E_N) for 145 sites. The green (=horizontal) line gives the (minimum least squared) estimated relation based on the data points. The red (=diagonal) line gives the relation that was used. This relation is based on expert judgment.

The above exercise gave the following equation for the conversion of N availability (Nav) into an Ellenberg N number (E_N):

$$E_N = a_N + b_N * \text{Nav} + e_N = 0.818472 + 0.445168 * \text{Nav} + e_N .$$

Using standard regression methods, the standard errors for a_N and b_N calculated from the residuals formed in the manner described above, are 0.35 and 0.049 respectively; the residual standard error is 1.45; and the correlation between a_F and b_F is -0.94.

Comparing these values to the expert judgments (0.4 and 0.2 for the standard errors for a_N and b_N, and 0.8 for the residual standard error), the regression values for b_N and the residual standard error are notably smaller than the expert judgments. It was therefore considered safe to use the expert judgments. Hence, the parameters of the multivariate normal distribution used to generate 15,000 pairs of values $\left[a_N, b_N, e_N\right]$ are given by:

VARCOV MATRIX Ellenberg N

	aN	bN	eN
aN	0.160000		
bN	-0.075200	0.040000	
eN	0.000000	0.000000	0.640000
MEANS	0.818472	0.445168	0.000000
SDS	0.400000	0.200000	0.800000

The first 3000 draws from this distribution resulted in a sample with means, variances and correlations:

Means and variances of samples

Mean[aN]	Mean[bN]	Mean[eN]
0.8064	0.4522	-0.02147

Var[aN]	Var[bN]	Var[eN]
0.1611	0.03940	0.6304

Correlations between sampled values

aN	1.000		
bN	-0.938	1.000	
eN	0.015	-0.020	1.000
	aN	bN	eN

These values agree with the parameters that were used to generate the sample.

8 The uncertainty analysis

8.1 General introduction

In this research we assumed 26 parameters uncertain for groundwater table, soil type, SMART2, SUMO2 and P2E. Because it is difficult to ascribe uncertainty to a parameter when this parameter depends on the value of another parameter, as in the case when there are rank correlations between parameters, the parameters were grouped such that parameters in different groups can be considered as independent The groundwater table and soil type were grouped with the soil parameters of SMART2 because these are not independent. The SUMO2 parameters were also grouped as were the P2E parameters. For MOVE4 the parameters for the response curves were not treated as uncertain, so the uncertainty in MOVE4 itself does not contribute to the uncertainty in the end result. This results in three separate parameter groups for which the uncertainty contributions were estimated.

This chapter describes the statistical aspects of the analysis carried out.

8.2 Definitions

As mentioned in the Introduction, the output variables will be considered one by one. Let *y* be the output variable under consideration and let $\boldsymbol{p} = (p_1, p_2, ... p_m)$ be a vector of input parameters. In this study, uncertainty is defined as the variance in *y* that is due to variation in the model input parameters. If the model is run a large number of times, say B times, with B different independent vectors of input parameters, the *total uncertainty in y* can be estimated as the variance of the simulated *y*-values. For this reason the total uncertainty is also known as the *total variance*. The total variance of *y* will be denoted as VTOT (Jansen, 1996; Jansen, 1999).

Let U and V be two groups of mutually independent input parameters. The *Top Marginal Variance for U*, TMV[U], is the expected reduction of the variance in *y* when U would be fully known, while the other input parameters would remain as uncertain as before. The *Bottom Marginal Variance for U*, BMV[U], is the expected value of the variance of *y* when all inputs except U would be fully known, and U would remain as uncertain as before. If U and V are complementary, i.e. U and V together contain all input parameters, then it follows from these definitions that

TMV[U] + BMV[V] = TMV[V] + BMV[U] = VTOT.

8.3 Formulas for VTOT and TMV

If a sample of independent simulation outputs is available, VTOT can be estimated by the sample variance $\hat{\mathrm{Var}}(y)$.

Jansen (1996) neatly and succinctly demonstrates how formulas for the BMV and TMV can be derived. The following is an almost literal citation from this work. Define f(U,V) as the model output with groups of input parameters U and V, The estimation of the bottom marginal variance is based on the following. Let U and V be independent complementary groups of sources, and let U_1 and U_2 denote two independent realizations of U. Then $f(U_1,V)$ and $f(U_2,V)$ are independent realizations of f(U,V), given V. Thus $f(U_1,V) - f(U_2,V)$ has expectation 0, while its variance, i.e. its expected square, given V, is twice the variance of f(U,V) given V. It follows that the unconditional expectation of $½ [f(U_1,V) - f(U_2,V)]^2$ is equal to the bottom marginal variance, BMV[U], from source U:

$$BMV(U) = ½ E [f(U_1,V) - f(U_2,V)]^2$$

The estimation of the top marginal variance is based on the following. As stated above, the top marginal variance from V is given by TMV(V) = VTOT – BMV(U). Thus we have

$$\begin{aligned} TMV(V) &= VTOT – ½ E [f(U_1,V) - f(U_2,V)]^2 \\ &= VTOT - ½ E \{[f(U_1,V) – f(U,V)] – [f(U_2,V)- f(U,V)]]^2 \\ &= [Covar[f(U_1, V), f(U_2, V)], \end{aligned}$$

since f(U1, V) and f(U2, V) both have variance VTOT.

This can easily be extended to the situation with more than two groups of parameters (see below).

Note that TMV(V) / VTOT, i.e. the *relative* TMV for group V (or the percentage 100 * TMV(V) / VTOT) is perhaps of even greater interest than the absolute value of the Top Marginal Variance itself.

Since the TMV is more interesting than the BMV, we will be concerned below with Top Marginal Variances only.

So TMV(V) is the uncertainty that can be ascribed to parameter group V, and the relative TMV(V) is this uncertainty as a proportion or percentage of the total uncertainty VTOT.

8.4 Design for the estimation of VTOT and TMV

In our case there are 4 groups of parameters, of which the group consisting of the MOVE4 parameters was eventually skipped. The groups of parameters are indicated as columns in Figure 17. The number of parameters in each group can be equal or greater than one. Now G+1 sets of parameter values are generated. The sets are denoted as S_0, S_1...S_G. In Figure 17 the output y for the five sets are coloured blue, yellow, orange, lilac and green. Each set consists of B=3000 draws. In Figure 17, the draws are represented by the rows. In each set S_g, the values drawn for the g-th group of parameters are *replaced* by the corresponding values in S_0. To denote this, they are coloured blue. Then for all G+1 sets of parameter values the simulation model is run, resulting in G+1 sets of simulation output y_0, y_1...y_G.

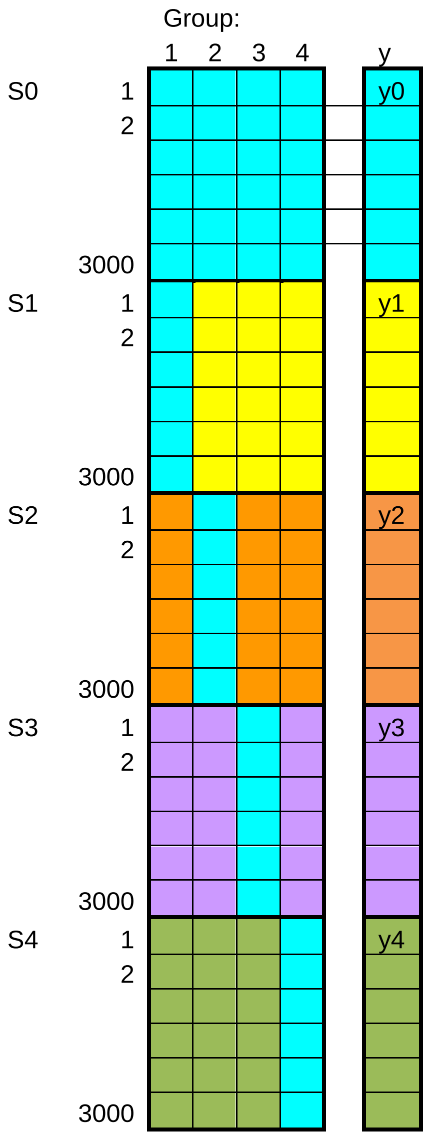


Fig. 17. Design for the estimation of VTOT and TMV.

The Top Marginal Variance for the parameters in group g (g = 1...G) is given by the covariance between y_0 and y_g:

$$TMV(g) = Cov(y_0, y_g) .$$

The TMV for group g can therefore be estimated as the sample covariance between y_0 and y_g.

The relative TMV accounted for by group G, given by $Perc(g) = \frac{TMV(g)}{Var(y)} * 100$, will be estimated as

$$Per\hat{c}(g) = \frac{C\hat{o}v(y_0, y_g)}{V\hat{a}r(y_0)} * 100 .$$

Note that Var(*y*) is estimated from S_0 only, because the y-values in the different sets are dependent.

8.5 Estimating the variance of VTOT and TMV

The uncertainty contributions are estimated from a finite sample of simulations. Therefore these estimates contain sampling error: another sample would yield different estimates for the TMV. To get an idea of the magnitude of the sampling error, expressions are needed for the variance and standard errors of the sample covariance between y_0 and y_g, and also for the variance of the estimated percentage. These expressions are derived in Appendix 4 and 5 (Stuart and Ord, 1987).

9 Results

9.1 Grassland

The average simulated soil pH per site varies between 3.8 and 7.2 (Fig. 18). Low and high pH values are spread all over the country, though lower values are often found on the sandy soils. For many sites the standard deviation in the simulated pH, based on 15,000 runs per site, is substantial (Fig. 18). For some sites the standard deviation is quite high, sometimes over 1.0 pH unit. In most of these cases the entropy (uncertainty) of the soil type is also relative high. For almost all sites uncertainty in soil parameters (soil type, groundwater table and SMART2 parameters) explain most of the uncertainty in the pH. Only for a minor number of sites the plant variables explain also a major part of the uncertainty of the pH (Fig. 18), based on the top marginal variance (TMV).

The uncertainty in the nitrogen availability simulated by SMART2 is on average for the major part determined by SUMO2 (Fig. 19), although SMART2 has also a substantial contribution, where for pH SUMO2 only contributes largely when the contribution of SMART2 is small. For most sites the uncertainty is relative small, compared with the predicted nitrogen availability (on average the coefficient of variation is 13%).

The simulated variance in total biomass at the sites is for a major part determined by SUMO2 parameters. At some sites the SUMO2 parameters totally dominate the uncertainty in the simulated biomass (Fig. 20). On average the uncertainty in the simulations is small; however, there are sites with a relative high uncertainty.

For Ellenberg F, R and N the %TMV for P2E is respectively 100%, 89% and 91% (Table 2). This leaves almost no other sources of uncertainty for F. For Ellenberg R 13% of VTOT can be attributes to SMART and 0% to SUMO. For Ellenberg N on the other hand SMART (4%) and SUMO (6%) have a similar but small contribution to the uncertainty.

The average predicted number of species by MOVE4 at the sites is at maximum 4 with a mean average of just above 1.5 species, out of a maximum of 30 (Fig. 24 and Table 2). Highest number of predicted species can be found in the south of the Netherlands. The standard deviation of the predicted number of species is quite large compared to the predicted number of species (Fig. 24). This indicates that there is a relative large uncertainty in the number of predicted species. For many sites the largest portion of uncertainty is caused by the uncertainty in the Ellenberg variables, although at some sites a significant part is caused by uncertainty in the soil variables, especially in the South. Some of the uncertainty is explained by (uncertainty in) the plant variables at some sites, but for the major part the influence on the uncertainty is negligible.

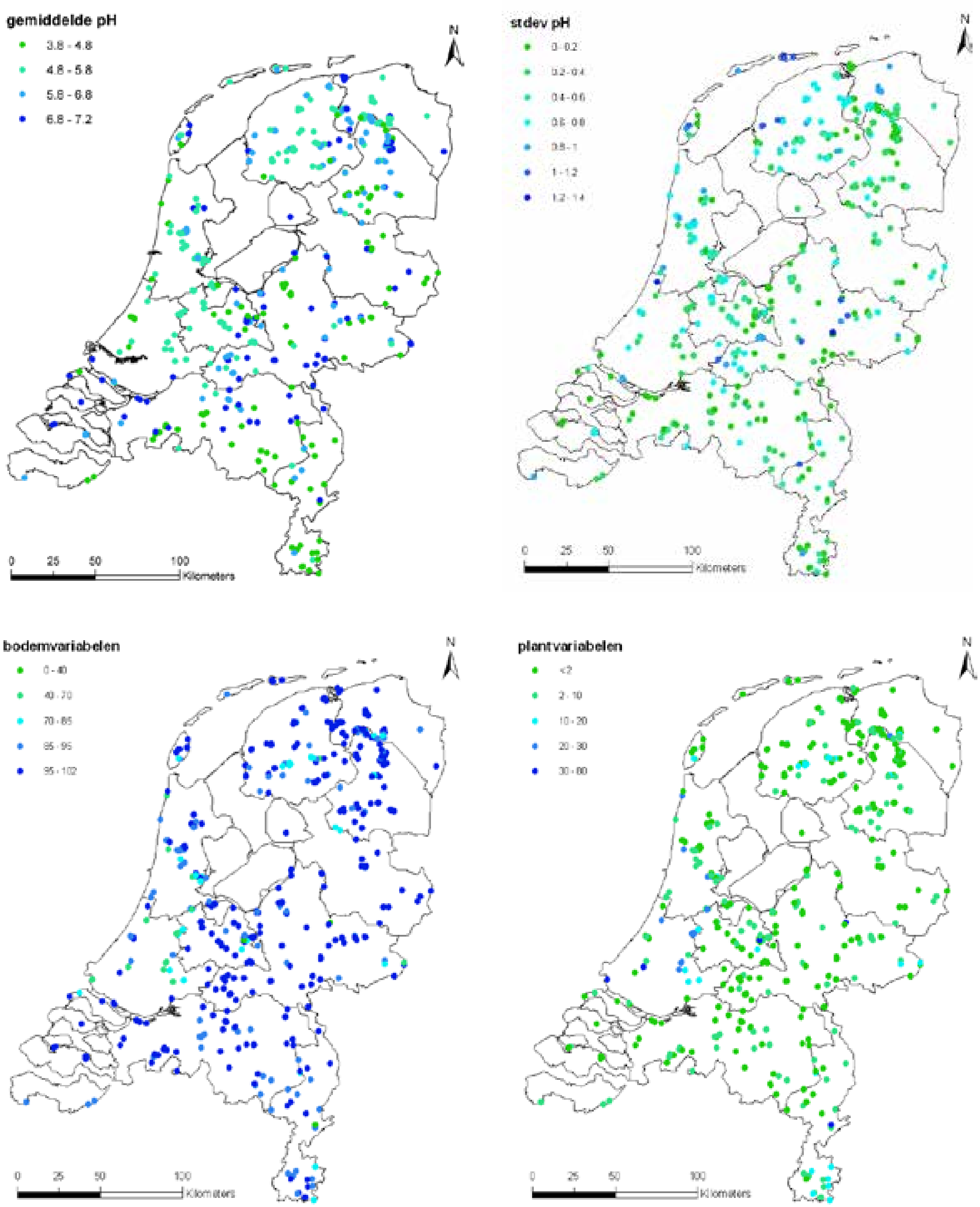


Fig. 18. Average simulated pH (by SMART2, top left), standard deviation of the pH (top right), percentage total variance for soil variables (bottom left) and plant variables (bottom right) per site.

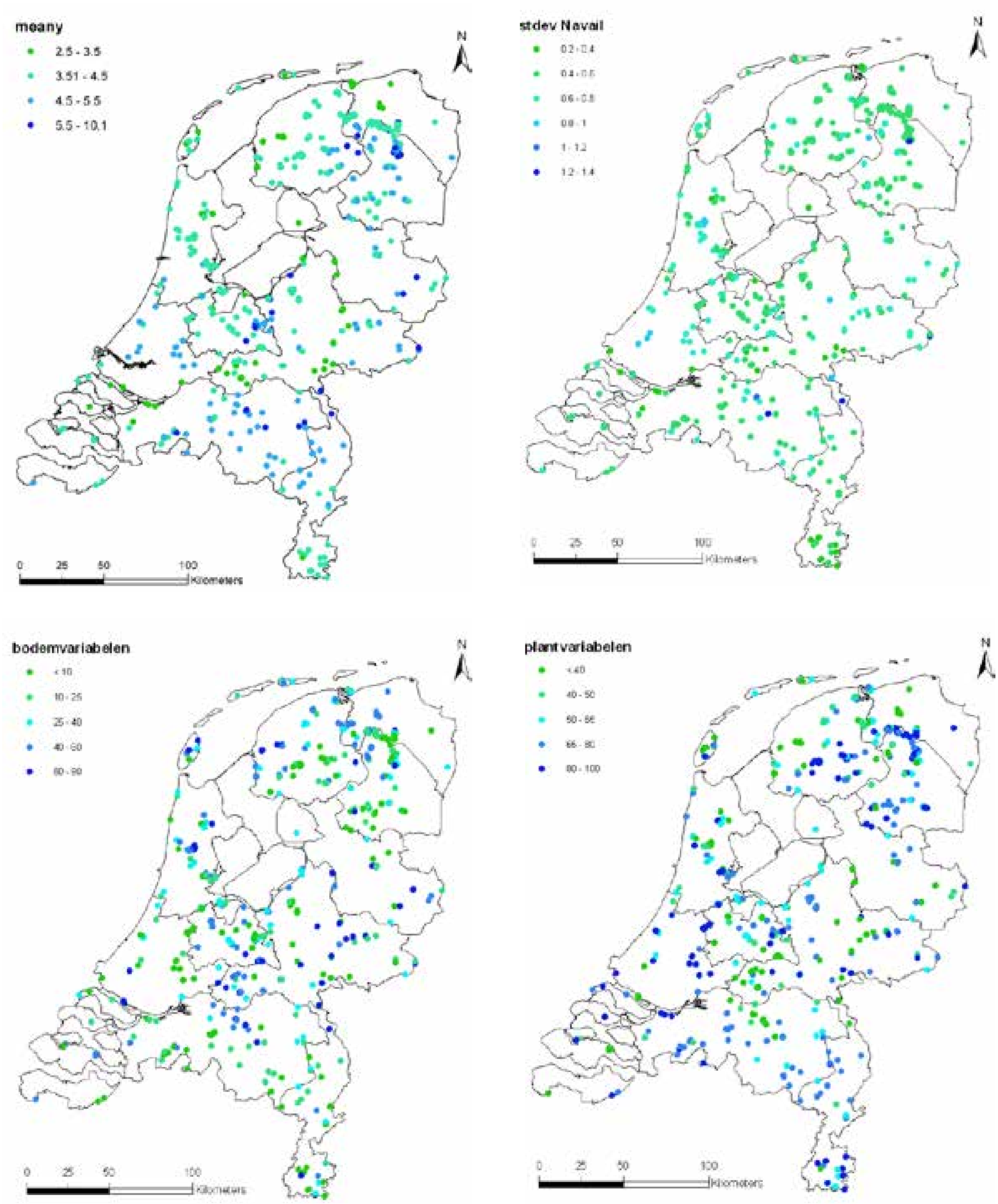


Fig. 19. Results for grassland. Output variable y: nitrogen availability (mol/ha/y). Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to soil variables (bottom left), and to plant variables (bottom right).

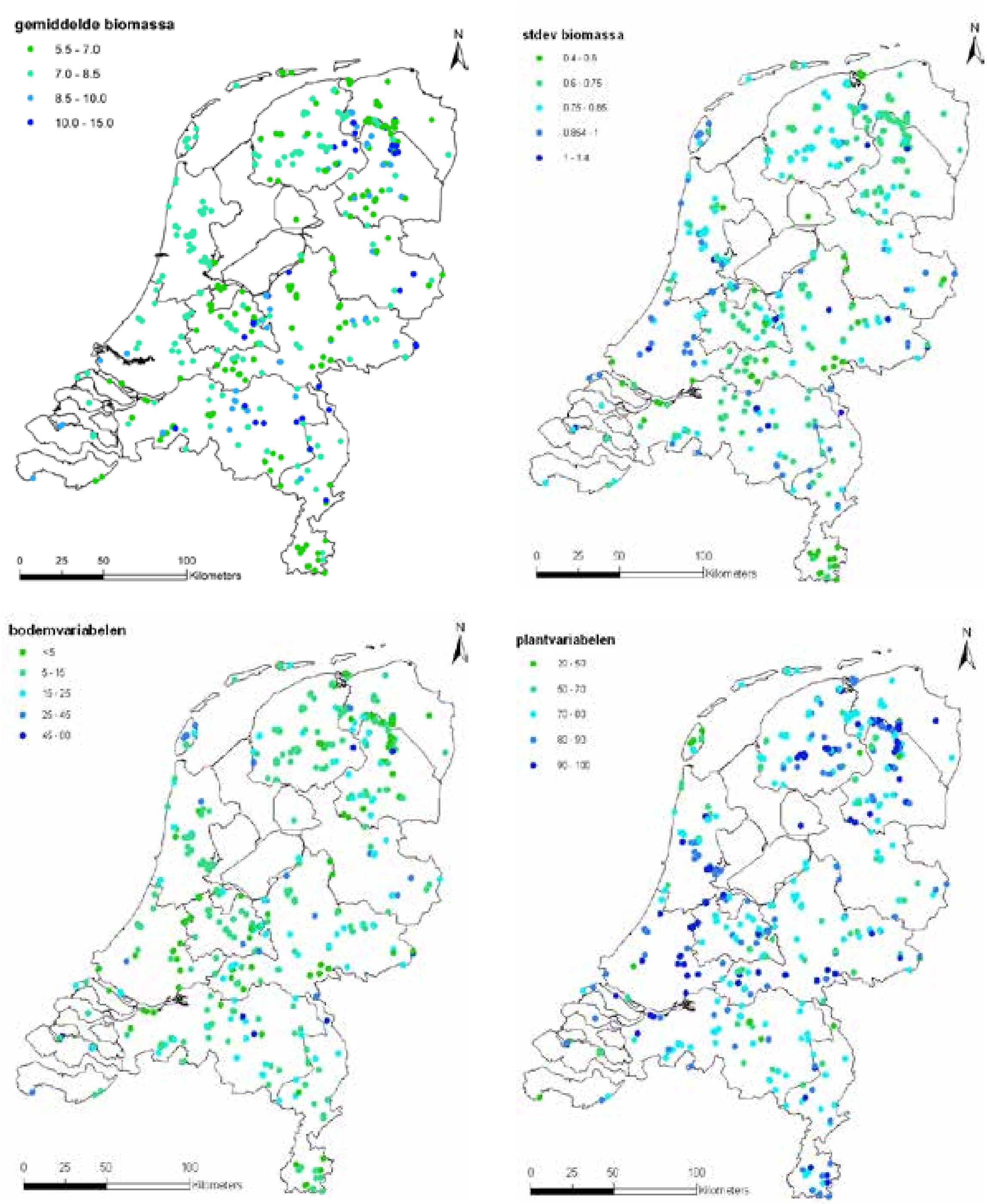


Fig. 20. Results for grassland. Output variable y: biomass (ton/ha). Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to soil variables (bottom left), and to plant variables (bottom right).

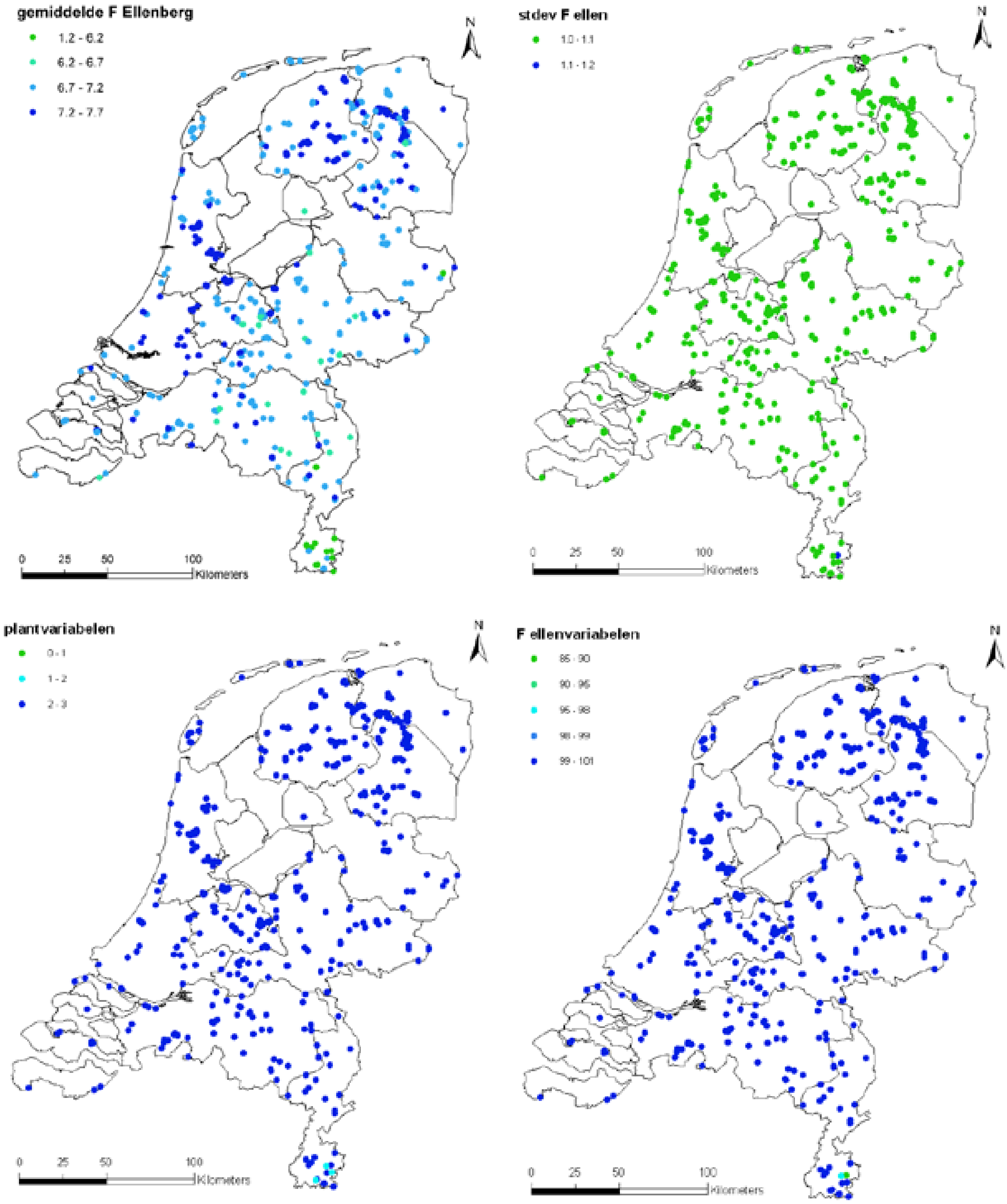


Fig. 21. Results for grassland. Output variable y: Ellenberg F. Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to plant variables (bottom left), and to P2E (bottom right). The contribution of the soil variables are not displayed, since they are very low. See Appendix 6 for more information.

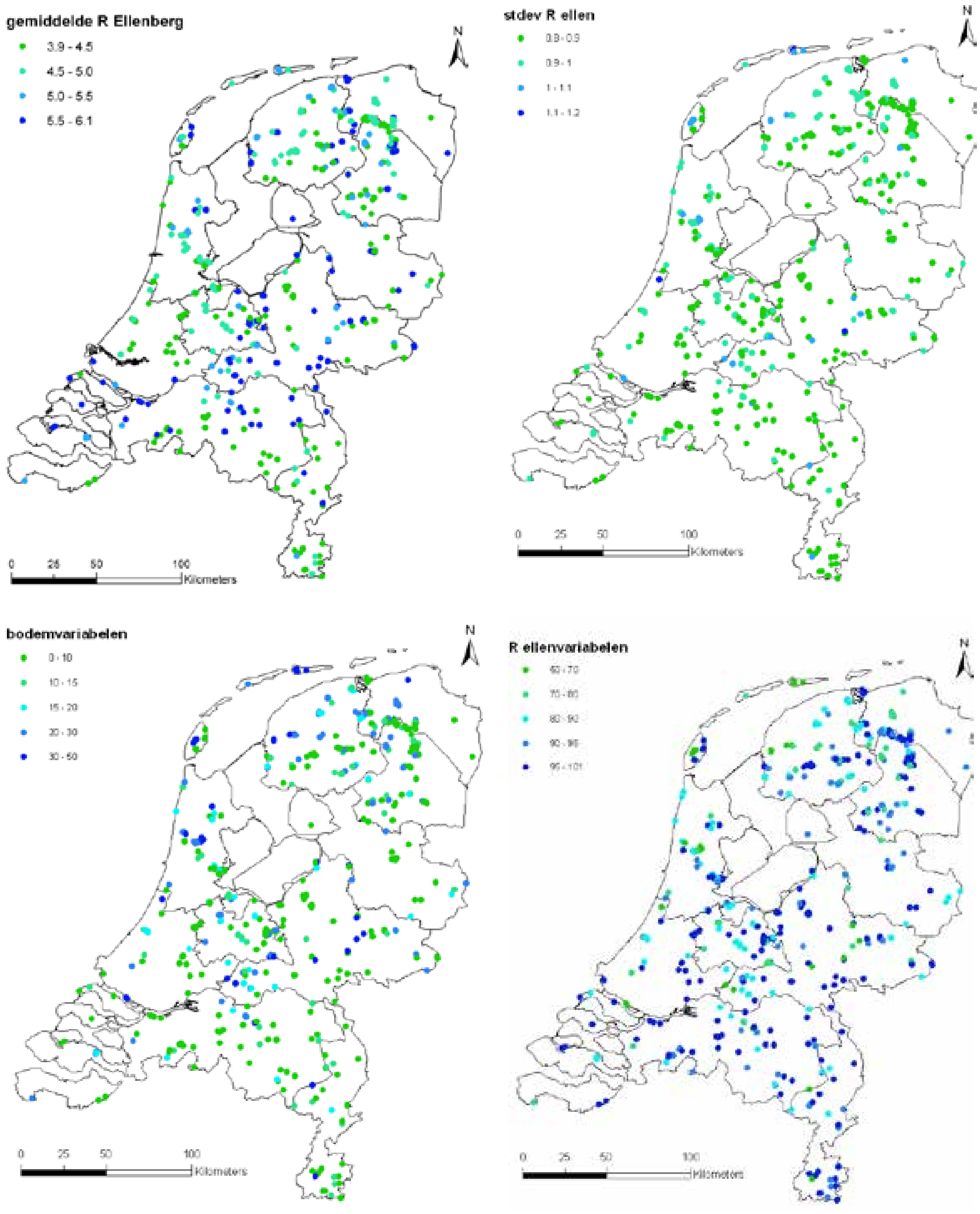


Fig. 22. Results for grassland. Output variable y : Ellenberg R. Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to soil variables (bottom left) and to P2E (bottom right). The contribution of the plant variables are not displayed since they are very low. See Appendix 7 for more information.

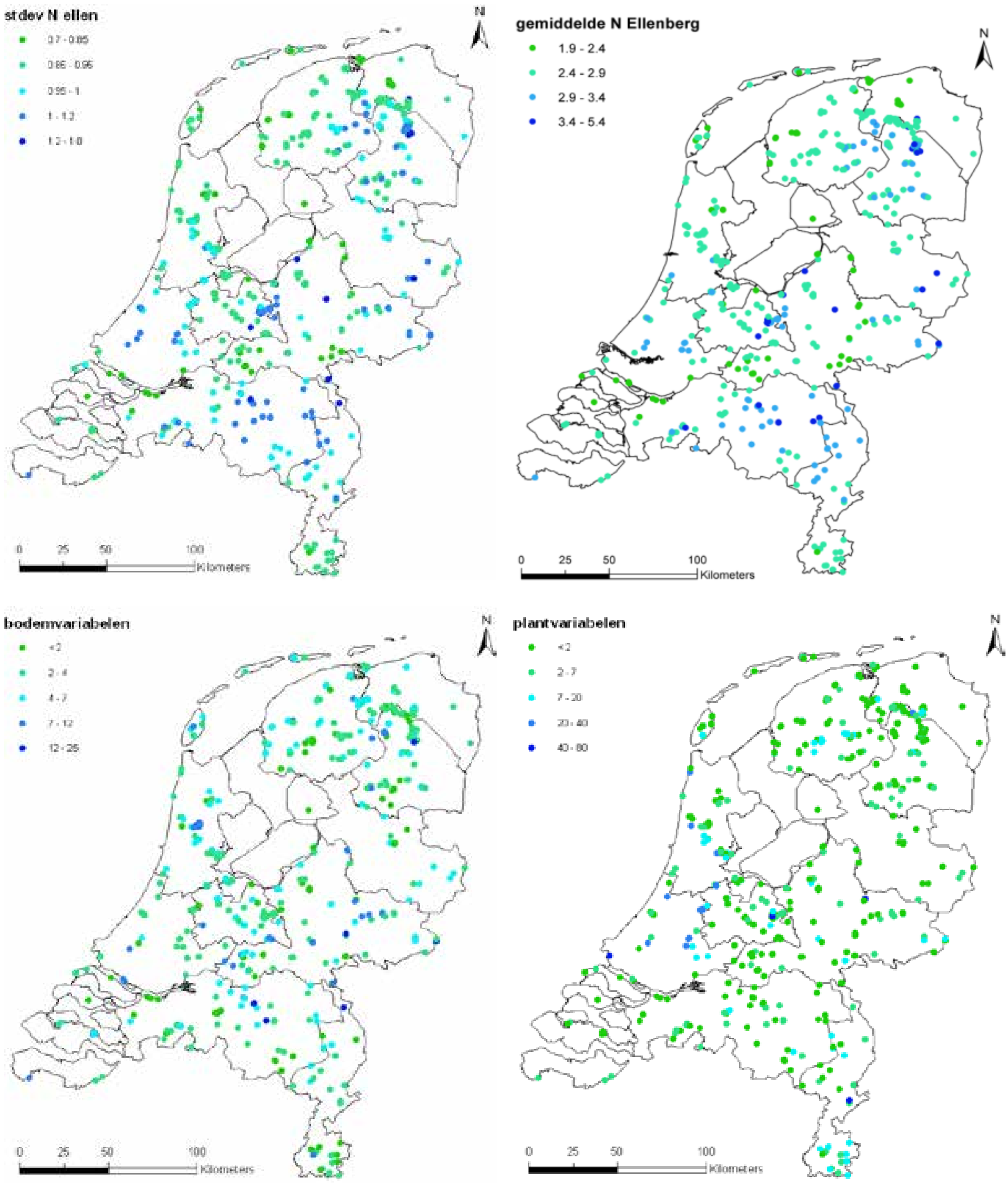


Fig. 23. Results for grassland. Output variable y : Ellenberg N. Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to soil variables (bottom left), to plant variables (bottom right), and to P2E (see next page).

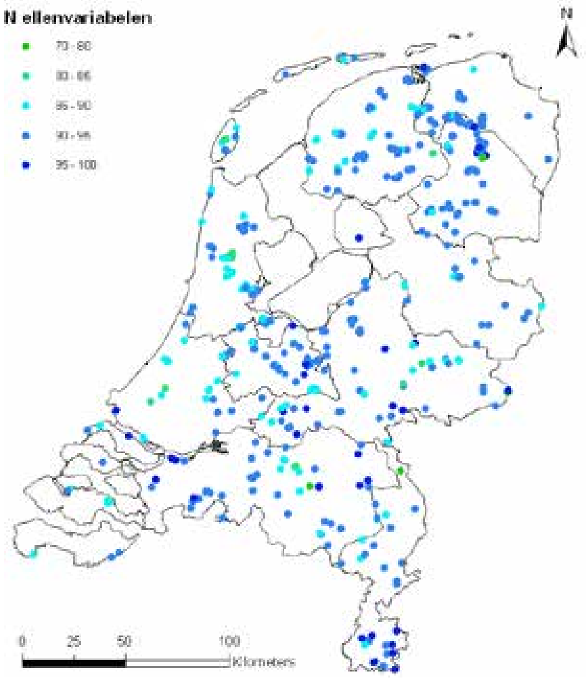
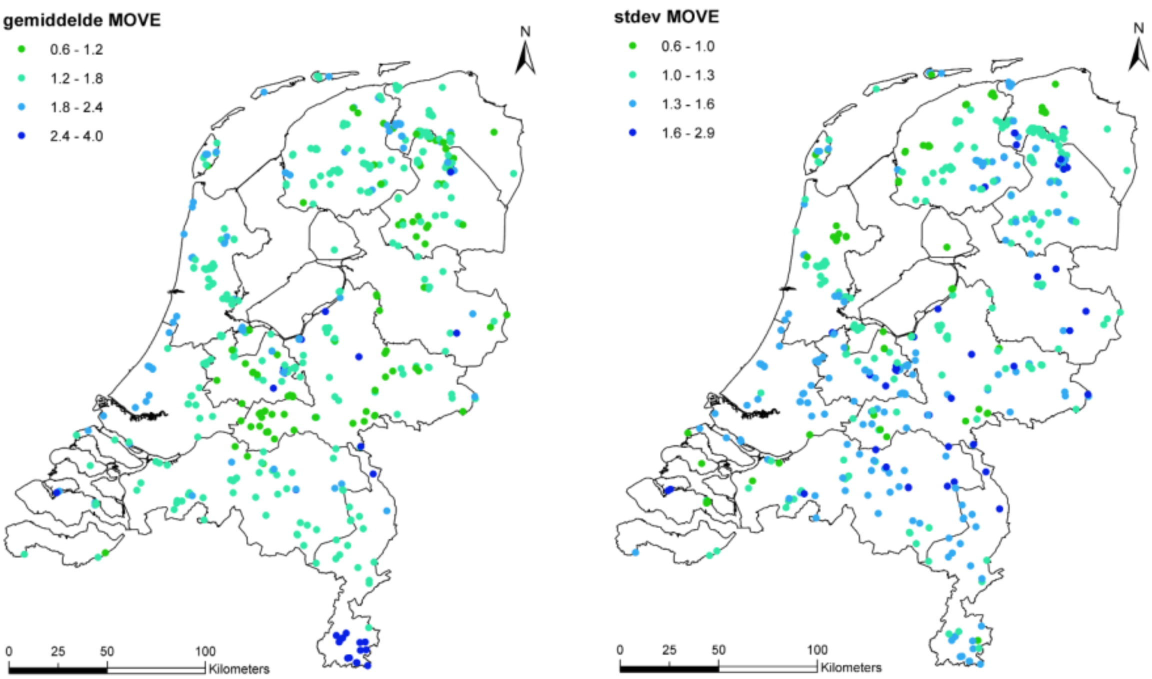
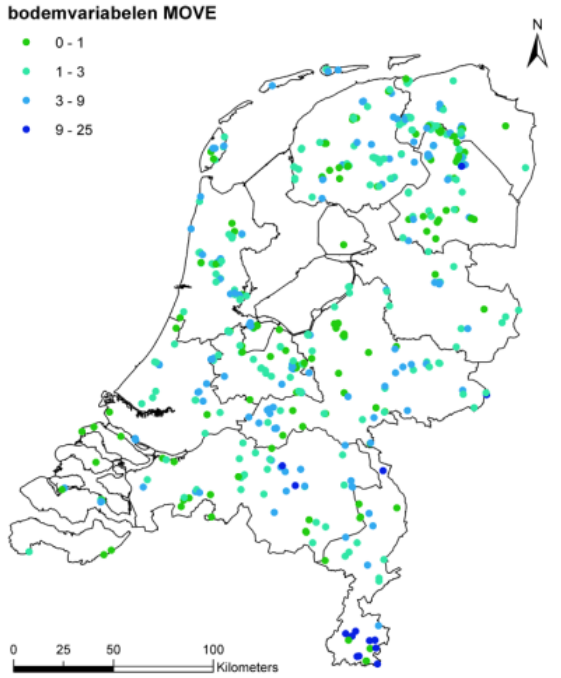


Fig. 23 (continued). Results for grassland. Output variable y : Ellenberg N. Per site: P2E





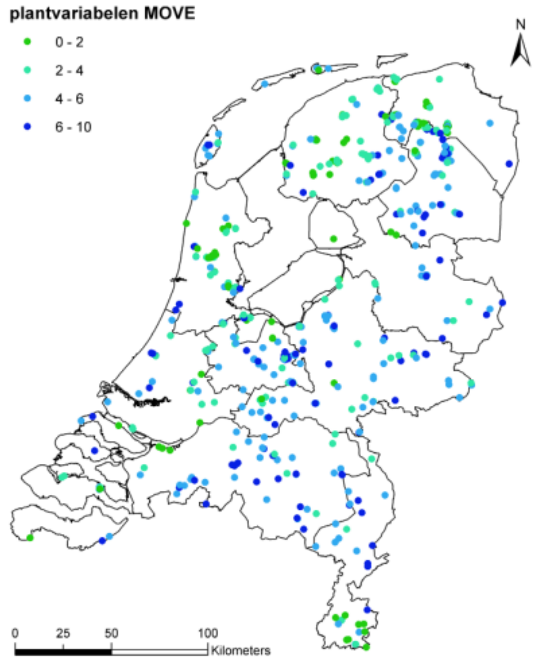


Fig. 24. Results for grassland. Output variable y : number of species. Per site: mean of y (top left, page 56), standard deviation of y (top right, page 56), percentage of the uncertainty in y due to soil variables (mid left), to plant variables (mid right), and to P2E (bottom left).

The uncertainty in the simulated soil pH by SMART2 almost totally depends on the soil parameters and maps (Table 2, Fig. 25). The uncertainty in the nitrogen availability, however, depends for a larger part on the uncertainty in the vegetation parameters in SUMO2. But also the SMART2/map uncertainty contributes for a significant part to the uncertainty in the nitrogen availability in the 500 inspected grassland sites. The uncertainty in the simulated biomass mostly depends on the vegetation parameters of SUMO2 itself, although also here the soil parameters have some influence.

Table 2. Results for Grassland for all output variables. For each site the output of the first 3000 Monte Carlo runs was averaged to obtain $\hat{y}$*, an estimate for the value of the output variable y. The mean, min, max and standard deviation of the 500 values for* $\hat{y}$ *are given in the first column. The variance of the first 3000 outputs, VTOT, is an estimate for the total uncertainty on that site. The mean, standard deviation, minimum and maximum of the 500 values for VTOT are given in the second columns. The next two columns contain these four statistics for* $\hat{S}(\hat{y}) = \sqrt{\mathrm{VTOT}}$ *and for the Coefficient of Variation* $CV = \hat{S} / \hat{y} * 100\%$*. Next, for each site an estimate and associated standard error is available for the fraction of the uncertainty that can be attributed to each of three parameter groups (p1=%TMV SMART2, en, p2=%TMV SUMO, p3=%TVM P2E). The mean, min, max and sd of these estimates over the 500 sites are given in the columns labelled p1 – p3, and se1 – se3 (being the standard errors in p1-p3).*

Output variable		$\hat{y}$	VTOT	√VTOT	CV	p1	p2	p3	se1	se2	se3
pH	mean	5.61	0.27	0.43	8	94	4		1	2	
	sd	1.03	0.3	0.29	5	11	8		1	1	
	min	3.8	0	0	0	9	0		0	0	
	max	7.14	1.88	1.37	25	102	77		20	14	
Navail	mean	4.3	0.33	0.56	13	29	61		2	2	
	sd	0.83	0.17	0.12	3	22	22		0	1	
	min	2.57	0.08	0.28	6	0	8		1	0	
	max	10.12	1.59	1.26	25	90	99		5	5	
Biomtot	mean	7.66	0.58	0.75	10	12	78		2	1	
	sd	1.41	0.2	0.12	2	10	13		0	0	
	min	5.64	0.24	0.49	5	0	21		1	0	
	max	15.03	1.87	1.37	15	76	99		3	3	
F	mean	7.86	1.08	1.04	13	0	2	100	2	2	0
	sd	0.02	0.01	0	0	0	0	1	0	0	0
	min	7.5	1.08	1.04	13	0	2	88	2	2	0
	max	7.86	1.22	1.1	15	11	2	100	2	2	1
R	mean	4.91	0.81	0.9	19	13	0	89	2	2	1
	sd	0.62	0.11	0.06	2	10	0	10	0	0	0
	min	3.99	0.71	0.85	14	3	0	52	1	2	0
	max	6.08	1.37	1.17	24	50	1	100	2	2	1
N	mean	2.74	0.91	0.95	35	4	6	91	2	2	1
	sd	0.37	0.23	0.11	1	3	2	3	0	0	0
	min	2	0.55	0.74	32	0	2	73	2	2	0
	max	5.35	3.23	1.8	38	24	13	97	2	2	2
MOVE4	mean	1.58	1.74	1.29	88	3	4	76	2	2	2
	sd	0.53	0.75	0.27	24	3	2	8	0	0	1
	min	0.68	0.46	0.68	21	0	0	33	1	2	1
	max	3.98	7.89	2.81	149	22	9	92	4	3	4

For the Ellenberg indicator values (F, R and N) the uncertainty (and the calculated values) almost totally depend only on the uncertainty in the regression parameters used for the translation into the indicator values (Table 2, Fig. 25). SMART2 and SUMO2 parameters and their uncertainty only contribute marginally to the calculated indicator values and the uncertainty in them.

The average predicted species occurrence by MOVE4 is rather low, with an average of just above 1.5 species. The uncertainty in it is relative high, also compared with the other parameters. On average almost all of the uncertainty in the MOVE4 predictions is explained by the P2E parameters (Ellenberg parameters). At some sites there is some influence of the soil parameters, but never higher than the P2E parameters.

The average uncertainty over the sites is relative small for the SMART2-SUMO2 output variables (Table 2). For pH, nitrogen availability and biomass it is all below 15% (with only 8% for soil pH). The spread in the average uncertainty is also small, although the highest uncertainties for soil pH and nitrogen availability are relative high. On average the uncertainty in the Ellenberg indicator values is higher, though for Ellenberg F it is comparable with the uncertainty in nitrogen availability. Especially the uncertainty in the Ellenberg indicator value for nutrient availability (N) is high, on average 35%, though the spread in the uncertainty is relative small. For the Ellenberg indicator value for moisture (E_F) a proper overall uncertainty cannot be estimated, since in the simulations all sites got the same value for the groundwater table (MSW), so the total variance is zero and hence there is no percentage of this variance that can be attributed to a parameter group. However, the uncertainty in the regression parameters for the P2E relation for E_F was included. As all groundwater table values are equal, the maximum, minimum and mean values are all equal.

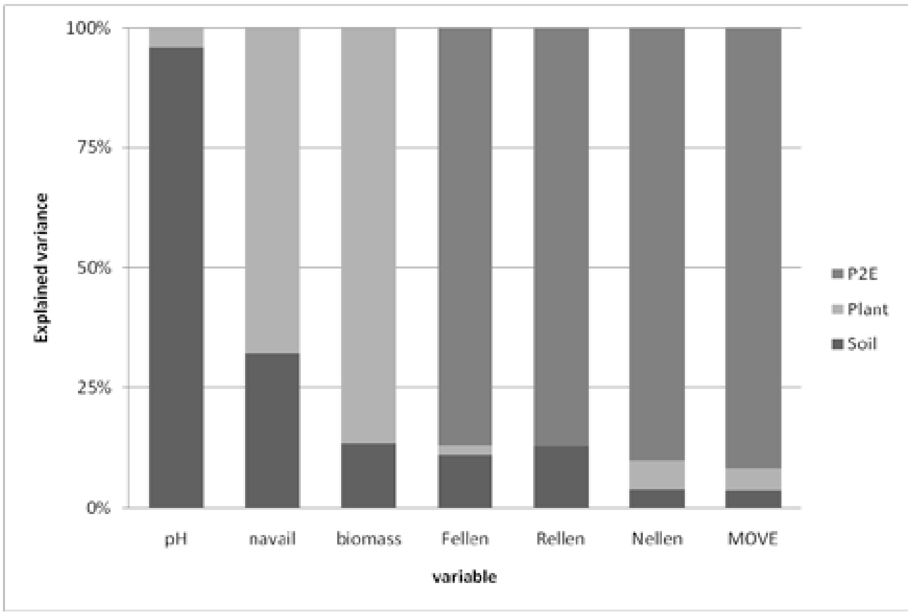


Fig 25. Results for grassland. Percentage of uncertainty attributable to the Soil, Plant and P2E parameters (totalized to 100%) for each of the seven output variables pH, nitrogen availability (navail), biomass, Ellenberg F, R and N and MOVE4.

For each vegetation type there are 500 sites. For each site, an estimate of the uncertainty due to the three parameter groups was obtained for each of the 7 output variables. So for each vegetation type four 7x7 correlation matrices can be given, with each correlation calculated from 500 observations. Thus, the value 0.806 in the first matrix, indicates that if soil (parameter group 1) is responsible for a large part of the uncertainty in variable 6 (N), then it is usually also responsible for a large part of the uncertainty in variable 2 (nitrogen availability). Fig. 26 shows these correlations. A high correlation indicates that there is a strong relation between two variables. The strongest correlations are present between total biomass and N for SMART2/maps (0.650), nitrogen availability and total biomass for SMART2/maps (0.564), nitrogen availability and N SMART2/maps (0.806), nitrogen availability and R SMART2/maps (0.595), nitrogen availability and biomass for SUMO2 (0.751) and nitrogen availability and N for SUMO2 (0.592). The correlations of these combinations are shown in Fig. 27, as scatter plots for the 500 sites. Scatter plots for all combinations are shown in Appendix 12. The strongest correlation is present for the explained variances between nitrogen availability and Ellenberg N for the SMART2/maps parameters. So when there is a high explained variance at a site for nitrogen availability for the SMART2/maps parameters it is very likely that SMART2/maps parameters will also explain a lot of variance in the uncertainty of Ellenberg N at that site. For MOVE4 results the correlations are all low.

Correlation matrix for %TMV due to SMART2

p[1][1]	1.000						
p[2][1]	0.436	1.000					
p[3][1]	0.266	0.564	1.000				
p[4][1]	0.106	-0.010	0.092	1.000			
p[5][1]	0.287	0.595	0.217	-0.047	1.000		
p[6][1]	0.250	0.806	0.650	-0.047	0.492	1.000	
p[7][1]	0.004	0.251	0.268	0.595	0.066	0.376	1.000
	p[1][1]	p[2][1]	p[3][1]	p[4][1]	p[5][1]	p[6][1]	p[7][1]

p[1][2]	1.000						
p[2][2]	0.407	1.000					
p[3][2]	0.324	0.751	1.000				
p[4][2]	0.021	-0.021	0.023	1.000			
p[5][2]	0.028	-0.050	-0.074	-0.038	1.000		
p[6][2]	0.341	0.592	0.373	0.041	0.046	1.000	
p[7][2]	-0.049	0.123	-0.120	0.011	0.084	0.233	1.000
	p[1][2]	p[2][2]	p[3][2]	p[4][2]	p[5][2]	p[6][2]	p[7][2]

p[1][3]	1.000						
p[2][3]	0.074	1.000					
p[3][3]	0.007	0.237	1.000				
p[4][3]	0.050	-0.127	-0.070	1.000			
p[5][3]	0.025	0.148	0.018	-0.043	1.000		
p[6][3]	-0.032	0.152	0.006	-0.202	0.532	1.000	
p[7][3]	0.015	-0.045	-0.075	0.510	0.298	0.349	1.000
	p[1][3]	p[2][3]	p[3][3]	p[4][3]	p[5][3]	p[6][3]	p[7][3]

p[1][4]	1.000						
p[2][4]	0.046	1.000					
p[3][4]	0.075	0.216	1.000				
p[4][4]	-0.023	-0.005	-0.055	1.000			
p[5][4]	0.132	0.030	0.004	-0.028	1.000		
p[6][4]	0.105	0.188	0.075	-0.020	0.015	1.000	
p[7][4]	-0.002	-0.024	-0.015	-0.027	0.094	0.114	1.000
	p[1][4]	p[2][4]	p[3][4]	p[4][4]	p[5][4]	p[6][4]	p[7][4]

Fig. 26. Results for grassland: For each of the four parameter groups, correlations are given between uncertainties attributable to that parameter group for the 7 output variables. First index: 1=pH, 2=nitrogen availability, 3=total biomass, 4=F, 5=R, 6=N, 7=npresent. Second index: 1= SMART2/maps, 2= SUMO2, 3= P2E, 4=MOVE4.

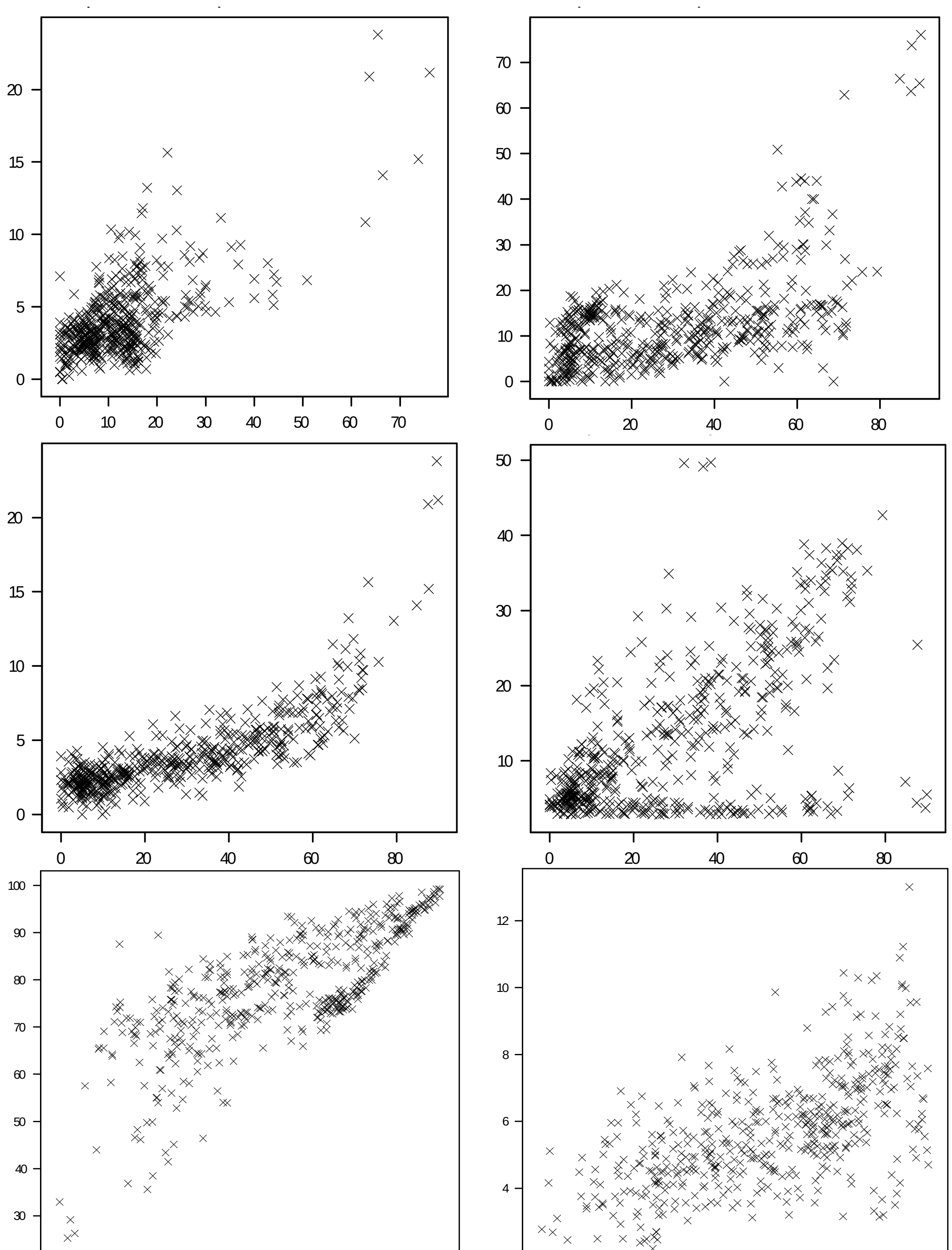


Fig. 27. Results for grassland. Bivariate scatter plots for variables with a high correlation in the above correlation matrix. 1. Total biomass vs N for SMART2/maps (0.650, top left); 2. nitrogen availability vs total biomass for SMART2/maps (0.564 top right); 3, nitrogen availability vs N SMART2/maps (0.806 middle left); 4. nitrogen availability vs R SMART2/maps (0.595 middle right); 5. nitrogen availability vs biomass for SUMO2 (0.751, bottom left); 6. nitrogen availability vs N for SUMO2 (0.592, bottom right).

9.2 Heathland

The average simulated soil pH is as expected relatively small with almost all average values below pH 4.3. Some sites have a high average pH. The lowest values can be found in the province of Noord-Brabant and the east of The Netherlands, known for their intensive agricultural activities. The uncertainty in the soil pH is mainly explained by uncertainty in soil type and mean spring groundwater level (Fig. 28). The explained variance ranges from 11 to 99%, with most of the explained variances between 85 and 95%. For some sites most of the uncertainty in the simulated soil pH is caused by the plant variables. For most of the sites however, the influence of the plant variables is minor, with most of the explained variances up to 21%.

The average simulated nitrogen availability ranges from 0.9 to 4.2 mol/y (Fig. 29), with most of the availability ranging from 0.9 to 1.7 mol/y. This is lower than the availability simulated for grassland. The uncertainty in the nitrogen availability is both caused by soil variables and plant variables.

Most of the uncertainty in the simulated biomass is explained by the plant parameters (Fig. 31). The contribution of the soil parameters is only minor. The average simulated biomass amount is as could be expected from natural grasslands.

The simulated Ellenberg indicator value for moisture (F) ranges between 4.7 and 7.5, moderate dry as may be expected for heathland (Fig. 30). The variation in the simulated F values between the sites is rather low, with most F values between 6.6 and 7.5. The variation simulated per site is relative large compared to the variation between the sites. Most of the uncertainty in the F value is explained by the Ellenberg variables (regression parameters for the translation of groundwater table into F). At a few sites the soil variables, in this case the uncertainty in the groundwater table map, also explain a substantial amount of uncertainty. The plant variables do not explain a substantial part of the uncertainty, as may be expected.

The results for Ellenberg R are comparable to the results for F (Fig. 32). The average R value for the sites is rather low as could be expected for heathers and the variation between the sites is minimal. The uncertainty in R is completely explained by the Ellenberg variables, the plant variables explain no uncertainty and the soil variables explain a negligible amount of variation.

For Ellenberg N the values are very low ranging from 1.4 till 2.7 (Fig. 33). Though Heathers are relative nutrient poor, these values are lower than expected. The uncertainty in the N values is almost completely caused by the uncertainty in the Ellenberg variables, with a negligible amount explained by soil variables.

All previous uncertainties end up in the simulation of the number of expected species by MOVE4. The number of species is low, but higher than for grasslands (Fig. 34). The uncertainty is for the major part caused by the Ellenberg variables, as could be expected from the results for the Ellenberg indicator values. The uncertainty in the plant variables does not really contribute to the uncertainty in the MOVE4 output, the soil variables contribute a little more, except for some sites where the influence of the soil variables is substantial.

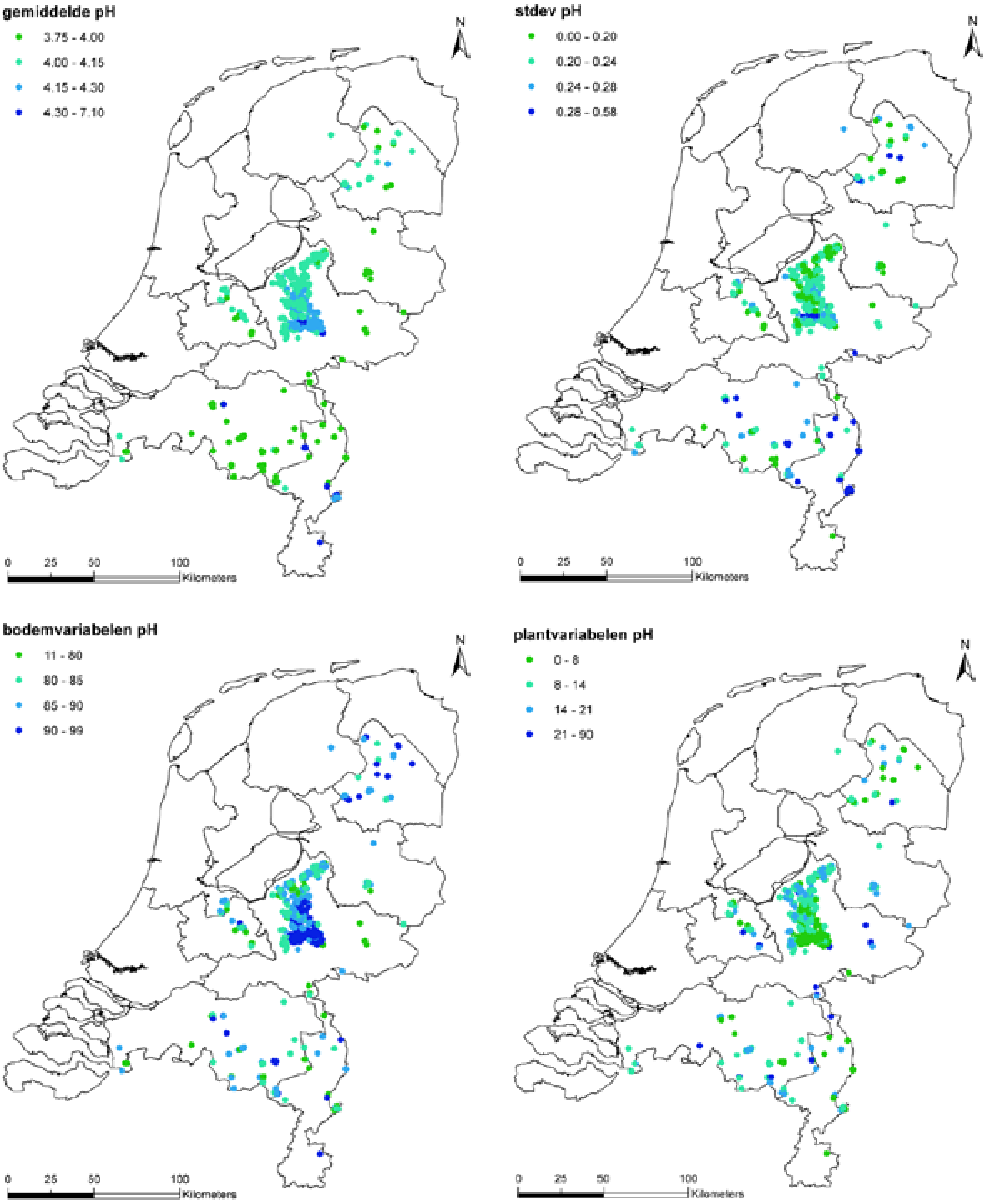


Fig. 28. Results for heathland. Output variable y: pH (mol/ha/y). Per site: mean of y (top left), standard deviation of y (top right), percentage of the uncertainty in y due to soil variables (bottom left), and to plant variables (bottom right).

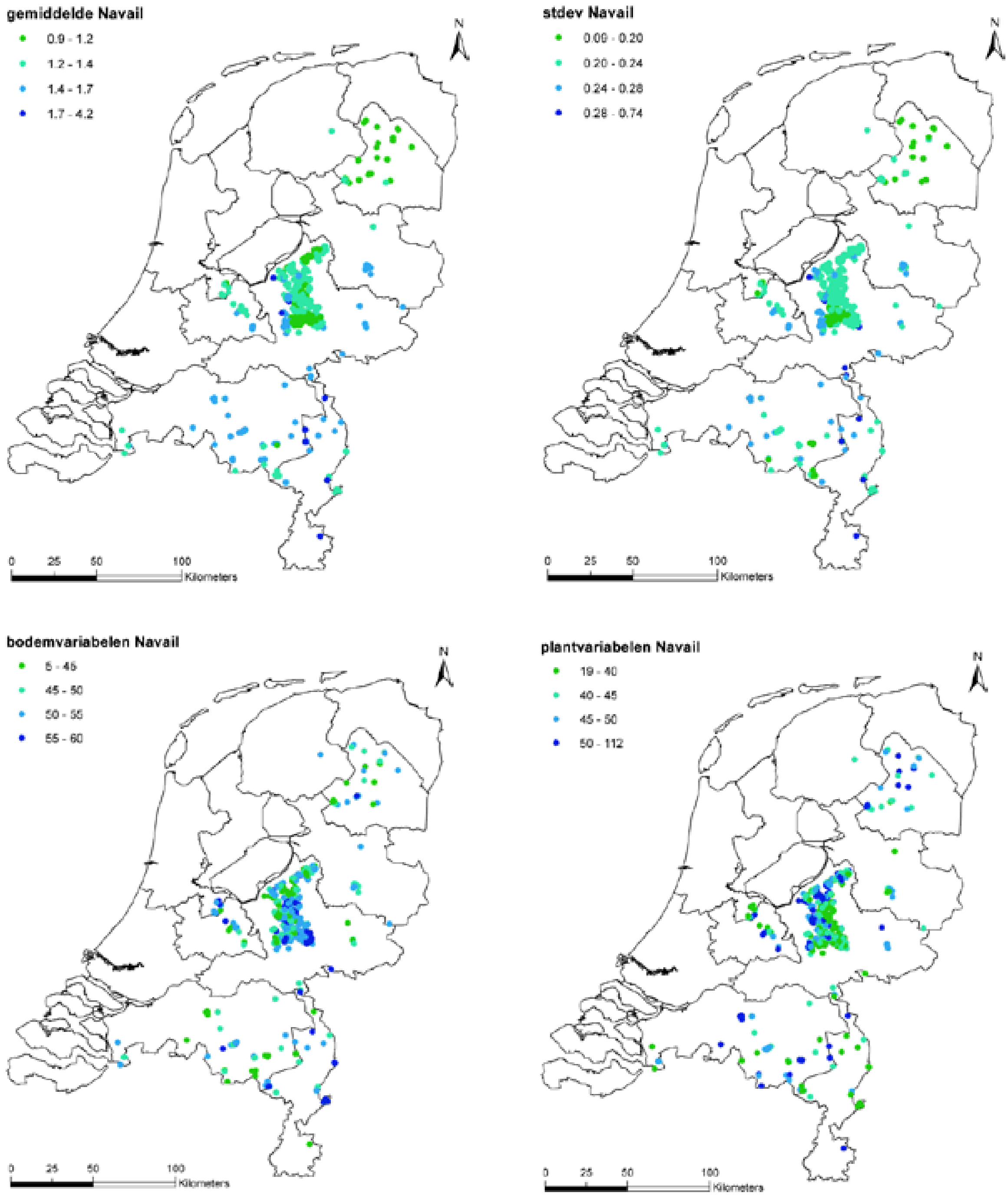


Fig. 29. Average simulated nitrogen availability in mol/ha/y for heathland (by SMART2, top left), standard deviation of the nitrogen availability (top right), total percentage variance for soil variables (bottom left) and plant variables (bottom right) per site.

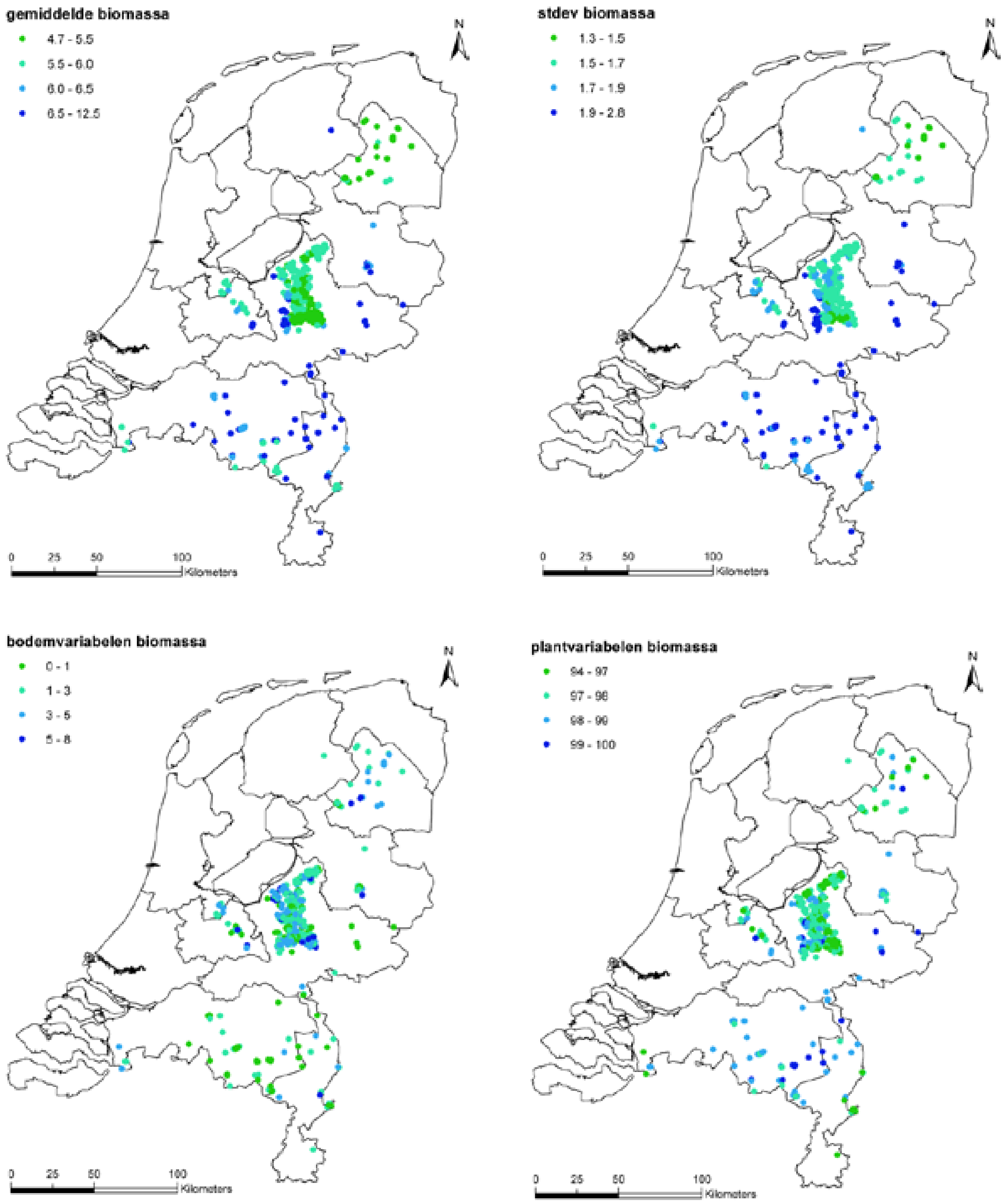


Fig. 30. Average simulated biomass in ton/ha for heathland (SUMO2, top left), standard deviation of the total biomass (top right), percentage total variance for soil variables (bottom left) and plant variables (bottom right) per site.

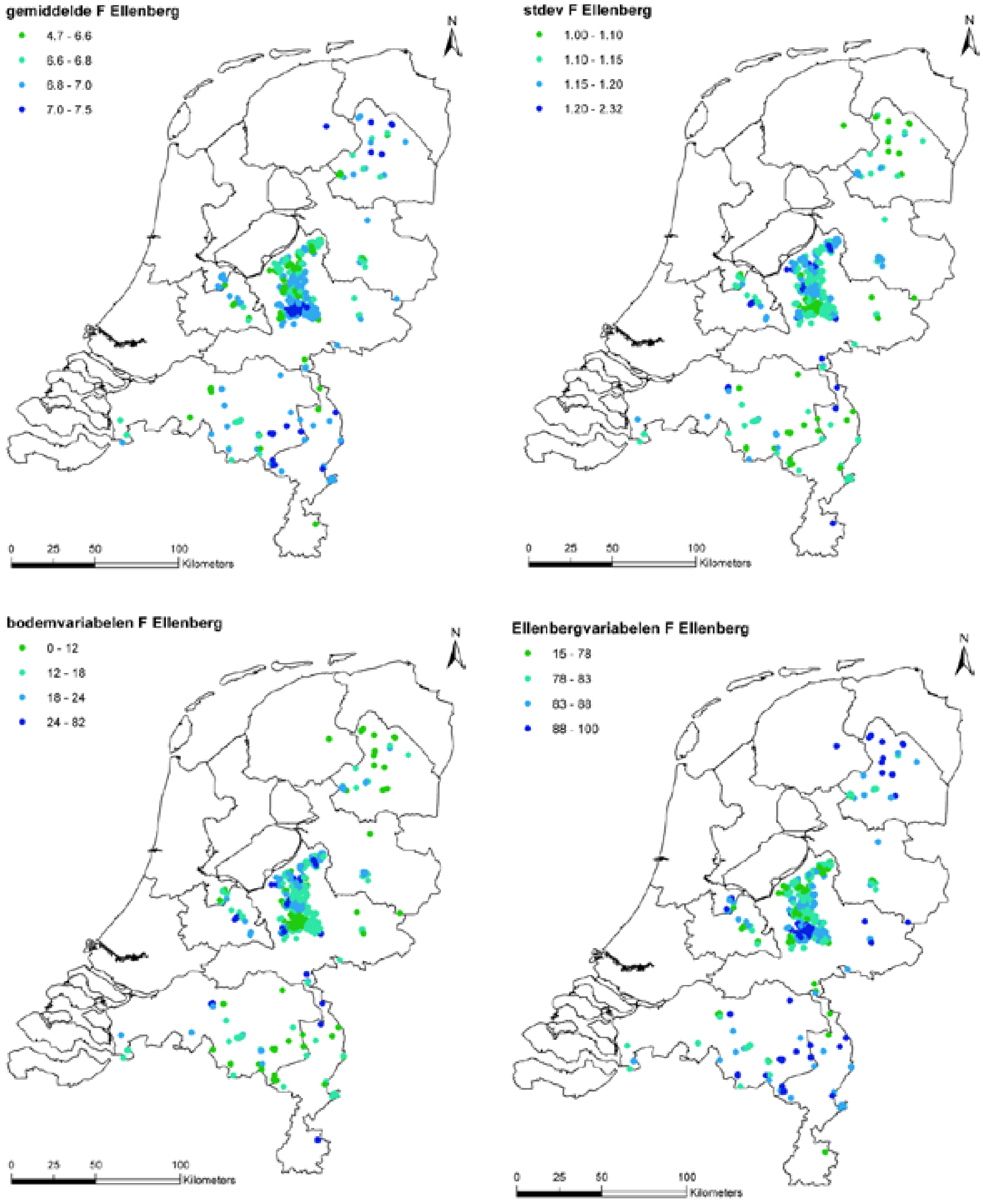


Fig. 31. Average simulated Ellenberg indicator value for moisture for heathland (P2E, top left), standard deviation (top right), percentage total variance for soil variables (bottom left) and the regression parameters (bottom right) per site. The plant variables are given in Appendix 8, since they are very low.

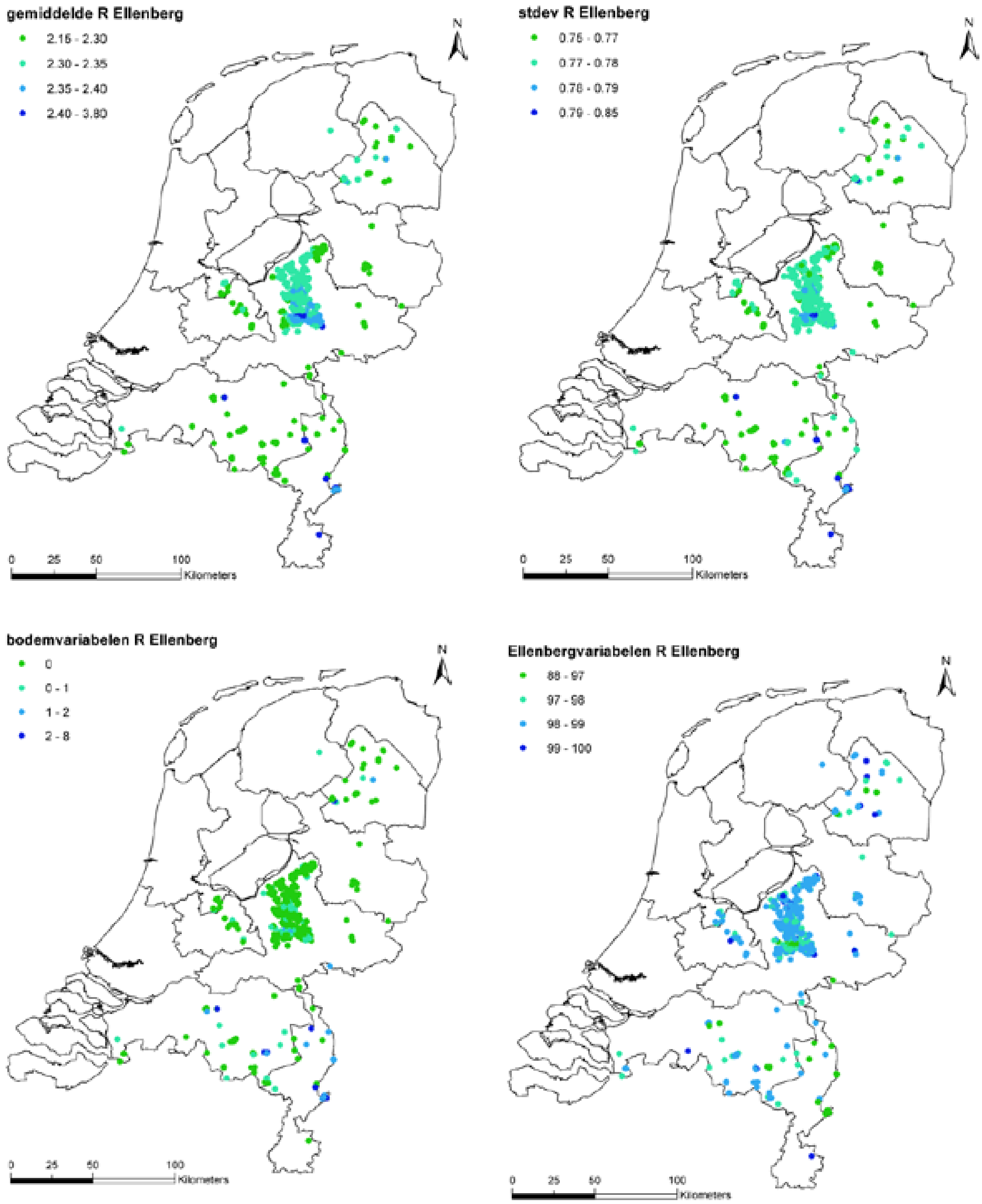


Fig. 32. Average simulated Ellenberg indicator value for acidity for heathland (P2E, top left), standard deviation (top right), percentage total variance for soil variables (bottom left) and regression parameters (bottom right) per site. The plant variables are given in Appendix 9, since they are very low.

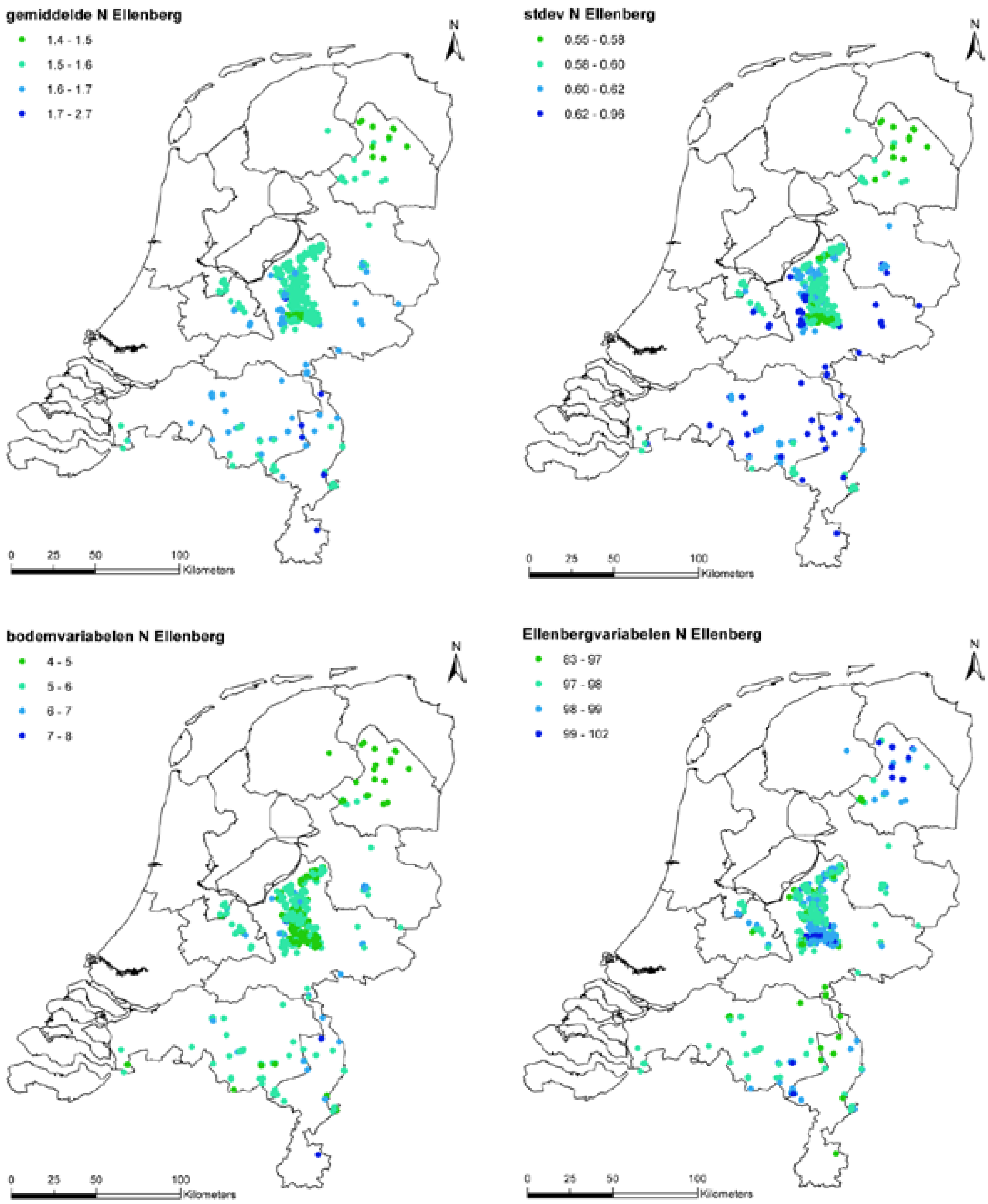


Fig. 33. Average simulated Ellenberg indicator value for nutrients for heathland (P2E, top left), standard deviation (top right), percentage total variance for soil variables (bottom left), and regression variables (bottom right) per site. Plant variables are given in Appendix 10, since the explained variance is marginal.

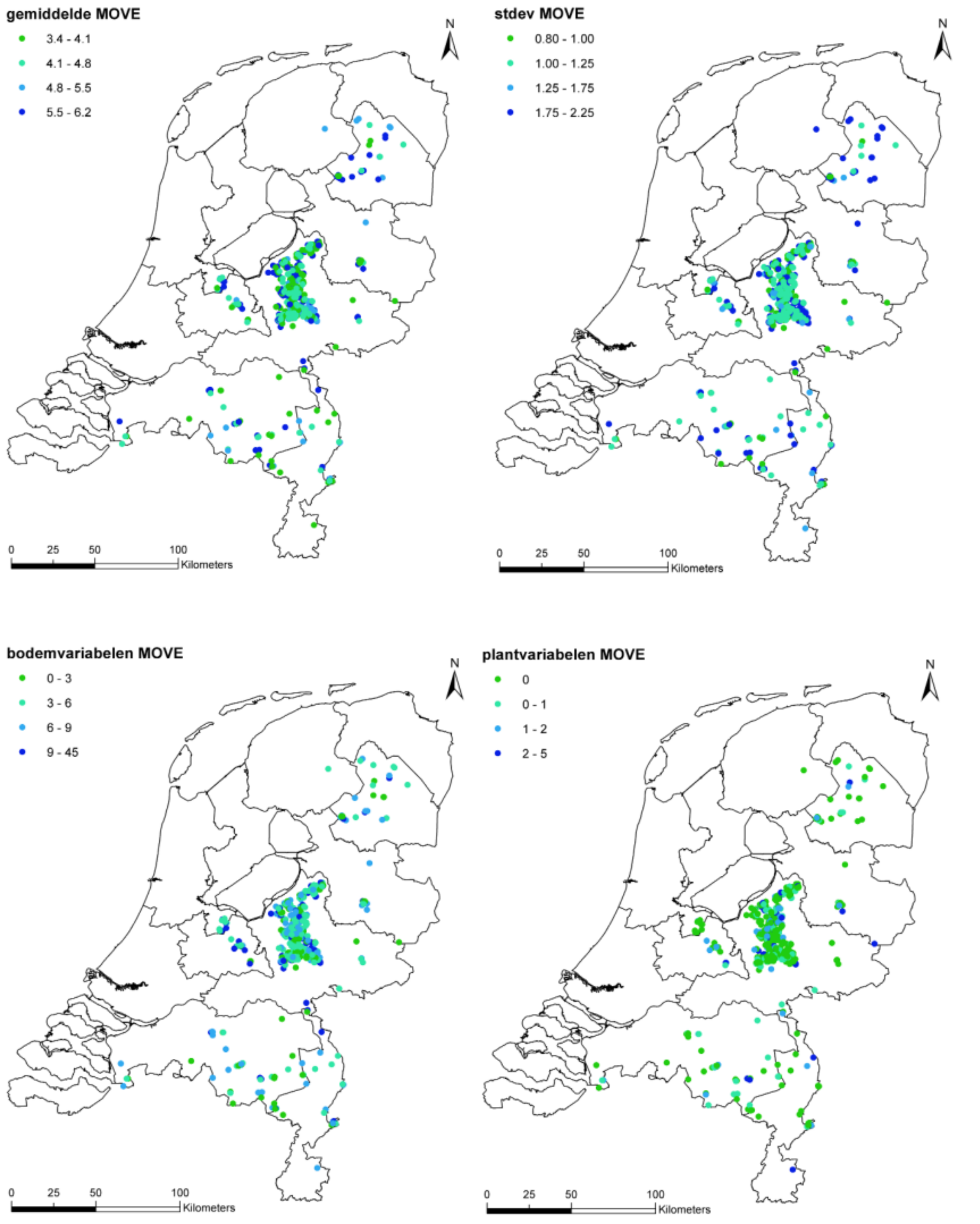


Fig. 34. Average simulated number of occurring species for heathland (MOVE4, top left), standard deviation (top right), percentage total variance for soil variables (bottom left), plant variables (bottom right) and regression variables (see next page) per site.

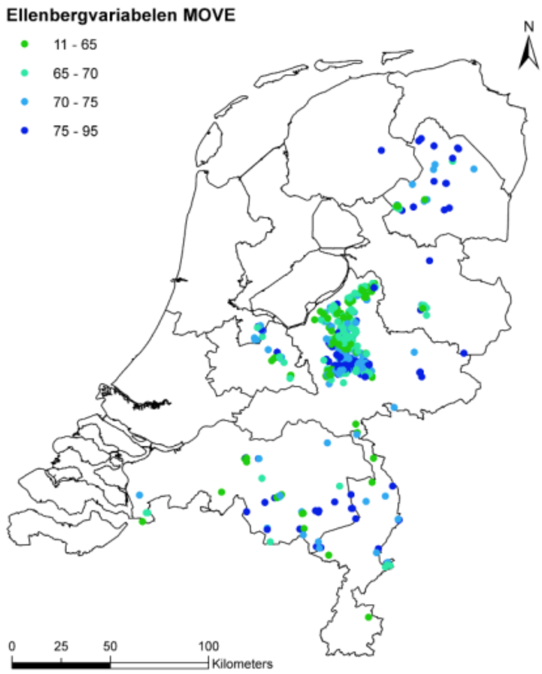


Fig. 34 (continued). The regression variables per site.

The uncertainty in the simulated soil pH for heathlands depends for a large part on the uncertainty in the soil parameters (SMART2 and soil map), although there are sites where the uncertainty mostly depends on the plant parameters (SUMO2, Table 3 and Fig. 35). The spread in the simulated pH values is low and the uncertainty in the percentages explained variances is also very low. For nitrogen availability soil and plant variables contribute more or less equally to the uncertainty on average. As for pH the uncertainty in the percentages explained variances is low as is the standard deviation of the predicted nitrogen availability. The latter indicates that there is not much variation in the nitrogen availability between the different sites. The average nitrogen availability, almost 1.3 mol/ha or almost 20 kg/ha, is rather low, even for heathland. The uncertainty in the simulated biomass almost totally depends on the uncertainty in the plant variables and again the uncertainty in the uncertainty is rather low.

The uncertainty in the Ellenberg indicator values (F, R and N) largely depends on the uncertainty of the regression equation to calculate the indicator values (P2E). Only for moisture (F), the soil (groundwater table map) also has a minor contribution to the uncertainty. Uncertainty in the Ellenberg indicator values is very low. For N and R this is in line with the small variation in the simulated nitrogen availability and pH.

As could be expected from the above, the uncertainty in the MOVE4 output is largely dominated by the uncertainty in the Ellenberg variables, though at some sites soil variables also contribute. The plant variables on average contribute nothing to the uncertainty of the MOVE4 outcome. The outcome of MOVE4, the number of simulated species present, is quite low, but higher than for grasslands. The standard deviation of the simulation is somewhat lower that 20%, which is lower than in grasslands.

Table 3. Results for heathland for all output variables. For each site the output of the first 3000 Monte Carlo runs was averaged to obtain $\hat{y}$, an estimate for the value of the output variable y. The mean, min, max and standard deviation of the 500 values for $\hat{y}$ are given in the first column. The variance of the first 3000 outputs, VTOT, is an estimate for the total uncertainty on that site. The mean, standard deviation, minimum and maximum of the 500 values for VTOT are given in the second columns. The next two columns contain these four statistics for $\hat{S}(\hat{y}) = \sqrt{\mathrm{VTOT}}$ and for the Coefficient of Variation $CV = \hat{S} / \hat{y} * 100\%$. Next, for each site an estimate and associated standard error is available for the fraction of the uncertainty that can be attributed to each of three parameter groups (p1=%TMV SMART2, en, p2=%TMV SUMO, p3=%TVM P2E). The mean, min, max and sd of these estimates over the 500 sites are given in the columns labelled p1 – p3, and se1 – se3 (being the standard errors in p1-p3).

Output variable		**ŷ**	**VTOT**	**√VTOT**	**CV**	**p1**	**p2**	**p3**	**se1**	**se2**	**se3**
pH	mean	4.12	0.05	0.23	6	87	11		1	2	
	sd	0.27	0.03	0.05	1	7	7		1	1	
	min	3.75	0	0	0	12	0		0	0	
	max	7.1	0.33	0.57	13	98	89		19	18	
Navail	mean	1.29	0.05	0.22	17	49	45		2	2	
	sd	0.22	0.03	0.05	2	8	9		0	0	
	min	0.93	0.01	0.09	9	6	19		2	1	
	max	4.16	0.54	0.73	24	60	112		3	4	
Biomtot	mean	5.75	3.03	1.72	30	2	98		2	0	
	sd	0.64	0.94	0.24	2	2	1		0	0	
	min	4.73	1.82	1.35	21	0	95		2	0	
	max	12.39	7.61	2.76	36	7	100		2	1	
F	mean	6.79	1.32	1.15	17	16	0	82	2	2	1
	sd	0.29	0.33	0.1	3	8	0	8	0	0	0
	min	4.75	1.08	1.04	14	0	0	15	1	1	0
	max	7.41	5.37	2.32	46	82	2	99	2	2	2
R	mean	2.33	0.6	0.77	33	0	0	98	2	2	0
	sd	0.12	0.01	0.01	1	1	0	1	0	0	0
	min	2.17	0.57	0.76	22	0	0	89	2	2	0
	max	3.75	0.71	0.85	35	7	0	100	2	2	1
N	mean	1.56	0.36	0.6	38	5	0	98	2	2	0
	sd	0.08	0.04	0.03	0	1	1	1	0	0	0
	min	1.46	0.31	0.55	36	4	0	83	2	2	0
	max	2.67	0.92	0.96	39	8	8	102	2	2	1
MOVE4	mean	4.87	2.24	1.43	29	6	0	71	2	2	1
	sd	0.82	1.29	0.44	6	4	1	9	0	0	0
	min	3.41	0.66	0.81	20	0	0	11	2	2	1
	max	6.19	4.85	2.2	48	44	4	93	2	2	2

Figure 36 shows the correlation matrix for the relations between the uncertainty in the output variables accounted for by the different models. High correlation are present for pH and nitrogen availability, pH and R and number of species simulated and F accounted for by the soil variables (SMART2/maps). For the %TVM related to SUMO2 there are high correlations between pH and nitrogen availability, total biomass and nitrogen availability and pH and N. For P2E high correlations are present for F and N and F and the number of species simulated. For MOVE4 only low correlations are present. The figures for all correlations are shown in Appendix 12.

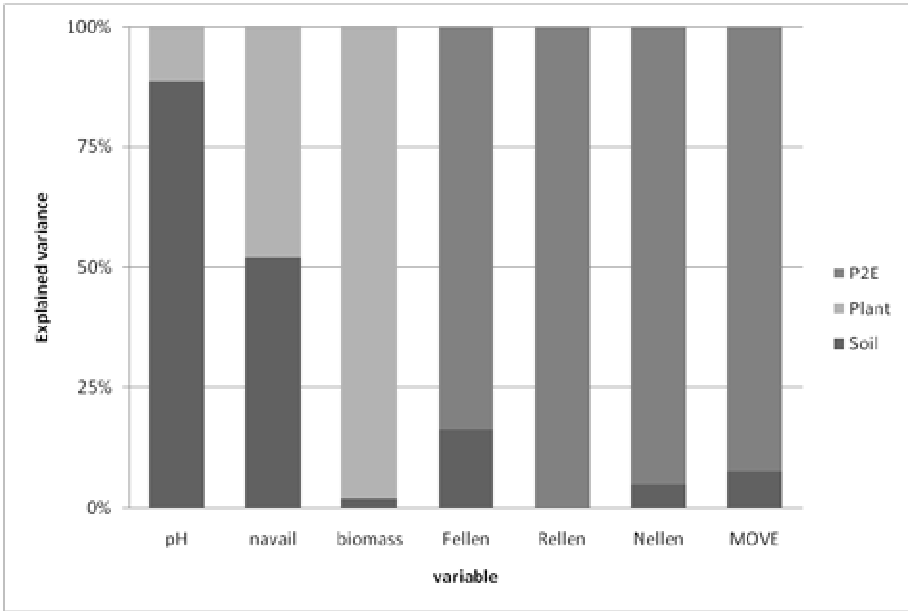


Fig 35. Results for heathland. Percentage of uncertainty attributable to the Soil, Plant and P2E parameters (totalized to 100%) for each of the seven output variables pH, nitrogen availability (navail), biomass, Ellenberg F, R and N and MOVE4.

Correlation matrix for %TMV due to SUMO2

p[1][1]	1.000						
p[2][1]	0.478	1.000					
p[3][1]	0.012	0.142	1.000				
p[4][1]	-0.314	-0.115	0.208	1.000			
p[5][1]	0.214	-0.004	-0.076	-0.151	1.000		
p[6][1]	-0.456	-0.195	-0.047	0.381	-0.014	1.000	
p[7][1]	-0.159	0.028	0.148	0.630	-0.084	0.196	1.000
	p[1][1]	p[2][1]	p[3][1]	p[4][1]	p[5][1]	p[6][1]	p[7][1]

p[1][2]	1.000						
p[2][2]	0.422	1.000					
p[3][2]	0.130	0.494	1.000				
p[4][2]	0.037	0.035	-0.080	1.000			
p[5][2]							
p[6][2]	0.418	0.332	-0.157	0.067	0.000	1.000	
p[7][2]	0.041	0.051	-0.016	0.139	0.000	0.136	1.000
	p[1][2]	p[2][2]	p[3][2]	p[4][2]	p[5][2]	p[6][2]	p[7][2]

p[1][3]	1.000						
p[2][3]	0.071	1.000					
p[3][3]	0.009	-0.007	1.000				
p[4][3]	-0.031	0.038	-0.006	1.000			
p[5][3]	0.001	0.033	-0.116	-0.264	1.000		
p[6][3]	-0.019	0.014	-0.014	0.409	-0.137	1.000	
p[7][3]	0.003	0.013	-0.032	0.870	-0.233	0.364	1.000
	p[1][3]	p[2][3]	p[3][3]	p[4][3]	p[5][3]	p[6][3]	p[7][3]

p[1][4]	1.000						
p[2][4]	0.030	1.000					
p[3][4]	-0.034	0.012	1.000				
p[4][4]	-0.003	0.075	-0.054	1.000			
p[5][4]	-0.048	-0.040	-0.009	-0.017	1.000		
p[6][4]	0.075	0.104	0.142	0.002	-0.020	1.000	
p[7][4]	-0.036	-0.066	-0.027	-0.017	0.019	0.064	1.000
	p[1][4]	p[2][4]	p[3][4]	p[4][4]	p[5][4]	p[6][4]	p[7][4]

Fig. 36. Results for heathland: For each of the four parameter groups, correlations are given between uncertainties attributable to that parameter group, for the 7 output variables. First index: 1=pH, 2=nitrogen availability, 3=total biomass, 4=F, 5=R, 6=N, 7=npresent. Second index: 1= SMART2/maps, 2= SUMO2, 3= P2E, 4=MOVE4.

9.3 Forest

As for heathland the range of the average pH for the sites is very low with most pH values between 3.8 and 5.0 pH units (Fig. 37). The range of the simulated pH values per site is also relative small with most of the standard deviations between 0.1 and 0.6 pH units. For most of the sites the uncertainty in the pH is mostly explained by the soil variables. At some sites the plant variables also contributes, minor, to the uncertainty in the soil pH.

The range in the average simulated nitrogen availability is reasonable (Fig. 38). The variation per site is moderate, implying that many different nitrogen availabilities are simulated per site. The uncertainty in the nitrogen availability is both caused by the soil and the plant variables. Mostly both more or less contribute at each site, though at some sites the uncertainty is largely caused by the plant variables. The simulated total biomass by SUMO2 gives similar results. There is a fair range of average biomass between the sites, with the highest biomasses in the south of The Netherlands (Fig. 39). The variation in the biomass at the sites is relative low mostly up till 7 ton/ha. The uncertainty in the biomass simulations is caused by both plant and soil parameters, where the influence of the plant variables is larger than the influence of the plant variables.

Similar to Grassland and Hethland, almost all uncertainty in Ellenberg F, R and N is caused by the Ellenberg regression parameters (P2E). The soil variables contribute also at some sites, especially for F, where the contribution of the plant variables is negligible except for Ellenberg N. For the latter the contribution for some sites is significant and of the same magnitude as the contribution of the soil variables.

The average predicted number of plant species varies per site from 1.5 to 6.0 (Fig. 43). The standard deviation of the sites shows that the variation per site is relative large, up to 50%. As could be expected from the previous results, the major part of the uncertainty in the MOVE4 predictions is caused by the uncertainty in the translation from the model output into the Ellenberg indicator values. At some sites the uncertainty of the soil variables also contributes a major part to the uncertainty. At some sites this contribution is equal to the contribution of the Ellenberg variables. The contribution of the plant variables to the uncertainty is at most sites low, with maxima up to 9%.

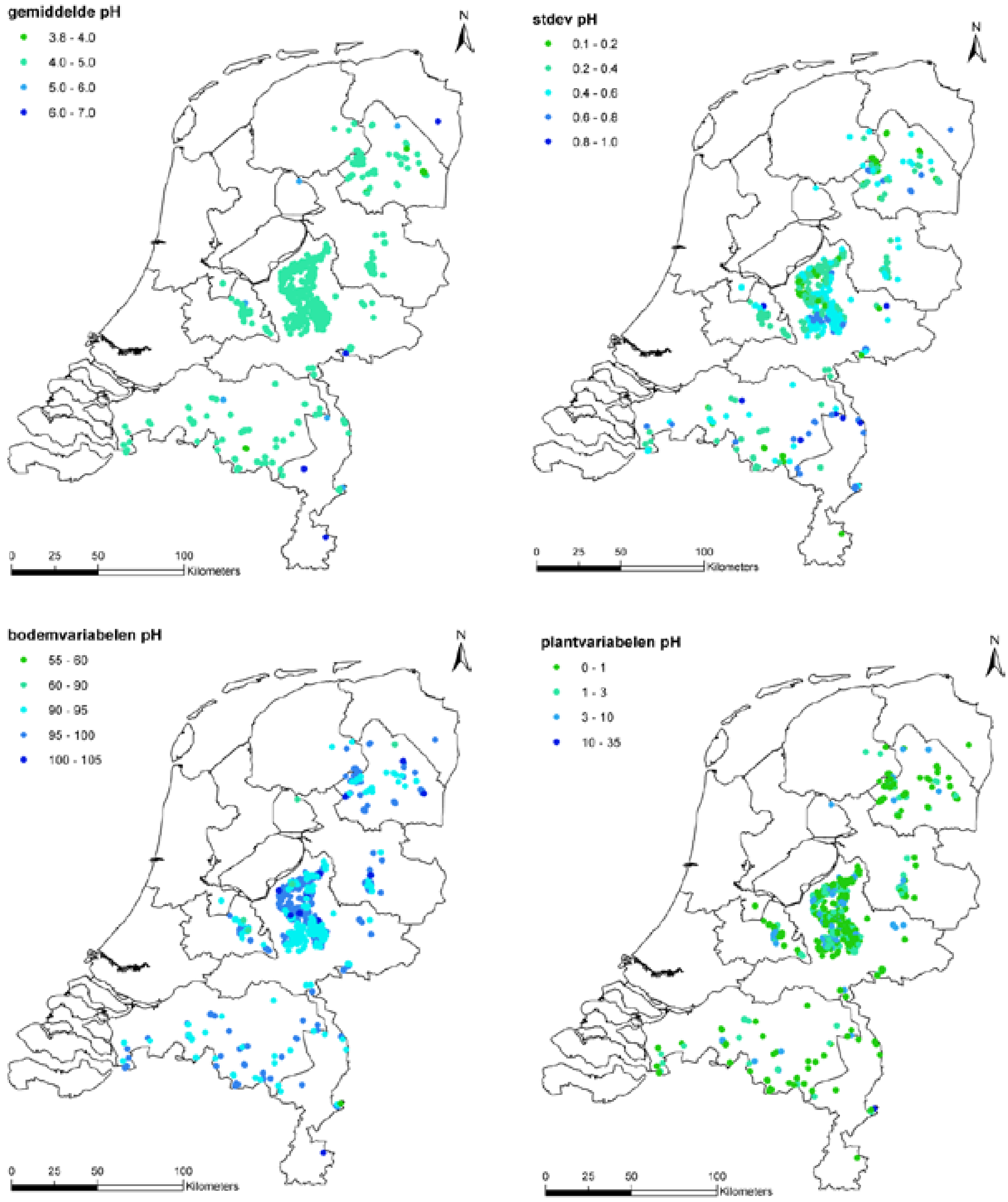


Fig. 37. Average simulated pH for forest (by SMART2, top left), standard deviation of the pH (top right), percentage total variance for soil variables (bottom left) and plant variables (bottom right) per site.

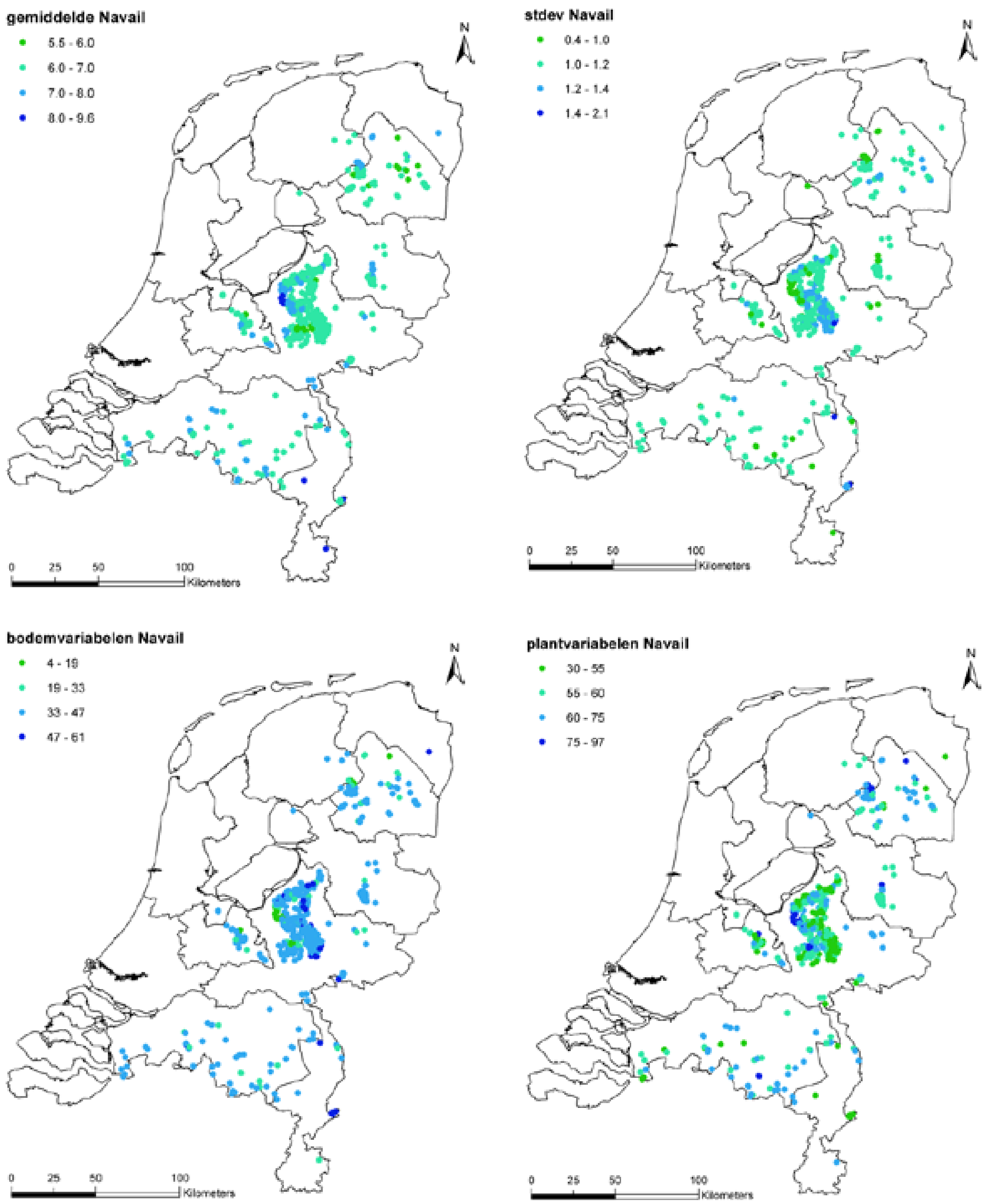


Fig. 38. Average simulated nitrogen availability for forest (by SMART2, top left), standard deviation of the nitrogen availability (top right), total percentage variance for soil variables (bottom left) and plant variables (bottom right) per site.

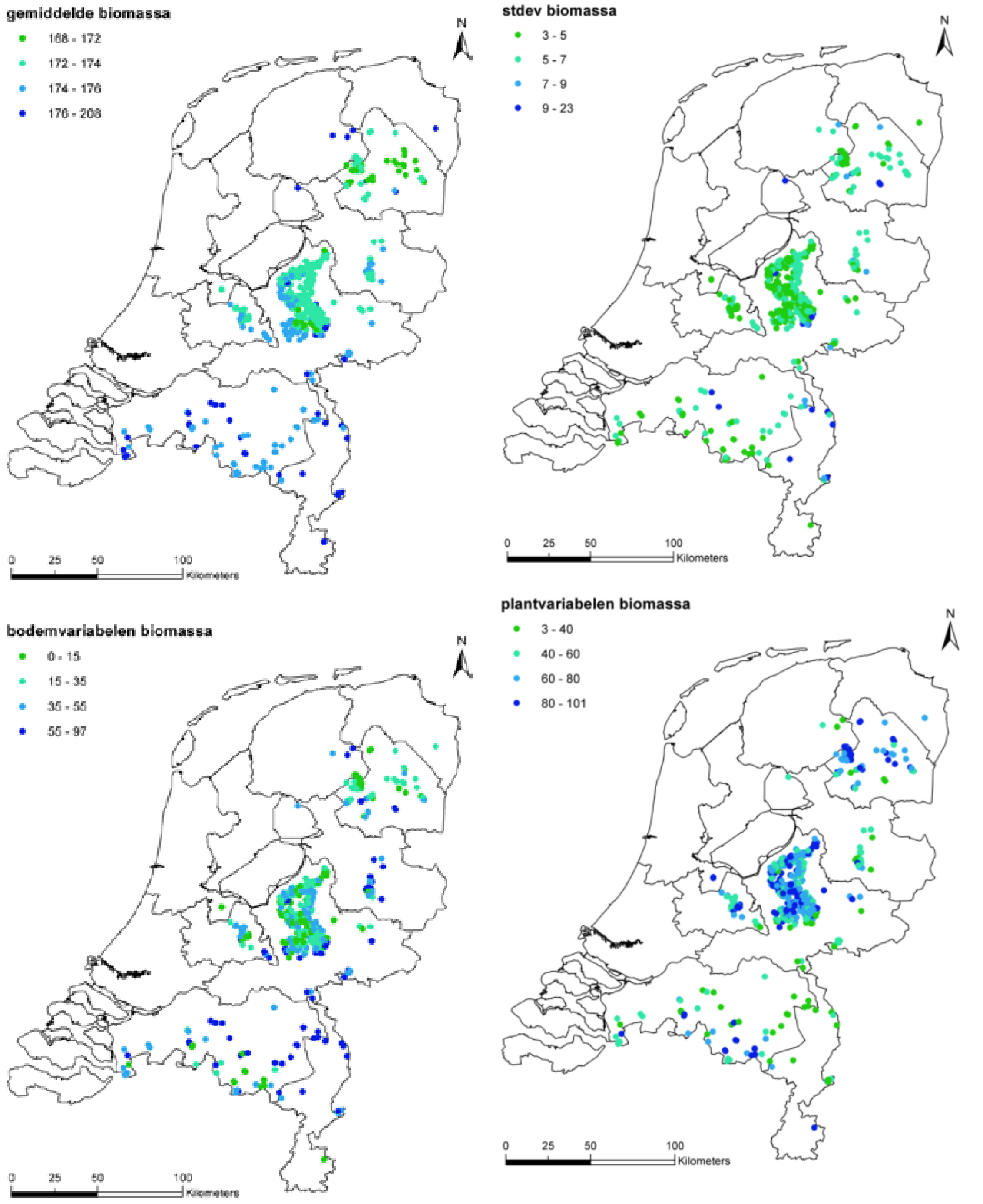


Fig. 39. Average simulated biomass for forest (SUMO2, top left), standard deviation of the total biomass (top right), percentage total variance for soil variables (bottom left) and plant variables (bottom right) per site.

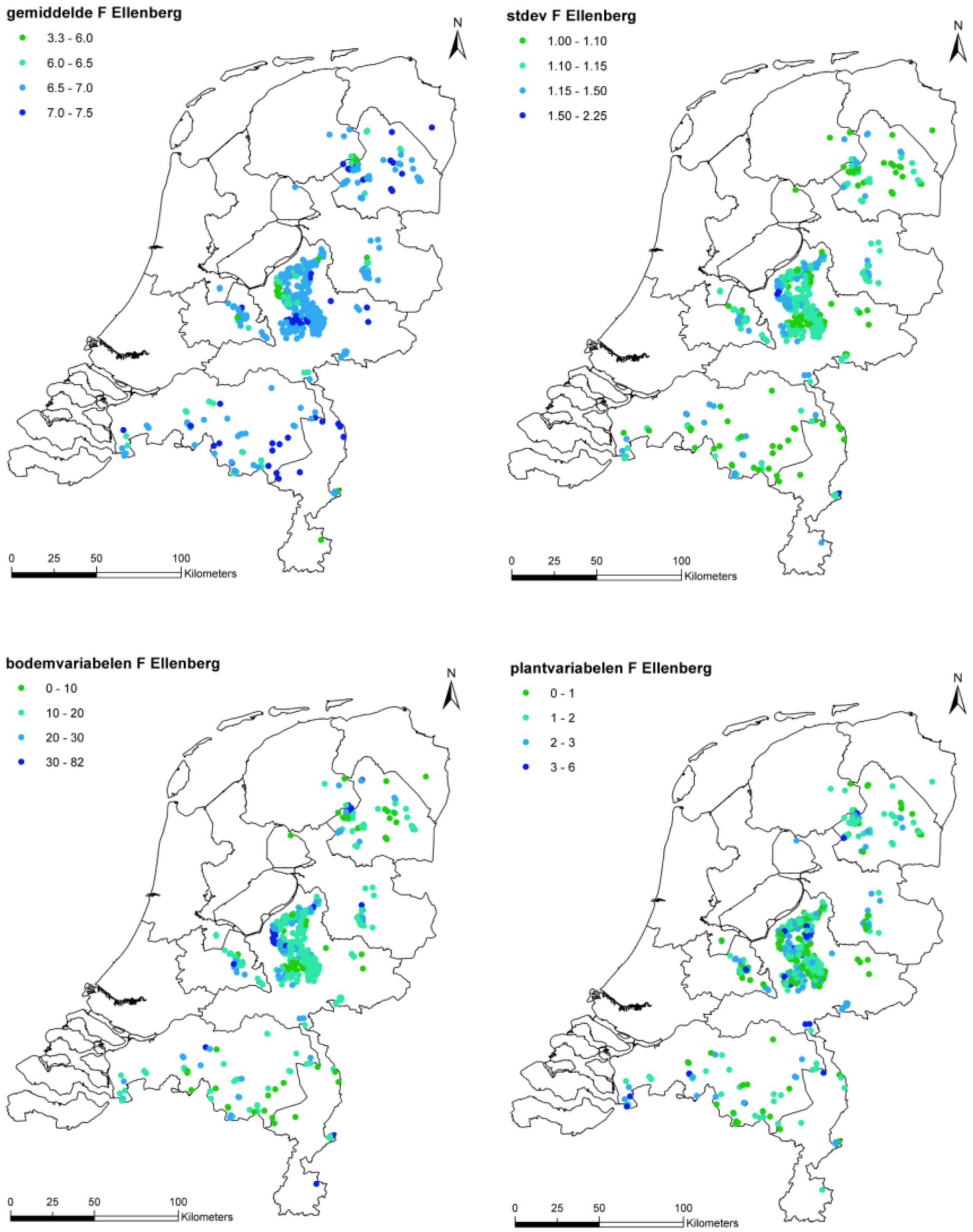


Fig. 40. Average simulated Ellenberg indicator value for moisture for forest (P2E, top left), standard deviation (top right), percentage total variance for soil variables (bottom left), plant variables (bottom right) and the regression parameters (see next page) per site.

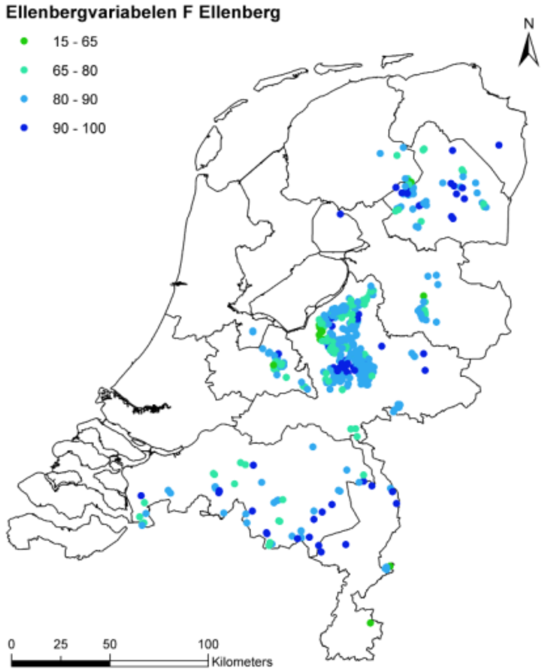
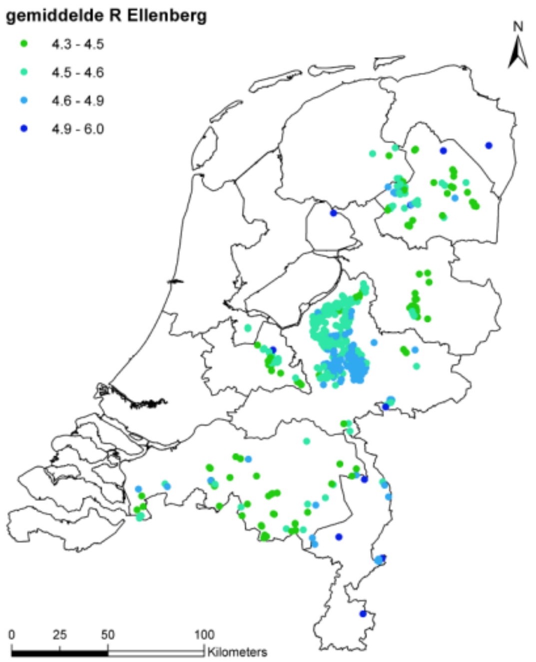
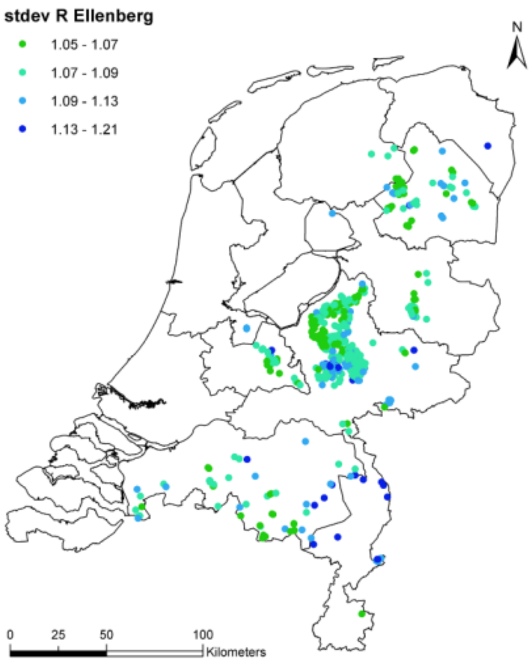


Fig. 40 (continued). The regression parameters per site.





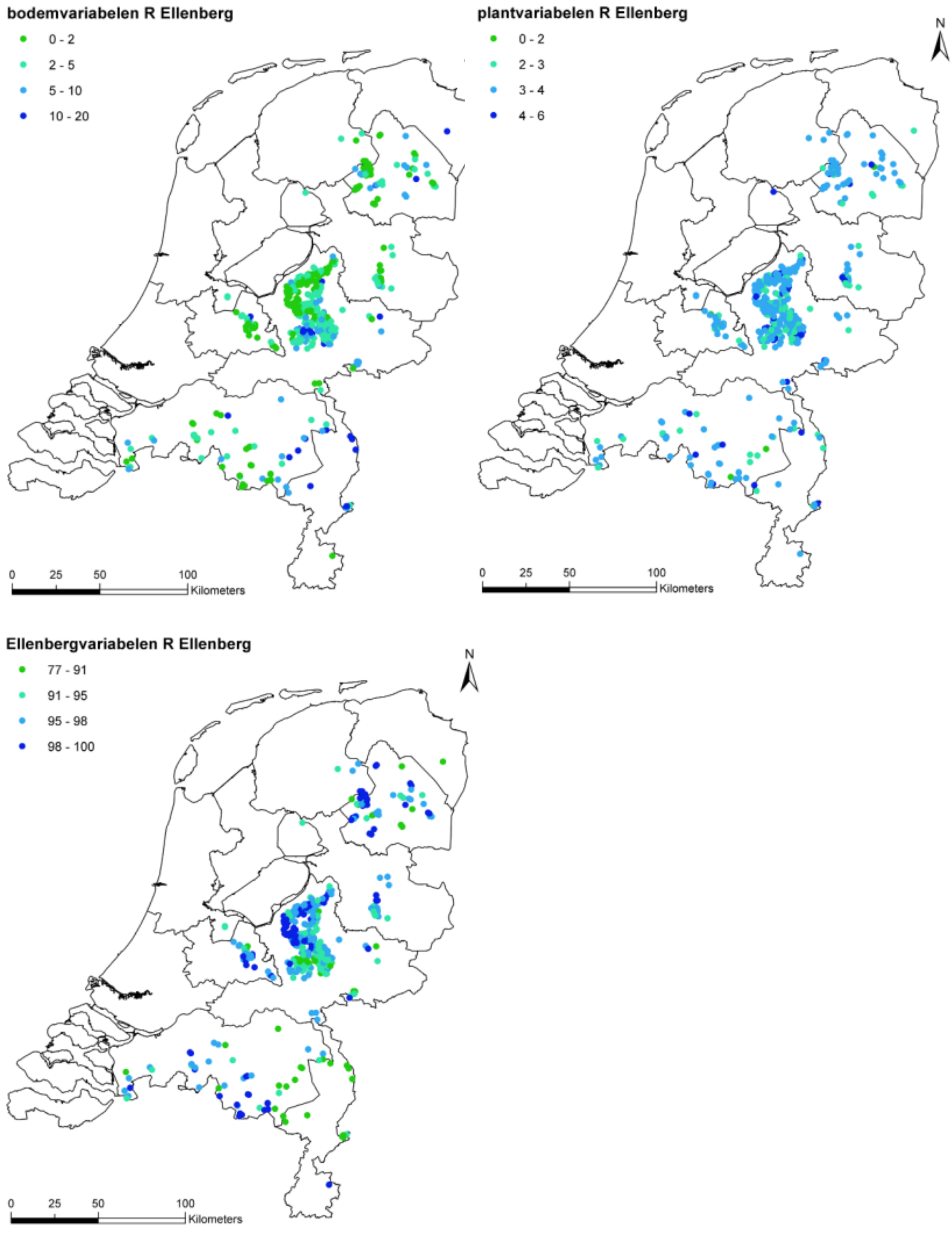
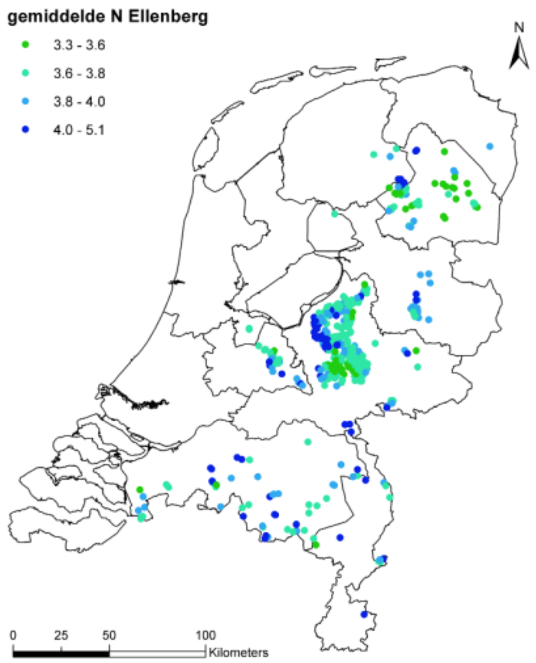
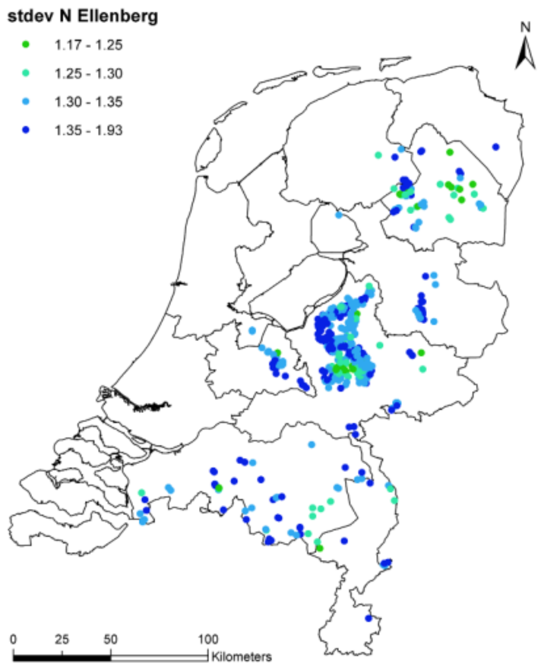
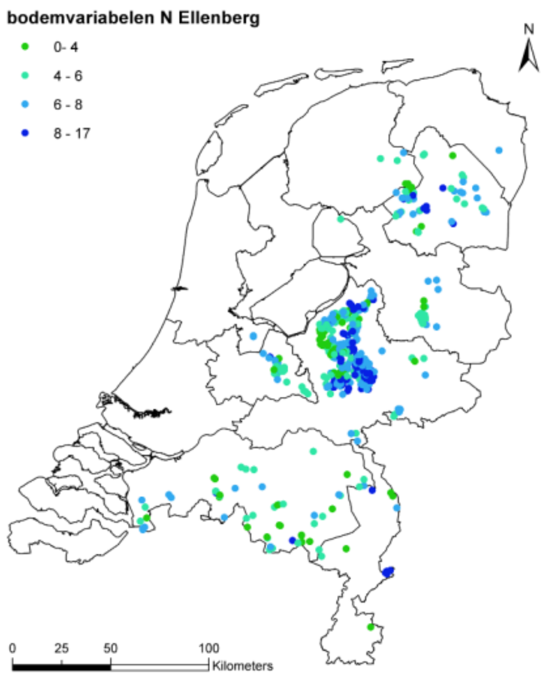
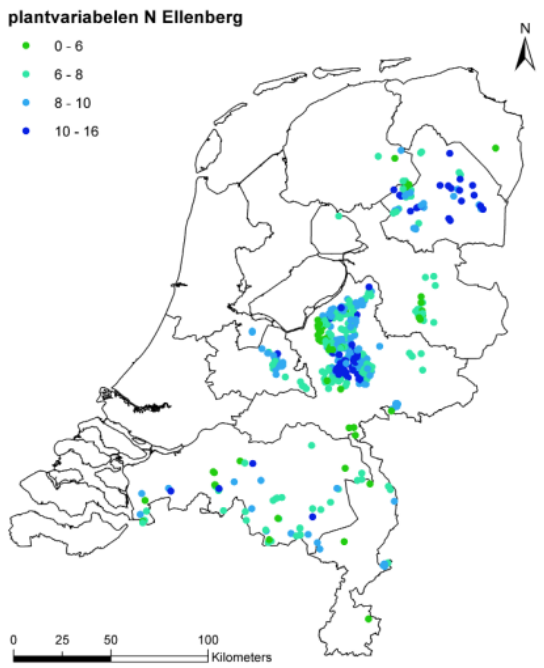


Fig. 41. Average simulated Ellenberg indicator value for acidity for forest (P2E, top left), standard deviation (top right), percentage total variance for soil variables (middle left), plant variables (middle right) and regression parameters (bottom left) per site.


gemiddelde N Ellenberg
3.3 - 3.6
3.6 - 3.8
3.8 - 4.0
4.0 - 5.1
N
0 25 50 100
Kilometers


stdev N Ellenberg
1.17 - 1.25
1.25 - 1.30
1.30 - 1.35
1.35 - 1.93
N
0 25 50 100
Kilometers


bodemvariabelen N Ellenberg
0- 4
4 - 6
6 - 8
8 - 17
N
0 25 50 100
Kilometers


plantvariabelen N Ellenberg
0 - 6
6 - 8
8 - 10
10 - 16
N
0 25 50 100
Kilometers

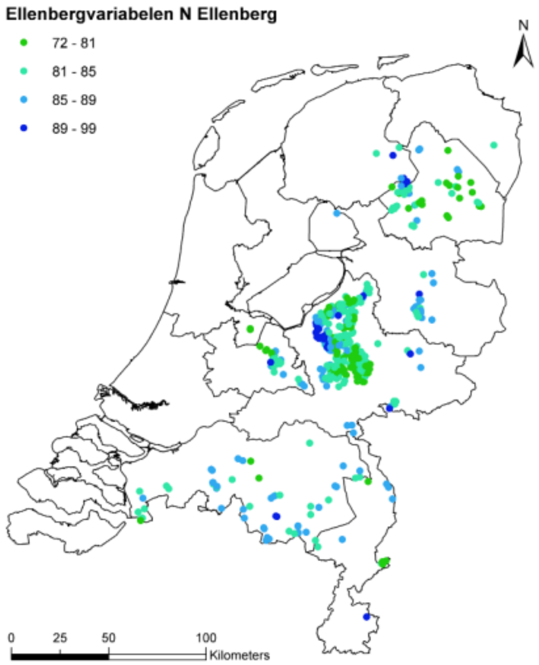
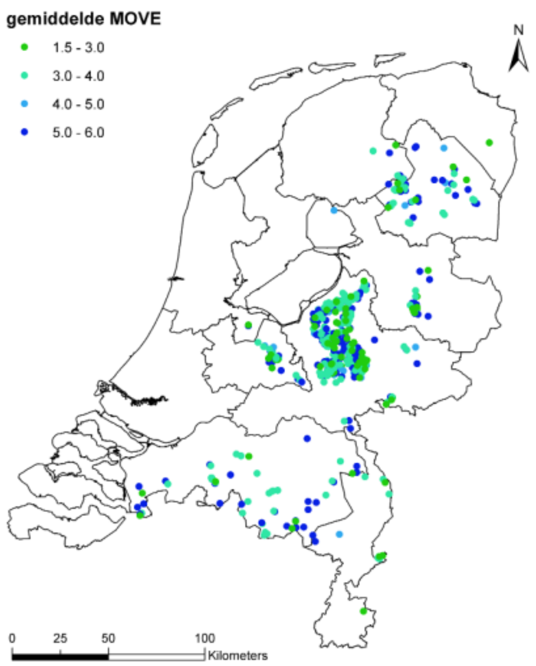
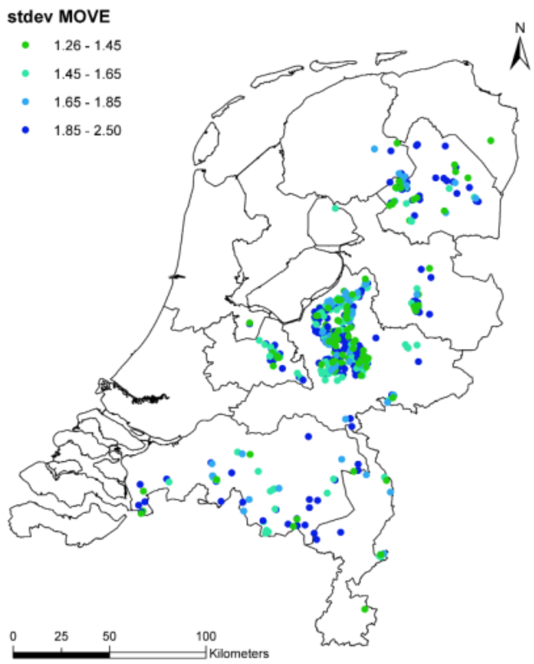


Fig. 42. Average simulated Ellenberg indicator value for nutrients for forest (P2E, top left), standard deviation (top right), percentage total variance for soil variables (middle left), plant variables (middle right) and regression variables (bottom left) per site.





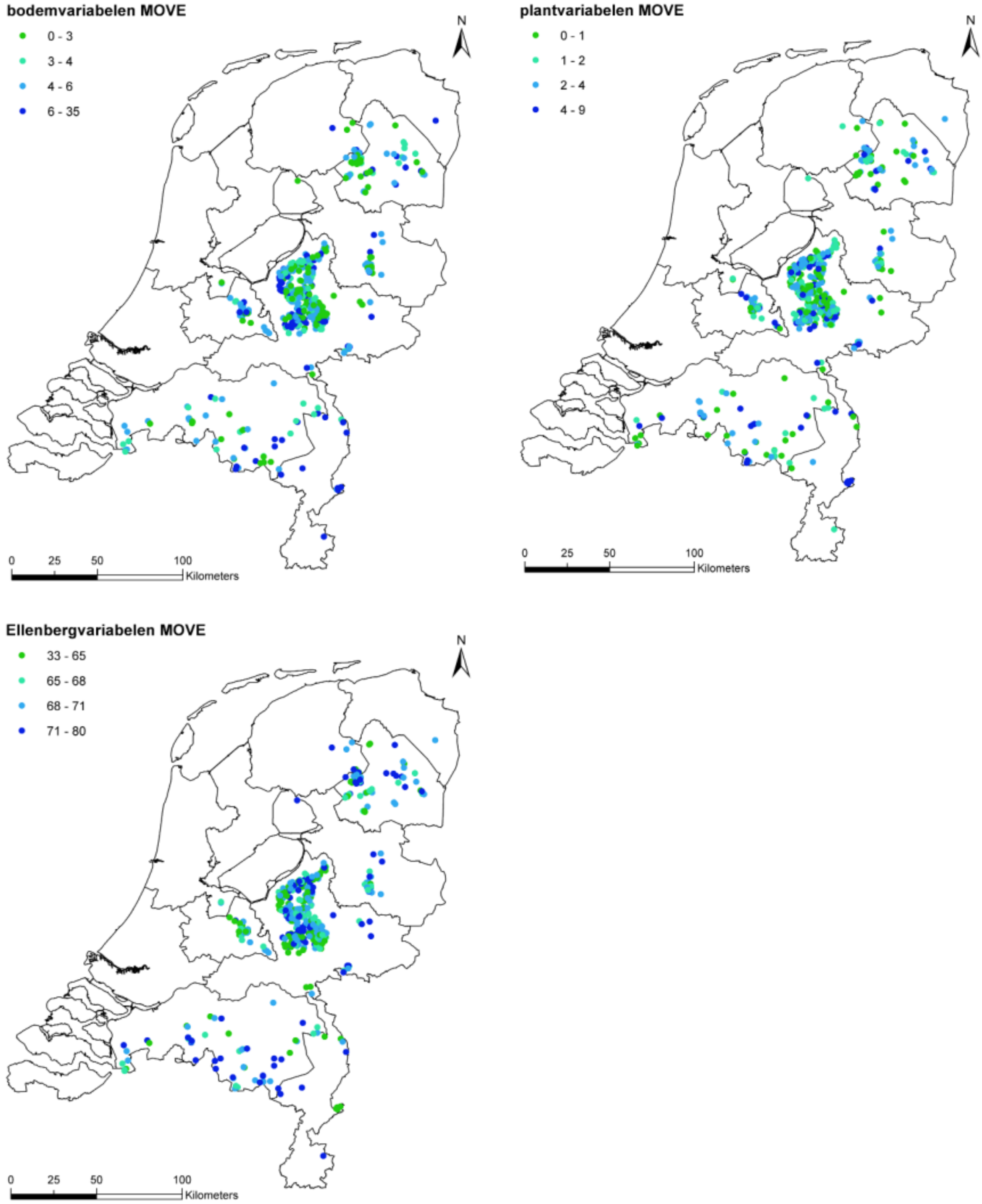


Fig. 43. Average simulated number of occurring species for forest (MOVE4, top left), standard deviation (top right), percentage total variance for soil variables (middle left), plant variables (middle right) and regression variables (bottom left) per site.

On average the uncertainty in the soil pH is almost totally explained by the soil parameters (Table 4 and Fig. 44). At some sites the plant variables also contribute. The uncertainty in the nitrogen availability is for the major part caused by the plant variables, though on average a lot of uncertainty is also explained by the soil parameters. This also applies for the biomass, though the effect of the plant variables is larger and thus the effect of the soil variables smaller. The uncertainty in the Ellenberg indicator values is largely caused by the variables of the regression equation to calculate them. Only for F there is also some influence of the soil variables on the uncertainty. This is also the case for the MOVE4 results, the number of simulated species. At some sites the soil variables also have some contribution to the uncertainty in the number of species. The total explained variance for the MOVE4 outcome is with 75% rather low. This indicates some problems with the applied model to estimate the explained variances; normally an explained variance of over 90% is advisable. The uncertainty in the given percentage explained variances are rather low, indicating that the values given are rather precise.

Table 4. Results for forest for all output variables. For each site the output of the first 3000 Monte Carlo runs was averaged to obtain $\hat{y}$ *, an estimate for the value of the output variable y. The mean, min, max and standard deviation of the 500 values for* $\hat{y}$ *are given in the first column. The variance of the first 3000 outputs, VTOT, is an estimate for the total uncertainty on that site. The mean, standard deviation, minimum and maximum of the 500 values for VTOT are given in the second columns. The next two columns contain these four statistics for* $\hat{S}(\hat{y}) = \sqrt{\mathrm{VTOT}}$ *and for the Coefficient of Variation* $CV = \hat{S} / \hat{y} * 100\%$*. Next, for each site an estimate and associated standard error is available for the fraction of the uncertainty that can be attributed to each of three parameter groups (p1=%TMV SMART2, en, p2=%TMV SUMO, p3=%TVM P2E). The mean, min, max and sd of these estimates over the 500 sites are given in the columns labelled p1 – p3, and se1 – se3 (being the standard errors in p1-p3).*

Output variable		**ŷ**	***VTOT***	***√VTOT***	***CV***	**p1**	**p2**	**p3**	**se1**	**se2**	**se3**
pH	mean	4.32	0.18	0.39	9	96	1		2	2	
	sd	0.29	0.15	0.16	3	3	2		1	0	
	min	3.88	0.01	0.11	2	55	0		0	0	
	max	6.81	0.97	0.98	20	102	34		4	5	
Navail	mean	6.69	1.27	1.12	17	40	59		2	1	
	sd	0.48	0.27	0.12	2	8	8		0	0	
	min	5.59	0.17	0.41	5	4	32		1	0	
	max	9.59	4.22	2.06	23	61	97		2	2	
Biomtot	mean	174	29.68	5.19	3	32	66		4	4	
	sd	2.98	32.33	1.66	1	20	20		1	1	
	min	168.5	9.79	3.13	2	0	3		0	0	
	max	207.6	522	22.85	11	96	101		8	9	
F	mean	6.72	1.29	1.13	17	17	1	82	2	2	1
	sd	0.38	0.22	0.08	3	8	1	9	0	0	0
	min	3.33	1.06	1.03	14	0	0	18	1	2	0
	max	7.49	4.89	2.21	47	82	5	99	2	3	4
R	mean	4.57	1.17	1.08	24	4	3	95	2	2	1
	sd	0.15	0.05	0.02	1	3	1	4	0	0	0
	min	4.34	1.12	1.06	18	0	1	78	2	2	0
	max	5.95	1.46	1.21	25	20	6	100	2	2	1
N	mean	3.79	1.79	1.34	35	6	8	83	2	2	1
	sd	0.21	0.17	0.06	1	2	2	4	0	0	0
	min	3.3	1.39	1.18	33	0	0	72	2	2	0
	max	5.06	3.7	1.92	38	17	15	98	2	2	2
MOVE4	mean	4.33	3.13	1.75	42	5	2	68	2	2	1
	sd	1.16	0.97	0.28	7	3	2	5	0	0	0
	min	1.68	1.59	1.26	33	0	0	33	2	2	1
	max	5.92	6.05	2.46	87	34	8	80	2	2	2

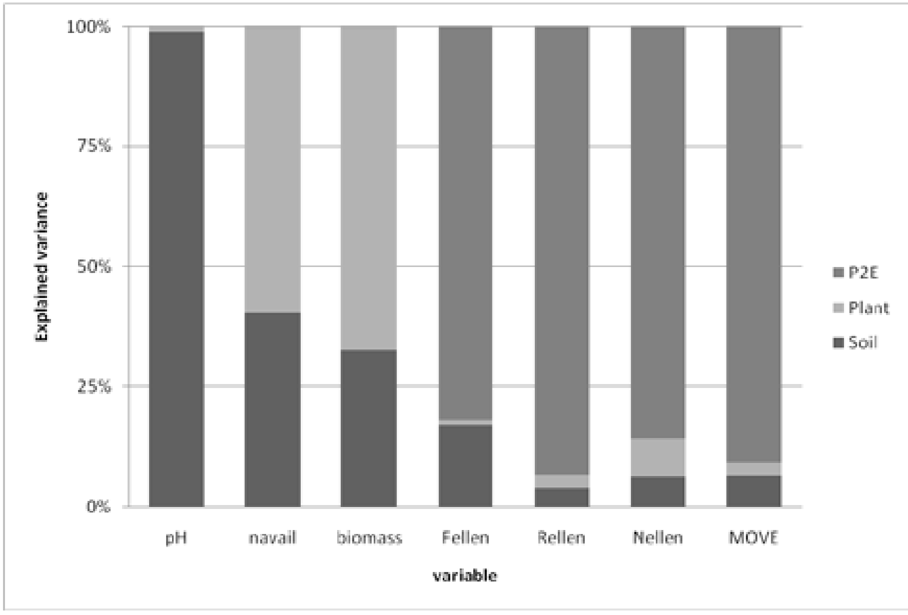


Fig 44. Results for forest. Percentage of uncertainty attributable to the Soil, Plant and P2E parameters (totalized to 100%) for each of the seven output variables pH, nitrogen availability (navail), biomass, Ellenberg F, R and N and MOVE4.

Correlation matrix for %TMV due to P2E

p[1][1]	1.000						
p[2][1]	-0.111	1.000					
p[3][1]	0.030	0.243	1.000				
p[4][1]	0.114	-0.146	-0.052	1.000			
p[5][1]	-0.288	-0.033	0.350	-0.553	1.000		
p[6][1]	-0.280	0.758	0.176	-0.231	0.266	1.000	
p[7][1]	-0.170	-0.323	0.107	0.544	0.095	-0.110	1.000
	p[1][1]	p[2][1]	p[3][1]	p[4][1]	p[5][1]	p[6][1]	p[7][1]

p[1][2]	1.000						
p[2][2]	0.057	1.000					
p[3][2]	-0.036	0.316	1.000				
p[4][2]	-0.016	-0.047	-0.052	1.000			
p[5][2]	0.306	-0.031	0.006	0.008	1.000		
p[6][2]	-0.015	-0.050	0.087	-0.012	-0.136	1.000	
p[7][2]	0.017	-0.010	-0.102	0.014	0.073	-0.061	1.000
	p[1][2]	p[2][2]	p[3][2]	p[4][2]	p[5][2]	p[6][2]	p[7][2]

p[1][3]	1.000						
p[2][3]	0.001	1.000					
p[3][3]	0.042	0.105	1.000				
p[4][3]	0.027	0.020	0.030	1.000			
p[5][3]	0.016	-0.023	-0.021	-0.529	1.000		
p[6][3]	-0.015	0.081	-0.073	-0.472	0.395	1.000	
p[7][3]	0.012	0.012	-0.011	0.494	-0.008	0.016	1.000
	p[1][3]	p[2][3]	p[3][3]	p[4][3]	p[5][3]	p[6][3]	p[7][3]

p[1][4]	1.000						
p[2][4]	-0.010	1.000					
p[3][4]	0.044	0.060	1.000				
p[4][4]	0.009	0.046	0.053	1.000			
p[5][4]	0.097	0.085	-0.037	-0.001	1.000		
p[6][4]	-0.019	0.042	0.132	-0.040	-0.040	1.000	
p[7][4]	0.018	0.086	-0.037	0.077	0.023	0.014	1.000
	p[1][4]	p[2][4]	p[3][4]	p[4][4]	p[5][4]	p[6][4]	p[7][4]

Fig. 45. Results for forest: For each of the four parameter groups, correlations are given between uncertainties attributable to that parameter group, for the 7 output variables. First index: 1=pH, 2=nitrogen availability, 3=total biomass, 4=F, 5=R, 6=N, 7=npresent. Second index: 1= SMART2/maps, 2= SUMO2, 3= P2E, 4=MOVE4.

Figure 45 shows the correlation matrix for the relations between the uncertainty in the output variables accounted for by the different models. High correlations are present between nitrogen availability and N, F and the number of species simulated and F and R for SMART2/maps. The latter has a negative correlation, indicating that the higher the percentage explained variance for F is the lower the explained variance for R is. For the SUMO2 model the correlation between the explained uncertainties of the output variables is low, though there is a weak correlation present between pH and R. For P2E high correlations are present for F with R, N and the number of species simulated. For MOVE4 the correlations are all rather low.

All figures for of the correlation matrix are shown in Appendix 12.

10 Discussion

The primary goal of this study was to quantify the uncertainty about four (three) distinct parameter groups, and to assess the relative contribution of each of these parameter groups to the variability in the model output. Due to technical problems with the model MOVE4 the number of groups was reduced to three. The uncertainty caused by the model MOVE4 is not included in the here given uncertainty, though the model was used to calculate the number of simulated species and the uncertainty in it.

The study has been carried out by means of a Monte Carlo setup. The available results also allow us to say something about the value of the outputs themselves, and its absolute variability. We start the discussion with some comments on these latter two points, and will then come back to the main subject of the investigation.

The number of predicted species is rather low. For grassland, only app. 1.5 species per site are predicted to be present out of possible 30 species. For the two other vegetation types the ratio is much higher (4 to 5 predicted present species out of possible 20), but still rather low, especially since a fair part of rather common species is included. Although assessing the actual number of species predicted was not part of the uncertainty analysis, it is a surprising result and should be investigated further. The results seem to suggest that the predicted number of species is underestimated. However, only a proper validation of MOVE4 can reveal the real performance of the model. Whether or not a species is assumed to be actually present depends on the predicted probability of occurrence and a species specific threshold value. This automatically generated threshold value may be too high (see further Van Adrichem *et al.* 2010). The low predictions may be caused by the fact that only a subset of the species was considered in this analysis. It might be that, when all species present in MOVE4 are selected, a relatively higher number of species will be predicted, because the number of general species is probably underrepresented in this research. But the small number of species predicted may also reveal an underlying problem with the model predictions (namely, that in general the probability of occurrence is underestimated). This may be caused by MOVE4 itself, but may also be caused earlier in the model chain. The translation of nitrogen availability into Ellenberg indicator value for nutrient availability may be a major cause, since the relationship is very weak and could be regarded as rather unscientific. Only field measurements can overcome these problems.

The absolute number of species predicted by MOVE4 is rather low, especially for grassland (1.58). The end result raises also questions about the number of predicted species and thus the accuracy of the model predictions itself as well as the uncertainty. See also the remarks about the value of VTOT below.

For the number of species, the average of the uncertainty estimate (i.e. the average of the estimated VTOT over the 500 sites) varies from 2.24 for heathland and 3.13 for forest to 1.74 for grassland (see Table 5 here below; the values were taken from Tables 2-4). The square roots of these VTOTS, which are of the same magnitude as the number of species predicted, are 1.43, 1.75 and 1.29, respectively. In the table, the numbers between brackets are averages of the estimated standard errors. These numbers are very small, which is entirely due to the large sample size of 3000 (see Appendix 4, 5, 11).

Table 5. Estimated number of species predicted with MOVE4, and estimated total uncertainty, averaged over the 500 sites for each vegetation type. Between brackets is the average, over the 500 sites, of the standard errors for each estimate.

Output variable: **Vegetation type**	$\hat{y}$	$\mathrm{VTOT} = \hat{\mathrm{Var}}(\hat{y})$	$\sqrt{\mathrm{VTOT}}$	$\mathrm{CV} = \sqrt{\mathrm{VTOT}} / \hat{y} \times 100\%$
Grassland	1.58 (0.02)	1.74 (0.08)	1.29 (0.05)	88 (1.9)
Heathland	4.87 (0.03)	2.24 (0.05)	1.43 (0.03)	29 (0.4)
Forest	4.33 (0.03)	3.13 (0.07)	1.75 (0.04)	42 (0.6)

It must be noted that in the table 5 the uncertainty within MOVE4 has not been taken into account (see further on).

Most of the variability in the MOVE4 output is caused by the uncertainty in P2E (Table 6): the translation of the groundwater table, simulated soil pH and simulated nitrogen availability (the latter two simulated by SMART2) into the Ellenberg indicator values. This is in line with earlier research by Schouwenberg *et al.* (2000), who also found that the translation function by the P2E model is the most uncertain step in the whole model chain. Efforts to reduce the variability of the end result, the number of predicted species, can therefore best be directed to improving these functions, or even to completely avoiding them, which could be achieved by replacing the Ellenberg indicator values in MOVE4 with measured values (Wamelink *et al.* 2005). These values, such as soil pH, should then have a direct relation with the simulated output of SMART2 or the values derived from the spring groundwater table map, thus avoiding the awkward step of the translation into Ellenberg indicator values. That this may reduce the uncertainty was shown by Wamelink *et al.* (2005) who compared the uncertainty in predictions with Ellenberg indicator value for R and predictions with pH indicator values. The prediction error for Ellenberg R was more than twice as large as predictions based on pH indicator values.

Table 6. Percentage explained variance of the output of MOVE4 for each parameter group and vegetation type. The soil parameter group includes the soil and groundwater table map.

Type	**Explained variance (%)**		
	Soil	Plant	Ellenberg
Grassland	3	4	76
Heathland	6	0	71
Forest	5	2	68

The conclusions on the relative large contribution of P2E to the overall uncertainty must be put in perspective. For P2E also the model uncertainty was included, where it was left out for SMART2 and SUMO2, though for the latter two models this cannot be neglected. However, estimations, even an educated guess, of the model uncertainty is not available at the moment. It may be clear that by leaving out the model uncertainty of the two models the overall uncertainty is underestimated. Also the relative contribution of the two models to the uncertainty is underestimated and thus the relative effect of P2E overestimated.

When looking at individual sites it becomes clear that there can be rather large differences between site variability and in the causes of these variabilities. For some sites the variability in the MOVE4 predictions is not primarily caused by the P2E variables but by uncertainty in the soil variables (SMART2/maps). The effect of uncertainty in the parameters for the plant model (SUMO2) is almost everywhere small.

The variability in the end result is caused by uncertainty in the parameter values. So assessing an adequate statistical distribution for the input parameters is of crucial importance, since both over- and underestimation of the parameter uncertainties may lead to a wrong estimate of the variability of the model output. For some of the model parameters, a value and uncertainty (mean and variance of the statistical distribution assumed) can be estimated from empirical data; for other model parameters these quantities are only available as expert judgments. We think it is advisable to collect (more) field data to make it possible to start with more reliable estimates for the uncertainty of the investigated parameters. As a by-product, these field data will also allow better calibration of parameters for 'ordinary' model runs.

The uncertainty in MOVE4 was not included in the analysis. Thus the model output does not contain any variability as a result of uncertainty in the responses of the plant species to the environment. Statistical distributions for the MOVE4 parameters of the selected species were determined and parameter values were simulated from them, but these values could not be used because of technical issues. One of the most important reasons was that in theory MOVE4 can run with different parameter values for each run, but that in practice this becomes almost impossible on the scale necessary here, because currently this process is not be automated. Changes in the model code would be necessary to make this possible. We believe that the uncertainty in the MOVE4 parameters is substantial and may be bigger than all other uncertainties put together (Wamelink *et al.* 2001), so the absolute variabilities (VTOT) found in this study should be regarded as minimum values only.

The results reflect the internal model uncertainty including the two input maps. For soil and vegetation, only a very limited number of model parameters could be included in the analysis. However, we believe that the most uncertain and most important parameters were included in the analysis. This assumption is also based on earlier work for both SMART2 and SUMO2 (Kros *et al.* 2002, Wamelink 2008). For P2E, all parameters of the translation module were included in the uncertainty analysis.

We only investigated the contributions of the three parameter groups to the uncertainty in the end result of the model chain; the prediction of plant species. We did not investigate the contribution of the uncertainty of a parameter group to the next step in the model chain. A follow-up could look at this and thus give insight in the uncertainty propagation between the several modules.

Note that an uncertainty analysis does not give any information on the model performance. This can only be obtained from validation studies by comparing field measurements with the simulated values.

The uncertainty analysis focuses on individual sites. The total variance and the percentage which can be ascribed to the three parameter groups are first calculated for each site separately. The tables of Results (Tables 2, 3 and 4) then give the mean of these values over the 500 sites. However one of the main uses of the Nature Planner is targeting the Netherlands as a whole, but it will also be used for provinces and larger nature areas such as De Veluwe. In that case the relevant uncertainty is some sort of spatial aggregation of the uncertainties at individual sites. This is only useful when spatial correlations are taken into account. This has already been done for the two parameter groups (soil and vegetation) and we assumed that the spatial correlation for Ellenberg is not spatial correlated. However, the results are only valid for the site level and for studies that are aggregated to a higher (national) level an extra step will be necessary to gain insight in the uncertainty on that level.

11 Conclusions

For each of the 500 sites for each vegetation type, the analysis has yielded a MOVE4 estimate of the number of species, and an estimate of the associated absolute uncertainty. For grassland the distribution of the 500 numbers of species predicted has mean 1.58, for heathland 4.87 and for forest 4.33 (see also Table 7). The distribution of the uncertainty has a mean of 1.74 for grassland, 2.24 for heathland and 3.13 for forest.

Table 7. Summary of results of the uncertainty analysis of the model chain Soil map, Groundwater table map, SMART2, SUMO2, P2E and MOVE4. Given are descriptive statistics (mean and sd) for the distribution, over the 500 sites for each vegetation type, of the following two variables: 1. the number of species predicted by MOVE4 (N pred); 2. the square root of the estimated uncertainty (VTOT) in the model output. Also given is the average percentage of the uncertainty in the model output that can be ascribed to the three parameter groups SMART2 + maps parameters, SUMO2 and P2E, with the average of its standard error.

Distribution of simulation results over 500 sites.

Descriptive statistics:	**Grassland**		**Heathland**		**Forest**	
	mean	sd	mean	sd	mean	sd
N. species predicted	1.58	0.53	4.87	0.82	4.33	1.16
$\sqrt{\text{VTOT}}$	1.29	0.27	1.43	0.44	1.75	0.28
Average of percentage of uncertainty attributable to (with average and standard error (se))						
SMART2/maps	3 (2)		6 (2)		5 (2)	
SUMO2	4 (2)		0 (2)		2 (2)	
P2E	76 (2)		71 (1)		68 (1)	

The average number of species predicted is low, especially for grassland (Table 7). This asks for a validation with field data. This raises more concern about the validity of the MOVE4 results than the here obtained uncertainty in the model chain. We therefore recommend that MOVE4 is validated thoroughly in the near future, or that a new model will be developed (see also here below).

The standard errors of the uncertainty contributions show that enough simulations have been used. They also show that in a future uncertainty analysis of this model chain possibly fewer simulations can be employed.

Almost all variance in the MOVE4 predictions is caused by uncertainty in the P2E module: the translation of the groundwater table, pH and nitrogen availability into the Ellenberg indicator values for moist, acidity and nutrient availability. At some of the sites however, the soil parameters cause the major part of uncertainty. There is no direct explanation for this and further research to reveal this is necessary.

For some of the parameters included in the model, e.g. Ellenberg N, no data were available to estimate their value and the uncertainty therein. Hence, these parameters, and their uncertainty, were estimated by means of an expert judgment, and hence they may be an over or under estimation of the real uncertainty. Only field measurements or experiments can solve this. Note that for P2E model uncertainty was included in the analysis, where it was left out for SMART2 and SUMO2. This may give an underestimation of the uncertainty in the MOVE4 output and the relative contribution of SMART2 and SUMO2 tot the overall uncertainty.

The uncertainty in the MOVE4 parameters was not included in the analysis, due to computational problems. Therefore the reported uncertainties in the MOVE4 predictions are most likely underestimated. Furthermore, when uncertainty in the MOVE4 parameters would be included, the major contributors to variability in the model output might also change, as a result of the uncertainty in the MOVE4 parameters.

To reduce the uncertainty (variability) in the model output we advise to solve the problem of the translation into Ellenberg indicator values (P2E). This could be done by basing the model MOVE4 or a new model on field measurements that can be linked directly with the model outputs of SMART2 and the groundwater table map or the newly developed national hydrological model (NHI). This solution would solve two problems, i.e. the uncertain step from physic parameters into Ellenberg indicator values and the general problems related to the use of Ellenberg indicator values (see Wamelink *et al.* 2002). Alternatively, Ellenberg indicator values could be linked to other model output parameters or with combined parameters or the relation between them could be improved. However, the first signs for the alternative are not very hopeful.

The uncertainties reported only reflect the model uncertainty. They do not give any information about the validity of the model outputs. For that a proper validation is necessary, i.e. comparing model simulations with field data. At the moment this is not planned. We advise first to develop a new model based on field measurements instead of Ellenberg indicator values, and then validate that new model.

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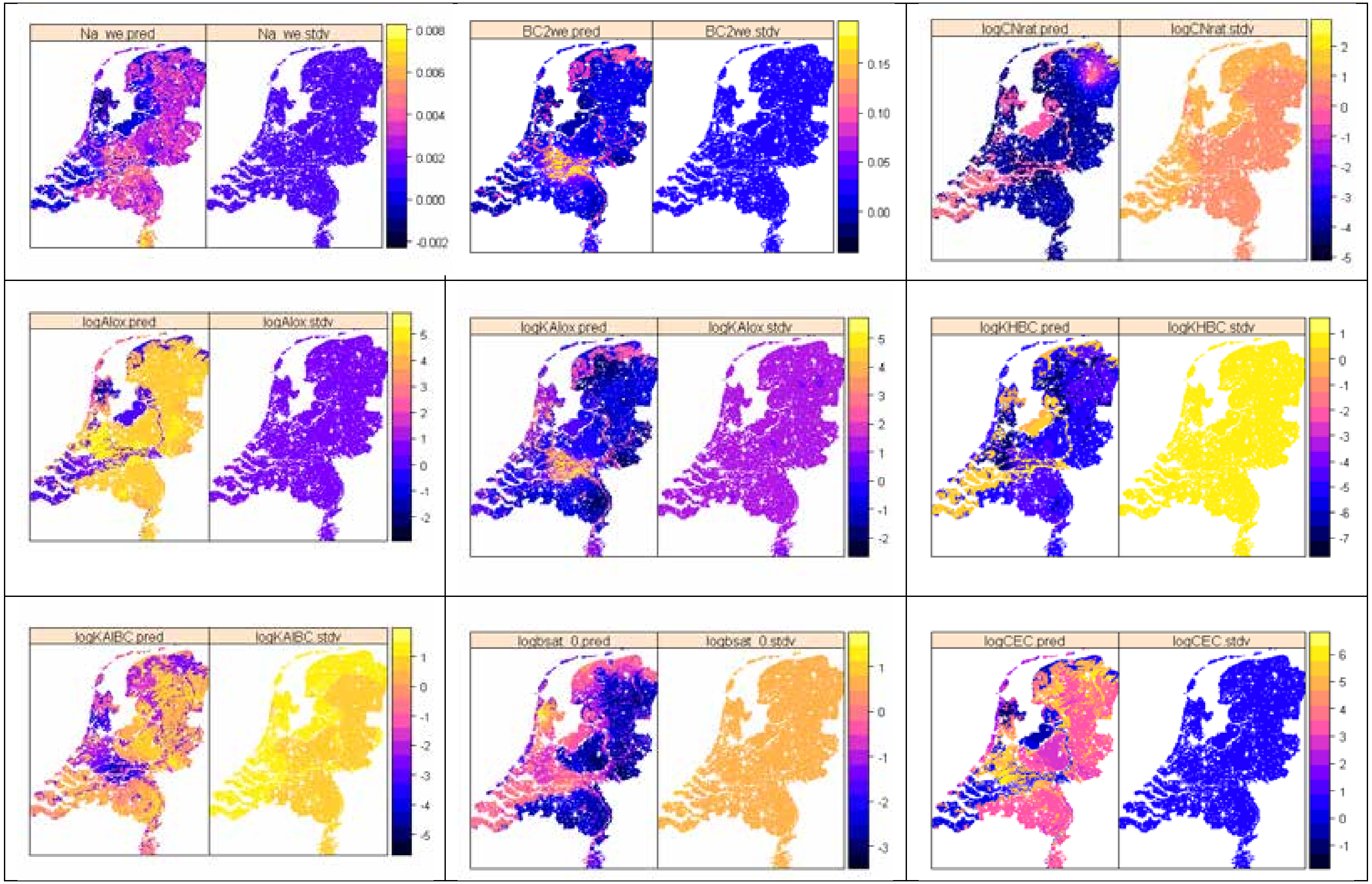
Appendix 1 SMART2 parameter conditions

Parameter	Distribution	Mean	St dev	Minimum	Maximum
logCEC_SP	normal	1.219	0.409	-Inf	Inf
logCEC_SR	normal	1.509	0.202	-Inf	Inf
logCEC_SC	normal	1.11	0.355	-Inf	Inf
logCEC_CN	normal	2.086	0.265	-Inf	Inf
logCEC_CC	normal	1.774	0.553	-Inf	Inf
logCEC_LN	normal	1.465	0.193	-Inf	Inf
logCEC_PN	normal	2.373	0.202	-Inf	Inf
logbsat_0_SP	normal	-0.981	0.448	-Inf	0
logbsat_0_SR	normal	-1.085	0.294	-Inf	0
logbsat_0_SC	normal	-0.03	0.027	-Inf	0
logbsat_0_CN	normal	-0.205	0.291	-Inf	0
logbsat_0_CC	normal	-0.004	0.021	-Inf	0
logbsat_0_LN	normal	-0.812	0.329	-Inf	0
logbsat_0_PN	normal	-0.436	0.256	-Inf	0
logKAlBC_SP	normal	0.005	1.328	-Inf	Inf
logKAlBC_SR	normal	0.362	0.759	-Inf	Inf
logKAlBC_SC	normal	-3.495	2.083	-Inf	Inf
logKAlBC_CN	normal	-3.029	2.112	-Inf	Inf
logKAlBC_CC	normal	-3.029	2.112	-Inf	Inf
logKAlBC_LN	normal	-0.088	1.199	-Inf	Inf
logKAlBC_PN	normal	-2.123	1.001	-Inf	Inf
logKAlox_SP	normal	7.605	0.69	-Inf	Inf
logKAlox_SR	normal	7.421	0.784	-Inf	Inf
logKAlox_SC	normal	11.991	1.636	-Inf	Inf
logKAlox_CN	normal	8.145	0.609	-Inf	Inf
logKAlox_CC	normal	10.95	2.601	-Inf	Inf
logKAlox_LN	normal	8.283	0.445	-Inf	Inf
logKAlox_PN	normal	6.809	0.739	-Inf	Inf
logAlox_SP	normal	1.647	0.576	-Inf	Inf
logAlox_SR	normal	1.959	0.257	-Inf	Inf
logAlox_SC	normal	0.78	0.15	-Inf	Inf
logAlox_CN	normal	2.031	0.191	-Inf	Inf
logAlox_CC	normal	1.818	0.311	-Inf	Inf
logAlox_LN	normal	2.014	0.125	-Inf	Inf
logAlox_PN	normal	1.916	0.301	-Inf	Inf
logCNrat_SP	normal	1.299	0.17	-Inf	Inf
logCNrat_SR	normal	1.312	0.097	-Inf	Inf
logCNrat_SC	normal	1.157	0.228	-Inf	Inf
logCNrat_CN	normal	1.059	0.109	-Inf	Inf

Parameter	Distribution	Mean	St dev	Minimum	Maximum
logCNrat_CC	normal	1.149	0.122	-Inf	Inf
logCNrat_LN	normal	1.25	0.094	-Inf	Inf
logCNrat_PN	normal	1.404	0.163	-Inf	Inf
logKHBC_SP	normal	4.004	1.005	-Inf	Inf
logKHBC_SR	normal	3.621	0.674	-Inf	Inf
logKHBC_SC	normal	5.667	0.884	-Inf	Inf
logKHBC_CN	normal	5.842	1.409	-Inf	Inf
logKHBC_CC	normal	5.842	1.409	-Inf	Inf
logKHBC_LN	normal	4.265	0.56	-Inf	Inf
logKHBC_PN	normal	3.762	0.502	-Inf	Inf

The figs below show the most likely value for the parameters and their standard deviation based on the measured values for 300 forest stands. The Country wide values are the result of a kriging process.



Appendix 2 SUMO2 parameter conditions

Parameter	Description	Distribution	Mean	Stdev	Min	Max	Condition	D or E[1]
biominikw	Initial biomass for roots herbs (ton/ha/y)	normal	3	1	0	*		E
biominidw	Initial biomass for roots dwarf shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominisw	Initial biomass for roots shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib1w	Initial biomass for roots tree 1 (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib2w	Initial biomass for roots tree 2 (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominiks	Initial biomass for stem herbs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominids	Initial biomass for stem dwarf shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominiss	Initial biomass for stem shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib1s	Initial biomass for stem tree 1 (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib2s	Initial biomass for stem tree 2 (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominikb	Initial biomass for leaves herbs (ton/ha/y)	normal	3	1	0	*		E
biominidb	Initial biomass for leaves dwarf shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominisb	Initial biomass for leaves shrubs (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib1b	Initial biomass for leaves tree 1 (ton/ha/y)	normal	0.1	0.0316	0	*		E
biominib2b	Initial biomass for leaves tree 2 (ton/ha/y)	normal	0.1	0.0316	0	*		E
verdelingkw	Biomass distribution for roots herbs	beta	0.49	0.0707	0.29	0.69	w+s+b=1	E
verdelingdw	Biomass distribution for roots dwarf shrubs	beta	0.4	0.0447	0.2	0.6	w+s+b=1	E
verdelingsw	Biomass distribution for roots shrubs	beta	0.4	0.0447	0.2	0.6	w+s+b=1	E
verdelingb1w	Biomass distribution for roots tree 1	beta	0.4	0.0447	0.2	0.6	w+s+b=1	E
verdelingb2w	Biomass distribution for roots tree 2	beta	0.4	0.0447	0.2	0.6	w+s+b=1	E
verdelingks	Biomass distribution for stem herbs	beta	0.01	0.0014	0.005	0.015	w+s+b=1	E
verdelingds	Biomass distribution for stem dwarf shrubs	beta	0.2	0.0316	0.1	0.3	w+s+b=1	E
verdelingss	Biomass distribution for stem shrubs	beta	0.1	0.01	0.05	0.15	w+s+b=1	E
verdelingb1s	Biomass distribution for stem tree 1	beta	0.15	0.0316	0.05	0.25	w+s+b=1	E
verdelingb2s	Biomass distribution for stem tree 2	beta	0.15	0.0316	0.05	0.25	w+s+b=1	E
verdelingkb	Biomass distribution for leaves herbs	beta	0.5	0.0707	0.3	0.7	w+s+b=1	E
verdelingdb	Biomass distribution for leaves dwarf shrubs	beta	0.4	0.0447	0.2	0.6	w+s+b=1	E
verdelingsb	Biomass distribution for leaves shrubs	beta	0.5	0.0707	0.3	0.7	w+s+b=1	E
verdelingb1b	Biomass distribution for leaves tree 1	beta	0.45	0.0447	0.25	0.65	w+s+b=1	E
verdelingb2b	Biomass distribution for leaves tree 2	beta	0.45	0.0447	0.25	0.65	w+s+b=1	E
verlieskw	Biomass loss for roots herbs	-	1	*	1	1		E
verliesdw	Biomass loss for roots dwarf shrubs	beta	0.7	0.0854	0	1		E
verliessw	Biomass loss for roots shrubs	beta	0.3	0.0854	0	1		E
verliesb1w	Biomass loss for roots tree 1	beta	0.3	0.0854	0	1		E
verliesb2w	Biomass loss for roots tree 2	beta	0.3	0.0854	0	1		E
verliesks	Biomass loss for stem herbs	beta	0.9	0.04	0	1		E
verliesds	Biomass loss for stem dwarf shrubs	beta	0.3	0.0854	0	1		E
verliesss	Biomass loss for stem shrubs	beta	0.04	0.0126	0	1		E

Parameter	Description	Distributio n	Mean	Stdev	Min	Max	Condition	D or E[1]
verliesb1s	Biomass loss for stem tree 1	beta	0.03	0.0084	0	1		E
verliesb2s	Biomass loss for stem tree 2	beta	0.03	0.0084	0	1		E
verlieskb	Biomass loss for leaves herbs	beta	0.9	0.0843	0	1		E
verliesdb	Biomass loss for leaves dwarf shrubs	beta	0.6	0.0854	0	1		E
verliessb	Biomass loss for leaves shrubs	-	1	*	1	1		E
verliesb1b	Biomass loss for leaves tree 1	-	1	*	1	1		E
verliesb2b	Biomass loss for leaves tree 2	-	1	*	1	1		E
uitdovingk	Light interception herbs	beta	0.7	0.2236	0.2	1		E
uitdovingd	Light interception dwarf shrubs	beta	0.7	0.1	0.4	1		E
uitdovings	Light interception shrubs	beta	0.6	0.1414	0.1	1		E
uitdovingb1	Light interception tree 1	beta	0.83	0.0316	0.4	0.9		E
uitdovingb2	Light interception tree 2	beta	0.83	0.0316	0.4	0.9		E
Nmink	Minimum N content herbs	beta	0.0085	0.001	0.0057	0.0093	Nmin<Nmax	D
Nmind	Minimum N content dwarf shrubs	beta	0.007	0.001	0.0042	0.0078	Nmin<Nmax	D
Nmins	Minimum N content shrubs	beta	0.007	0.001	0.0042	0.0078	Nmin<Nmax	D
Nminb1	Minimum N content tree 1	beta	0.007	0.001	0.0042	0.0078	Nmin<Nmax	D
Nminb2	Minimum N content tree 2	beta	0.007	0.001	0.0042	0.0078	Nmin<Nmax	D
Nmaxk	Maximum N content herbs	beta	0.025	0.0036	0.02	0.032	Nmin<Nmax	D
Nmaxd	Maximum N content dwarf shrubs	beta	0.018	0.0028	0.0145	0.025	Nmin<Nmax	D
Nmaxs	Maximum N content shrubs	beta	0.033	0.0032	0.02858	0.0398	Nmin<Nmax	D
Nmaxb1	Maximum N content tree 1	beta	0.033	0.0032	0.02858	0.0398	Nmin<Nmax	D
Nmaxb2	Maximum N content tree 2	beta	0.033	0.0032	0.02858	0.0398	Nmin<Nmax	D
Gmaxk	Maximum growth herbs (ton/ha/y)	normal	24	5	*	*		E
Gmaxd	Maximum growth dwarf shrubs (ton/ha/y)	normal	12	2	*	*		E
Gmaxs	Maximum growth shrubs (ton/ha/y)	normal	16	3	*	*		E
Gmaxb1	Maximum growth tree 1 (ton/ha/y)	normal	24	5	*	*		E
Gmaxb2	Maximum growth tree 2 (ton/ha/y)	normal	24	5	*	*		E
Aantal	Number of grazers	beta	0.2	0.2236	0	2		E
Eten	Food eaten by a cow (ton/ha/y)	normal	2.288	0.2236	*	*		E

[1]) D: based on field measurements, E: based on expert judgement

Appendix 3 Correlation matrixes for SUMO2 parameters

For an explanation of the parameter names see Appendix 2. Included are the spatial correlation between the parameters and within each parameter (that is why the latter is not 1). None given values imply that the correlation between the parameters is zero. All correlations are based on expert judgement.

parameter	biominikw	biominidw	Biominisw	biominib1w	biominib2w	biominiks	biominids	biominiss	biominib1s	biominib2s	biominikb	biominidb	biominisb	biominib1b	biominib2b
biominikw	0.9														
biominidw	-0.2	0.9													
biominisw	-0.2	-0.2	0.9												
biominib1w	-0.2	-0.2	-0.2	0.9											
biominib2w	-0.2	-0.2	-0.2	-0.2	0.9										
biominiks	0.8	-0.2	-0.2	-0.2	-0.2	0.9									
biominids	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9								
biominiss	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9							
biominib1s	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9						
biominib2s	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9					
biominikb	0.8	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9				
biominidb	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9			
biominisb	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9		
biominib1b	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9	
biominib2b	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.8	-0.2	-0.2	-0.2	-0.2	0.9

parameter	verdelingks	verdelingds	verdelingss	verdelingb1s	verdelingb2s	verdelingkb	verdelingdb	verdelingsb	verdelingb1b	verdelingb2b
verdelingks	0.99					-0.3				
verdelingds		0.99					-0.3			
verdelingss			0.99					-0.3		
verdelingb1s				0.99					-0.3	
verdelingb2s					0.99					-0.3
verdelingkb	-0.3					0.99				
verdelingdb		-0.3					0.99			
verdelingsb			-0.3					0.99		
verdelingb1b				-0.3					0.99	
verdelingb2b					-0.3					0.99

For all root parameters :1-s-b.

parameter	verlieskw	verliesdw	verliessw	verliesb1w	verliesb2w	verliesks	verliesds	verliesss	verliesb1s	verliesb2s	verlieskb	verliesdb	verliessb	verliesb1b	verliesb2b
verlieskw	1	-0.5	-0.5	-0.5	-0.5	0					0				
verliesdw	-0.5	1	-0.5	-0.5	-0.5		0					0			
verliessw	-0.5	-0.5	1	-0.5	-0.5			0					0		
verliesb1w	-0.5	-0.5	-0.5	1	-0.5				0					0	
verliesb2w	-0.5	-0.5	-0.5	-0.5	1					0					0
verliesks	0					1					0				
verliesds		0					1					0			
verliesss			0					1					0		
verliesb1s				0					1					0	
verliesb2s					0					1					0
verlieskb	0					0					1				
verliesdb		0					0					1			
verliessb			0					0					1		
verliesb1b				0					0					1	
verliesb2b					0					0					1

The correlation matrix for verliessw is repeated for stem and leaves, including between the three organs.

parameter	Nmink	Nmind	Nmins	Nminb1	Nminb2	Nmaxk	Nmaxd	Nmaxs	Nmaxb1	Nmaxb2
Nmink	0.99									
Nmind		0.99				0.5				
Nmins			0.99				0.5			
Nminb1				0.99				0.5		
Nminb2					0.99				0.5	
Nmaxk	0.5					0.99				0.5
Nmaxd		0.5					0.99			
Nmaxs			0.5					0.99		
Nmaxb1				0.5					0.99	
Nmaxb2					0.5					0.99

	Gmaxk	Gmaxd	Gmaxs	Gmaxb1	Gmaxb2
Gmaxk	1				
Gmaxd		1			
Gmaxs			1		
Gmaxb1				1	
Gmaxb2					1

‘Aantal’ and ‘eten’ are fully correlated (1) with themselves and fully uncorrelated with each other.

Appendix 4 Obtaining a sample of input parameters

If a distribution can be specified for the input parameters, a sample of size say B could be generated from this distribution. Performing B model runs with these B different vectors of input parameters, will result in B values for *y*. The variance of this vector *y* can be used as an estimate of VTOT, the total uncertainty due to the model parameters.

The distributions assumed for these parameters have been discussed above. In the present section, the required size of B is addressed. Note that the entire sample drawn will be of size (G + 1) x B, where G is the number of distinct parameter groups.

Required sample size B

To invest the required size of B, a preliminary analysis was undertaken with several 'fake' deterministic simulation models. In total, 4 (different fake simulation models, see below) x 5 (different sample sizes: 10, 100, 1000, 3000, 10000) = 20 situations were investigated.

The following 4 models were investigated:

1. $y = \sum_{g=1}^{5} x_g$,with

   $$x_1 \sim N(100,20),\ x_2 \sim N(100,15),\ x_3 \sim N(100,30),\ x_4 \sim N(100,10),\ x_5 \sim N(100,25)$$

2. $y = \sum_{g=1}^{5} \frac{1}{x_g}$, with distributions as in Model 1

3. $y = x_1 x_2 + \frac{x_3}{x_4} + \frac{x_5}{100}$, with distributions as in Model 1

$y = x_1 x_2 + \frac{x_3}{x_4} + \frac{x_5}{100}$ with

$$x_1 \sim N(10,2),\ x_2 \sim N(100,15),\ x_3 \sim N(50,10),\ x_4 \sim N(0.01,0.00001),\ x_6 \sim N(8,2)$$

For Model 1 the TMV's can be analytically derived. The other models were meant to mimic nonlinear respons of the fake simulation model to some of the parameters. In the table below, the estimated relative TMVs for all parameter groups and their estimated standard errors are given.

Table

Estimated Relative Top Marginal Variances, with estimated SE, as function of B, for 4 fake models

Model 1: y = sum (x)							
		Par1	**Par2**	**Par3**	**Par4**	**Par5**	
	Simulated Mean:	100	100	100	100	100	
	Simulated Variance:	20	15	30	10	25	
B	**Nsimulations**	**Estimated Relative TMVs**					**SE**
10	60	42	55	68	6	32	**20**
100	600	42	-3	40	-5	29	**9.2**
1000	6000	17	17	30	16	30	**3.0**
3000	18000	23	18	30	8	24	**1.7**
10000	60000	22	14	31	9	24	**0.95**
Model 2: y = sum (1/x)							
	Simulated Mean:	100	100	100	100	100	
	Simulated Variance:	20	15	30	10	25	
B	**Nsimulations**	**Estimated Relative TMVs**					**SE**
10	60	44	54	68	7	34	**20**
100	600	41	-1.8	39	-6	29	**9.2**
1000	6000	17	17	30	16	30	**3.0**
3000	18000	22	17	30	8	24	**1.7**
10000	60000	22	14	31	9	24	**0.96**
Model 3: y = x1* x2 + x3 / x4 + x5 / 100							
	Simulated Mean:	100	100	100	100	100	
	Simulated Variance:	20	15	30	10	25	
B	**Nsimulations**	**Estimated Relative TMVs**					**SE**
10	60	66	86	28	-7	4	**19**
100	600	56	23	9	-18	7	**8.6**
1000	6000	53	47	-2	-2	4	**2.8**
3000	18000	58	44	-1	0	0	**1.6**
10000	60000	57	44	-0	-1	-1	**0.90**
Model 4: y = x1* x2 + x3 / x4 + x5 / 100							
	Simulated Mean:	10	100	50	0.01	8	
	Simulated Variance:	2	15	10	0.0001	2	
B	**Nsimulations**	**Estimated Relative TMVs**					**SE**
10	60	-5 (17)	79(26)	-26 (21)	99 (0.6)	36 26)	**7**
100	600	1 (5)	11 (4)	4 (7)	100 (0.4)	1 (7)	**2.1**
1000	6000	0 (1)	0 (2)	0 (2)	99 (0.5)	-1 (3)	**0.6**
3000	18000	0 (0)	0 (1)	0 (1)	99 (0.3)	0 (2)	**0.22**
10000	60000	0 (0)	0 (0)	0 (1)	99 (0.4)	0 (0)	**0.11**

The estimated standard error can be different for each parameter, but the values found were all very close to each other, so for clarity only 1 value is given, in a single column (except for model 4).

In Model 1, which consists of simply adding the independent input parameters, the TMV's are equal to the parameter variances. With B=1000 the estimated TMVs start resembling the population variances, but instead of the neat sequence 10, 15, 20, 25, 30, the estimates seem to indicate two parameters with contributions of about 30 %, and 3 parameters with contributions of about 15 %. Furthermore, with B=1000 the estimated standard error is still 3, which is rather large. With this standard error the

TMV for parameter 1 has a confidence interval from about 14 to 26. With B=10000 the standard error is more or less equal to 1. For B=10000 the results are very good, and with B=3000 they are in between.

The results for Model 2 are strikingly similar to those for Model 1. This is because in Model 2, the TMVs are equal to the population variances as well (the expectations are equal for all parameters, so all terms in the Taylor expansion of var(*y*) have the same denominator).

With Model 3 the simulated *y* is mainly determined by parameters 1 and 2, because the terms x3/x4 and x5/100 have average 1, whereas x1 * x2 equals 10.000 on average. With B=1000 there are still negative variance estimates (these should be interpreted as 0). Unexpectedly, this happens again with B=10000. The variance contributions for parameters 1 and 2 should be around 57 en 43 percent, and from B=3000 they do so. With B=1000 the TMV estimates are also all right, but there the standard errors still have values around 3. Perhaps this large standard error is not such a big problem, however, as it is clear anyway that the big contributions are caused by parameters 1 and 2, not by parameters 3, 4 and 5.

Model 4 has the same form as Model 3, but the parameters have now been drawn from different distributions, leading to a larger contribution of parameter 4: x1*x2 now has average 1000, but x3/x4 has average 5000, which is caused mainly by x4 in the numerator. In this extreme case, the major contribution of parameter 4 is clear from B=1000 (and perhaps even from B=100). The standard errors are small throughout here, but the differences in estimated standard errors are larger than with the previous models, so all SE's have been given between brackets as well. Note that the 0's are not real zeros but rounded values.

For all models, estimates for the standard errors were also obtained numerically, after running the entire set-up 100 times. In most situations the numerical estimates closely resemble the estimates obtained with the formula.

To investigate if the results above depend on the number of groups, a similar exercise was undertaken with 3 parameter groups instead of 5. The results were completely comparable.

Conclusion: if good standard errors are needed, B=10000 seems best, but if computational time is an issue, B=3000 will probably also give acceptable values for the standard error. Of course it must be borne in mind that this was only a very limited investigation, and that the actual simulation models that will be investigated may behave differently.

Appendix 5 Estimating the variance of VTOT and TMV

Notation

Univariate population moments:
The r-th central population moment, i.e. the moment about the population expectation, is given by

$$\mu_r = E(x - Ex)^r$$

so that

$$\mu_0 = E\left(x - Ex\right)^0 = E(1) = 1 \text{ and } \mu_1 = E\left(x - Ex\right)^1 = E\left(x - Ex\right) = 0 .$$

Bivariate population moments:
In the bivariate distribution of x and y, the r,s-th central population moment is given by

$$\mu_{rs} = E\left(x - Ex\right)^r \left(y - Ey\right)^s ,$$

so that for example

$$\mu_{10} = E\left(x - Ex\right)^1 \left(y - Ey\right)^0 = E\left(x - Ex\right) = 0 .$$

The population covariance C is the first bivariate central moment μ_{11}:

$$C = E\left(x - Ex\right)^1 \left(y - Ey\right)^1 = \mu_{11}$$

Bivariate sample moments are indicated by m instead of μ; they are obtained as follows:

$$m_{rs} = \frac{1}{n} \sum_{i=1}^{n} \left(x_i - \bar{x}\right)^r \left(y_i - \bar{y}\right)^s .$$

In particular, in a bivariate distribution of x and y:

- m_{20} denotes the sample variance of x;
- m_{02} denotes the sample variance of y; and
- S = m_{11} denotes the sample covariance between x and y.

Variance of the absolute TMV

In our case, we consider the bivariate distribution not of *x* and *y*, but of y_0 and y_g, and we are interested in the variance of a sample covariance. The sample covariance is given by $S = \Sigma(y_0 - m_{y0})(y_g - m_{yg})/(n - 1) = m_{11}$, and hence the variance of S is the variance of a central moment. Stuard and Ord show that the necessary formula is:

$$Var(S) = Var(m_{11}) = \frac{1}{n}\left[\mu_{22} - \mu_{11}^2\right].$$

Estimating the terms on the right hand side with their corresponding sample moments (possibly with corrected df's) leads to

$$V\hat{a}r(S) = V\hat{a}r(m_{11}) = \frac{1}{n}\left[\hat{\mu}_{22} - \hat{\mu}_{11}^2\right]$$

with $\hat{\mu}_{11} = \frac{1}{n} \sum \left(y_0 - \bar{y}_0\right)\left(y_g - \bar{y}_g\right)$ and $\hat{\mu}_{22} = \frac{1}{n} \sum \left(y_0 - \bar{y}_0\right)^2 \left(y_g - \bar{y}_g\right)^2$.

Variance of the relative TMV

As noted above, the relative contribution of the g-th group of parameters to the total variance, is estimated as

$$Per\hat{c}(g) = \frac{100C\hat{o}v(y_0, y_g)}{\left[V\hat{a}r(y_0)\right]}.$$

Considering the bivariate distribution of y_0 and y_g , the expression for the estimated percentage can therefore be rewritten as

$$Per\hat{c}(g) = \frac{100m_{11}}{m_{20}}$$

Now first note that, in general, in a univariate distribution, $Var(a) = E(a - Ea)^2$ so disregarding the bias correction n/(n-1), we can estimate a variance by the second sample moment: $V\hat{a}r(a) = m_2$. In a bivariate distribution this would become $V\hat{a}r(a) = m_{20}$ or m_{20}.

Next, using a Taylor expansion, the variance of a/b is approximately given by:

$$Var(a/b) \approx \left\{\frac{Ea}{Eb}\right\}^2 \left\{\frac{Var(a)}{[Ea]^2} + \frac{Var(b)}{[Eb]^2} - \frac{2\operatorname{cov}(a,b)}{EaEb}\right\}$$

so that we find

$$Var\left[Per\hat{c}(g)\right] \approx 100^2 \left\{\frac{Em_{11}}{Em_{20}}\right\}^2 \left\{\frac{Var(m_{11})}{[Em_{11}]^2} + \frac{Var(m_{20})}{[Em_{20}]^2} - \frac{2\operatorname{cov}(m_{11}, m_{20})}{Em_{11}Em_{20}}\right\}.$$

Expectation and variance of m_{11}

The expectation of m_{11} is its corresponding population moment, and its variance was already given above, so we have

$$\begin{aligned} E(m_{11}) &= \mu_{11} \\ Var(m_{11}) &= \frac{1}{n}\left[\mu_{22} - \mu_{11}^2\right]. \end{aligned}$$

Expectation and variance of m_{20}

The expectation of m_{20} is given by

$$E(m_{20}) = \sigma^2(y_0)$$

and its variance is obtained using a formula from Stuart and Ord:

$$Var(m_{20}) = \frac{1}{n}\left(\mu_{40} - \mu_{20}^2 + 4\mu_{2,0}\mu_{10} + 0 + 0 - 4\mu_{30}\mu_{10} - 0\right)$$

$$= \frac{1}{n}\left(\mu_{40} - \mu_{20}^2\right)$$

where the last equality follows because $\mu_{10} = \mu_{01} = 0$).

Covariance of of m_{11} and m_{20}

With Stuart & Ord's formula for $Cov(m_{r,s}, m_{u,v})$ we find

$$Cov(m_{11}, m_{20}) = \frac{1}{n}\left(\mu_{31} - \mu_{11}\mu_{20}\right)$$

Combining the results

Substituting the above 5 expressions into

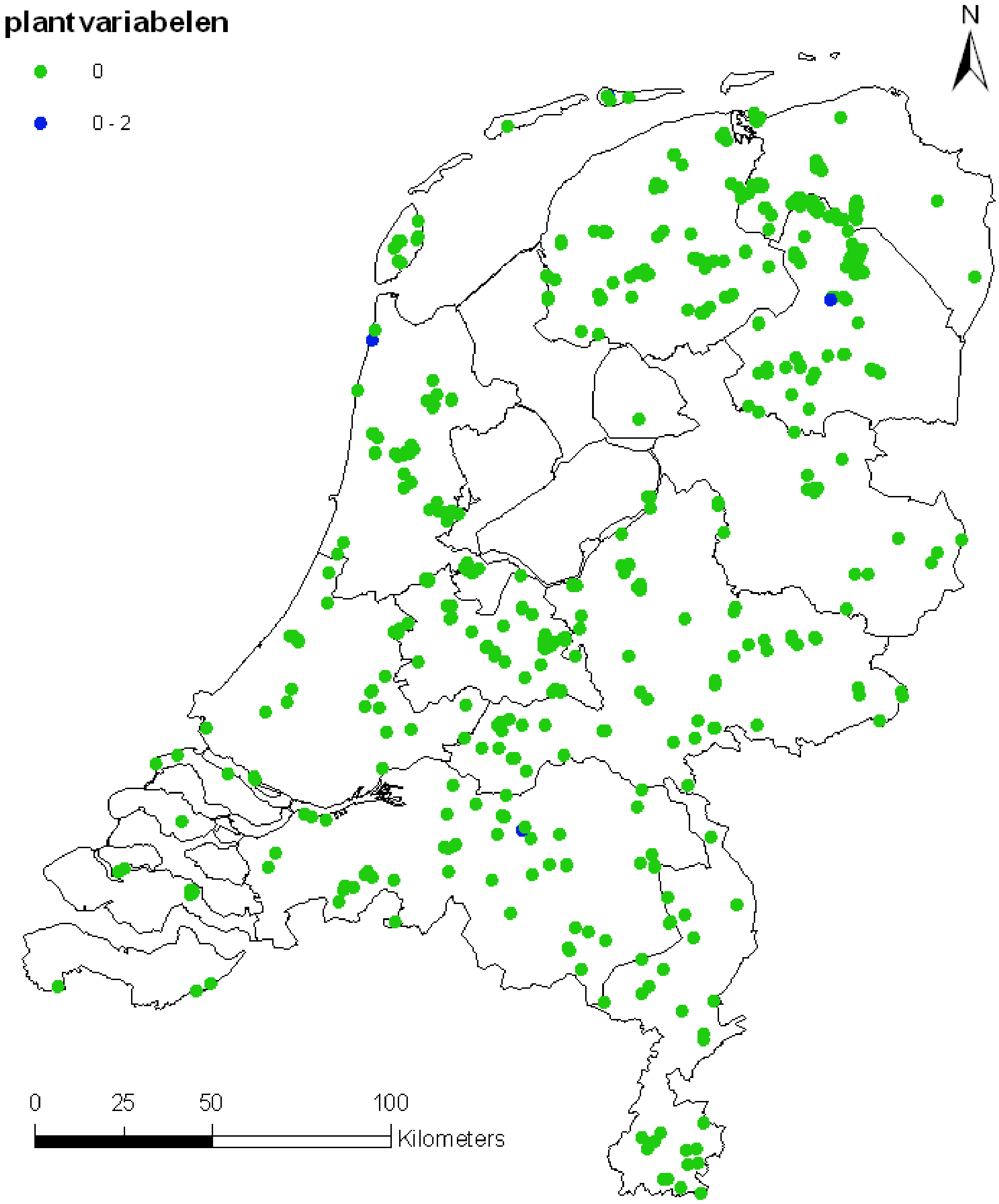
$$Var\left[Pe\hat{r}c(g)\right] \approx 100^2 \left\{\frac{Em_{11}}{Em_{20}}\right\}^2 \left\{\frac{Var(m_{11})}{[Em_{11}]^2} + \frac{Var(m_{20})}{[Em_{20}]^2} - \frac{2\,\mathrm{cov}(m_{11}, m_{20})}{Em_{11}Em_{20}}\right\}$$

will give the formula for the variance of the relative TopMarginalVariance.

An estimator for this variance can be obtained upon replacing the required moments by their method-of-moments estimators.

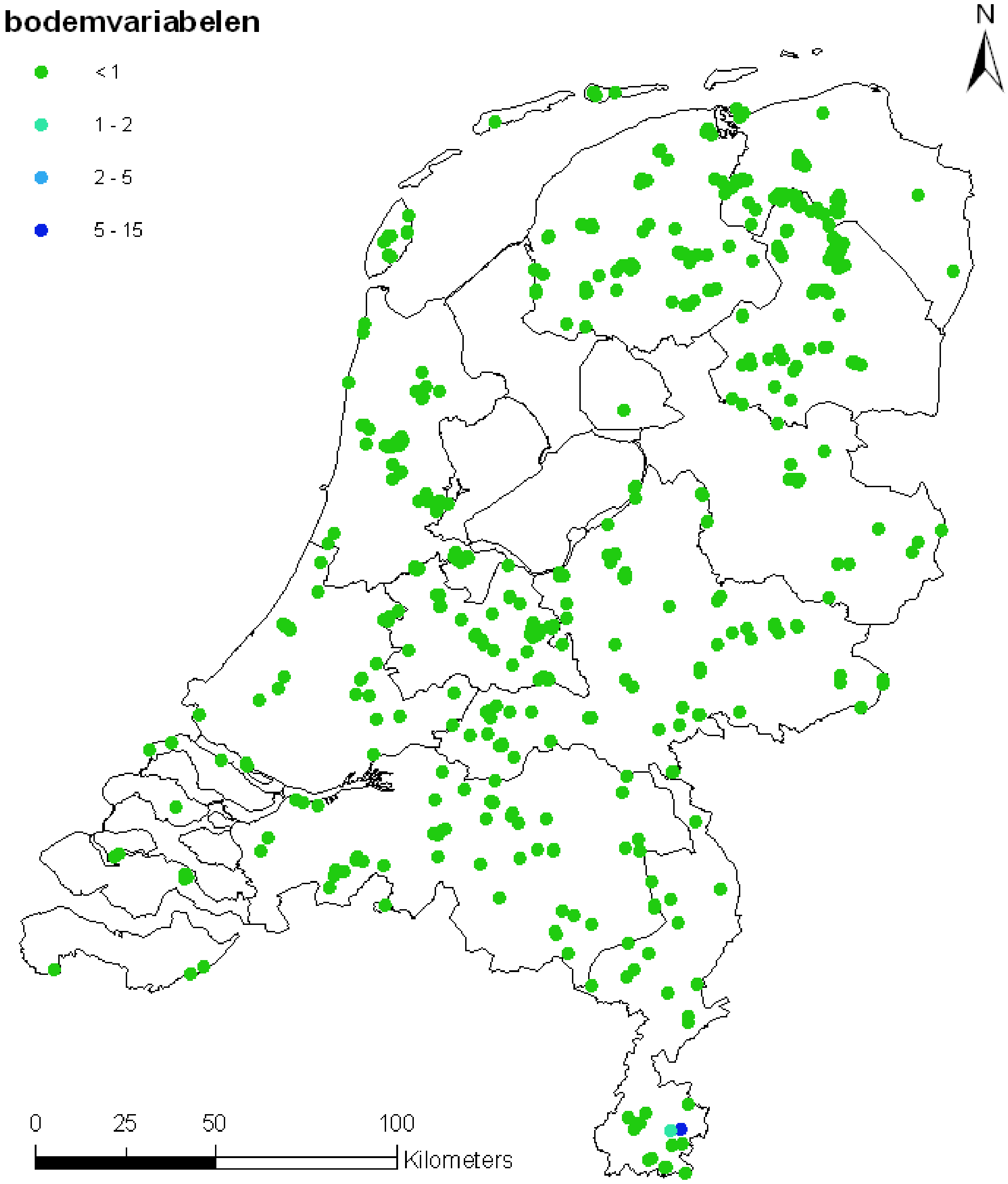
Appendix 6 Effect of plant variables on the Ellenberg indicator value for acidity (R) for grassland

The effect of the plant variables subjected to the uncertainty analysis is for almost all sites none existing. Only for two sites there is a very small, negligible effect.



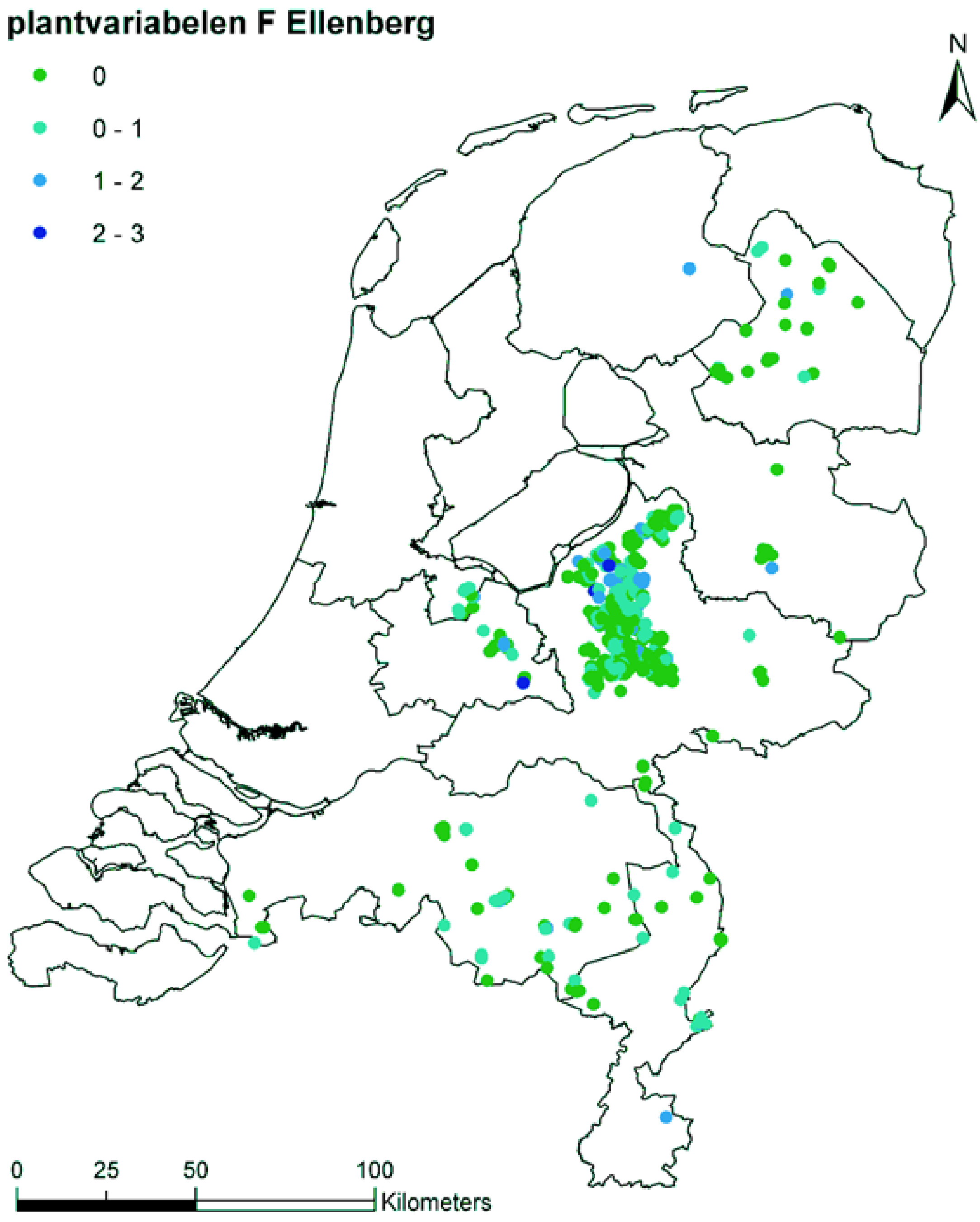
Appendix 7 Explained variance of soil variables on the Ellenberg indicator value for moisture (F) for grassland

The effect of the soil variables subjected to the uncertainty analysis is for almost all sites very low implying that the influence of the soil parameters on F is negligible.



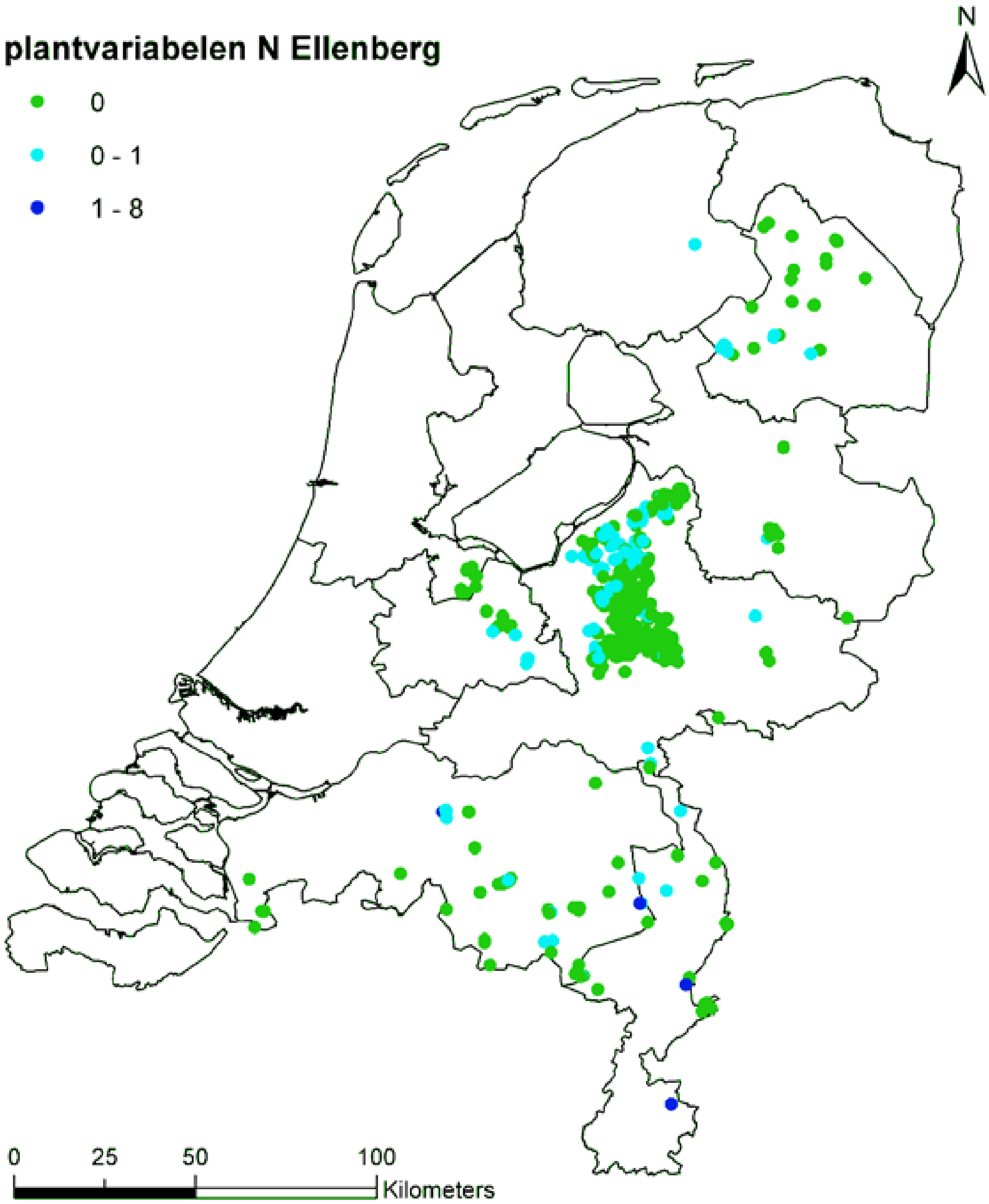
Appendix 8 Explained variance of the plant variables for the Ellenberg indicator value for moisture (F) for heathland

The effect of the plant variables subjected to the uncertainty analysis is for almost all sites very low implying that the influence of the plant parameters on F is negligible.



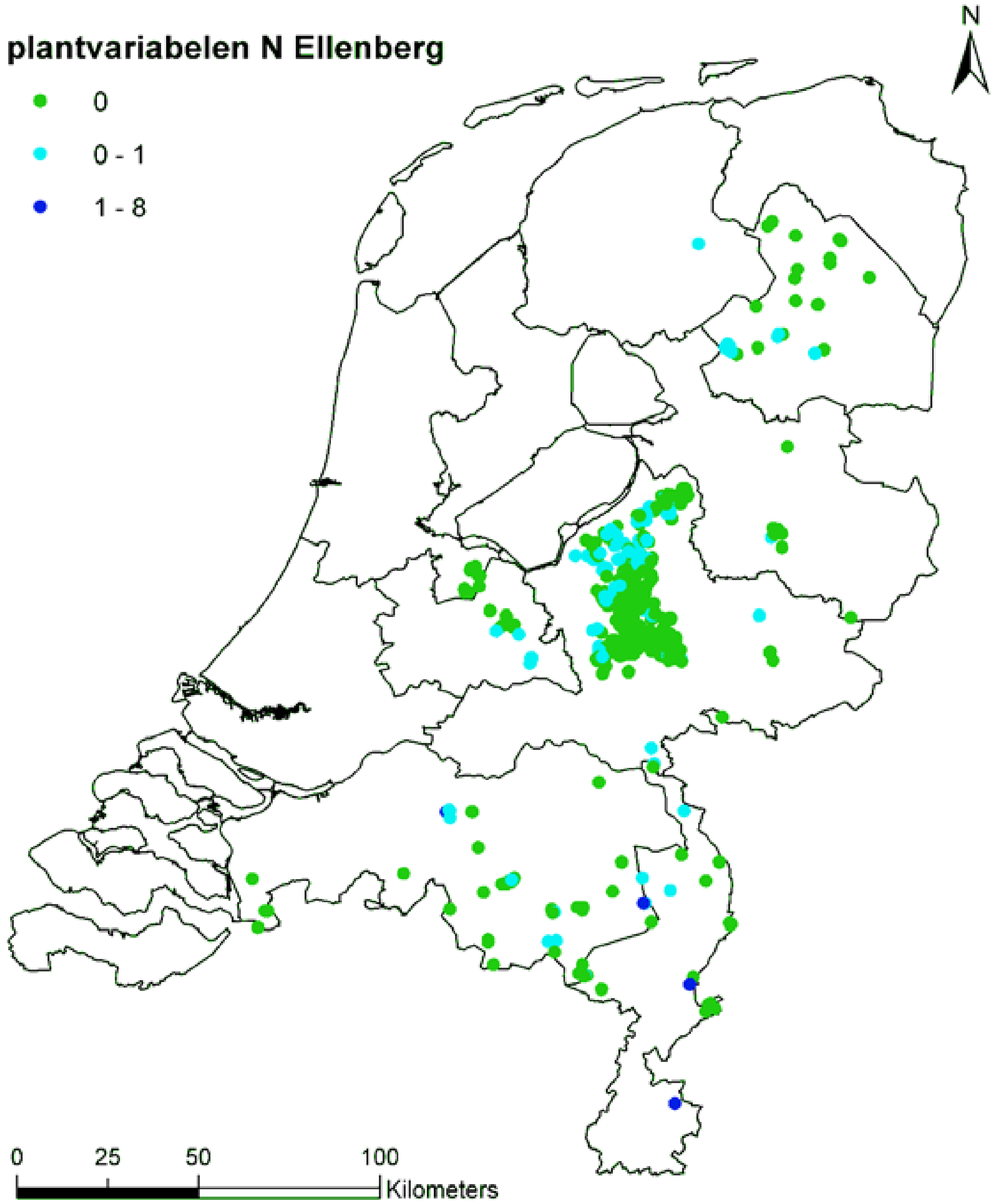
Appendix 9 Explained variance of the plant variables for the Ellenberg indicator value for nutrients (N) for heathland

The effect of the plant variables subjected to the uncertainty analysis is for almost all sites very low implying that the influence of the plant parameters on N is negligible.



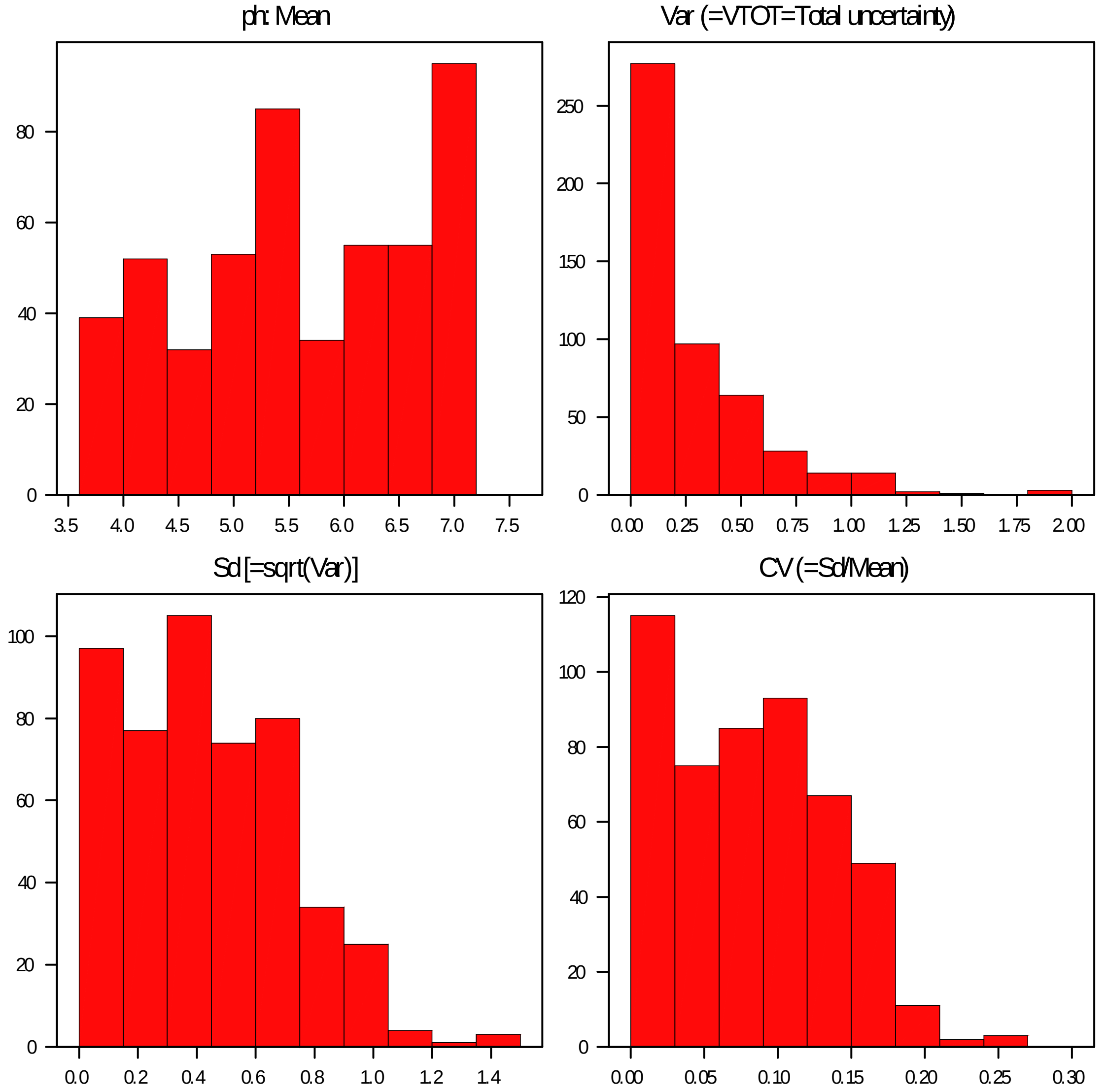
Appendix 10 Explained variance of the plant variables for the Ellenberg indicator value for nutrients (N) for heathland

The effect of the plant variables subjected to the uncertainty analysis is for almost all sites very low implying that the influence of the plant parameters on N is negligible.

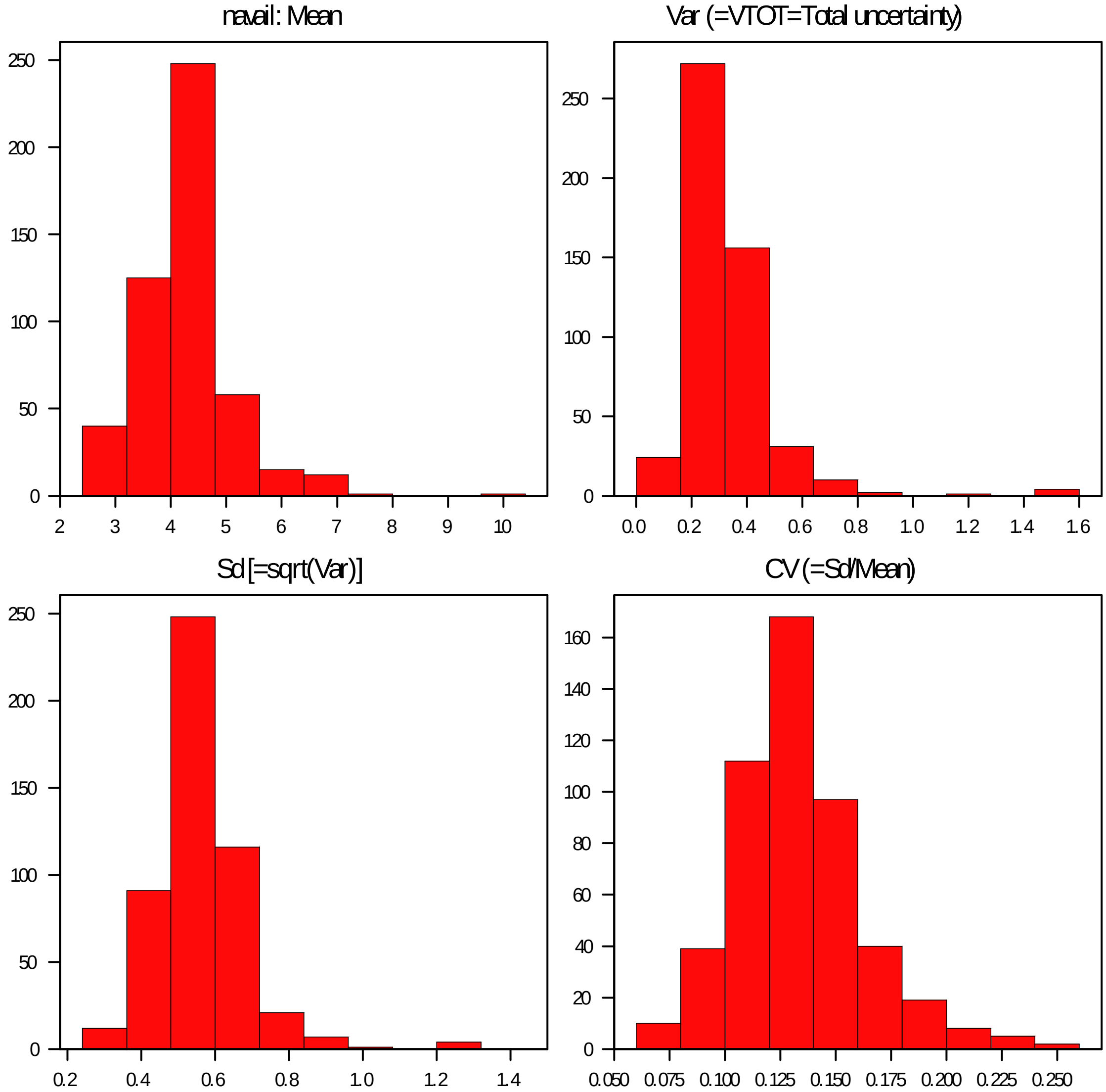


Appendix 11 Statistics tabulated for the sites

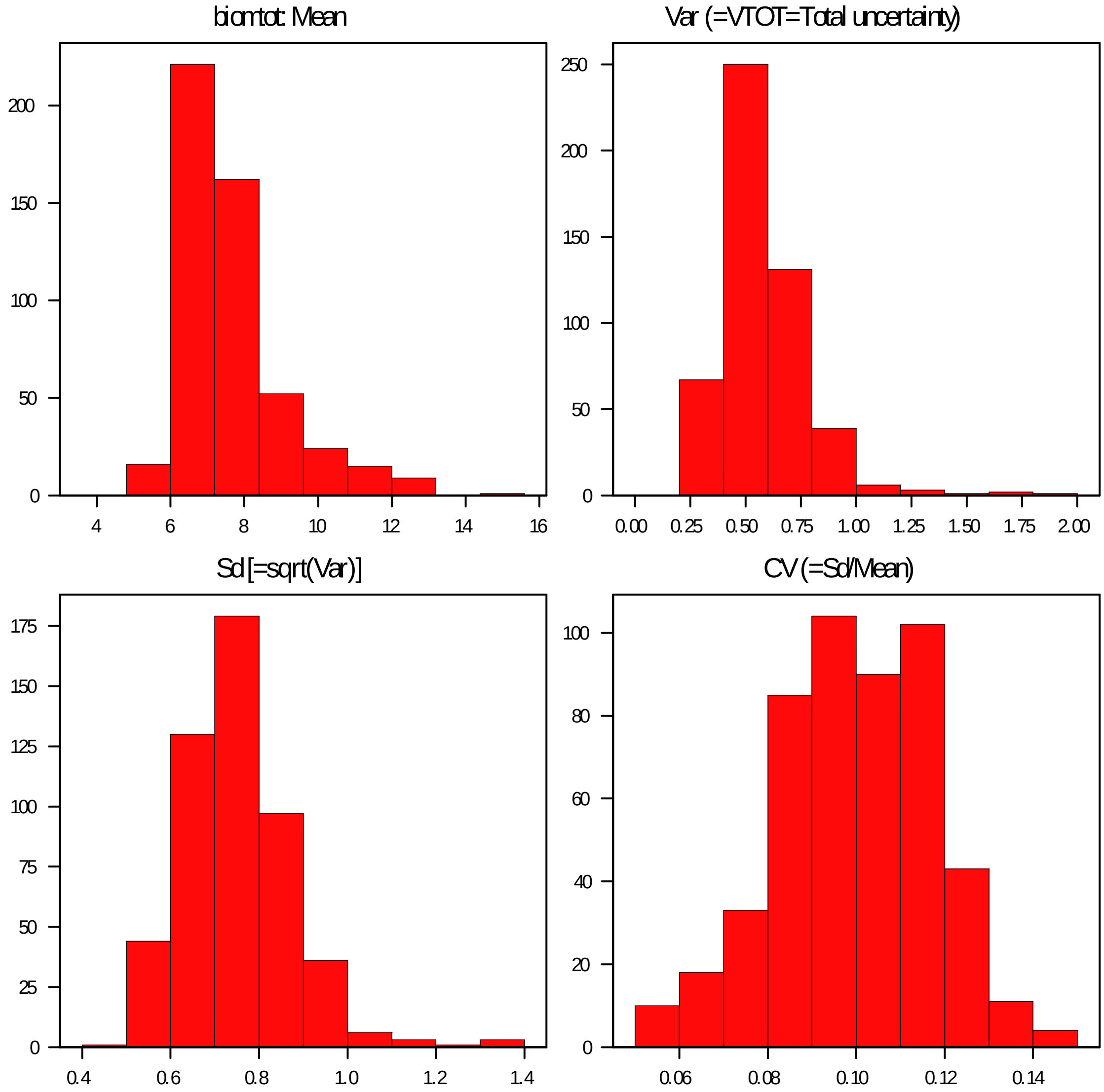
Grassland



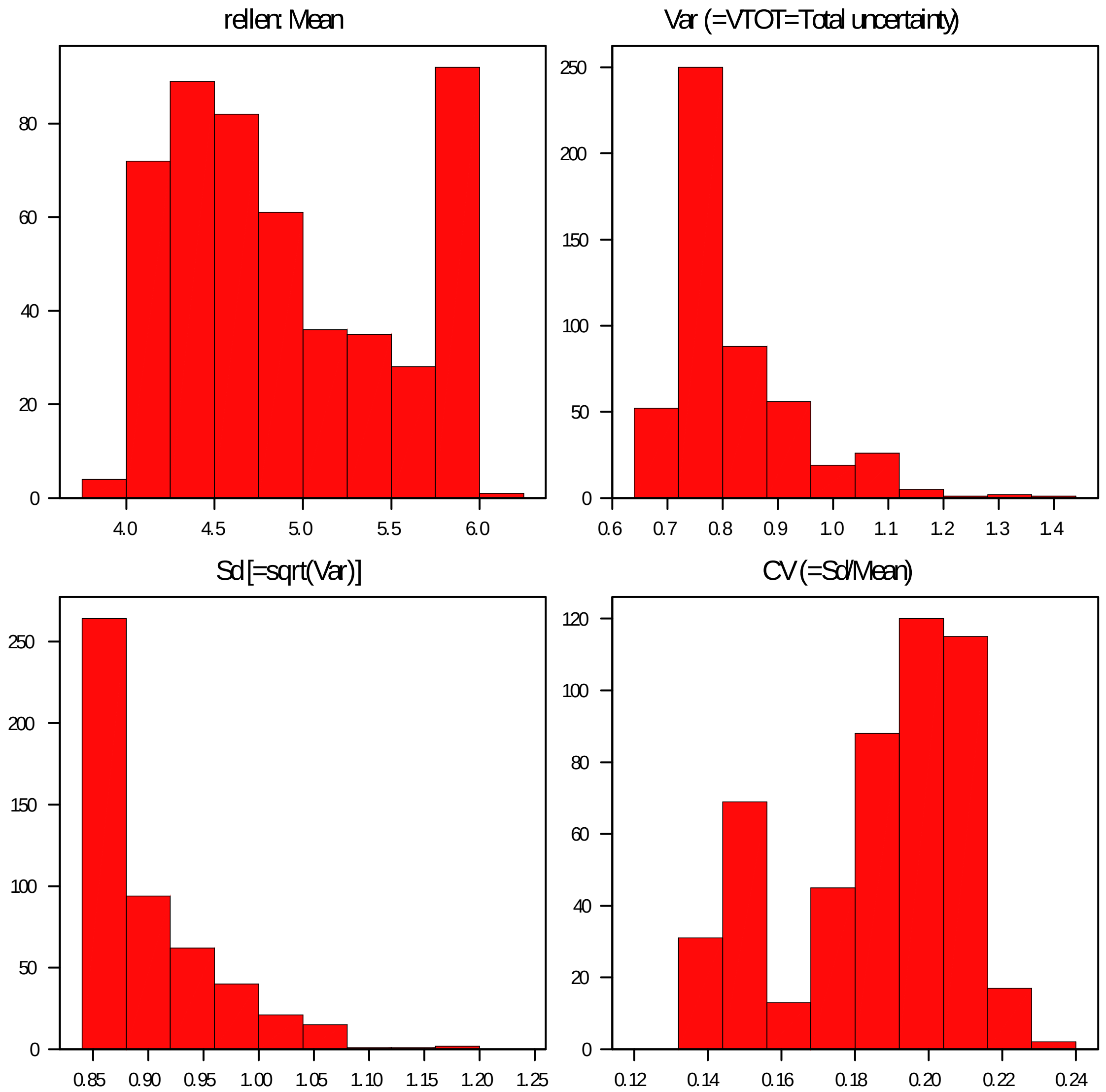
Tabulation of the number of sites of mean pH (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean for grassland as fraction.

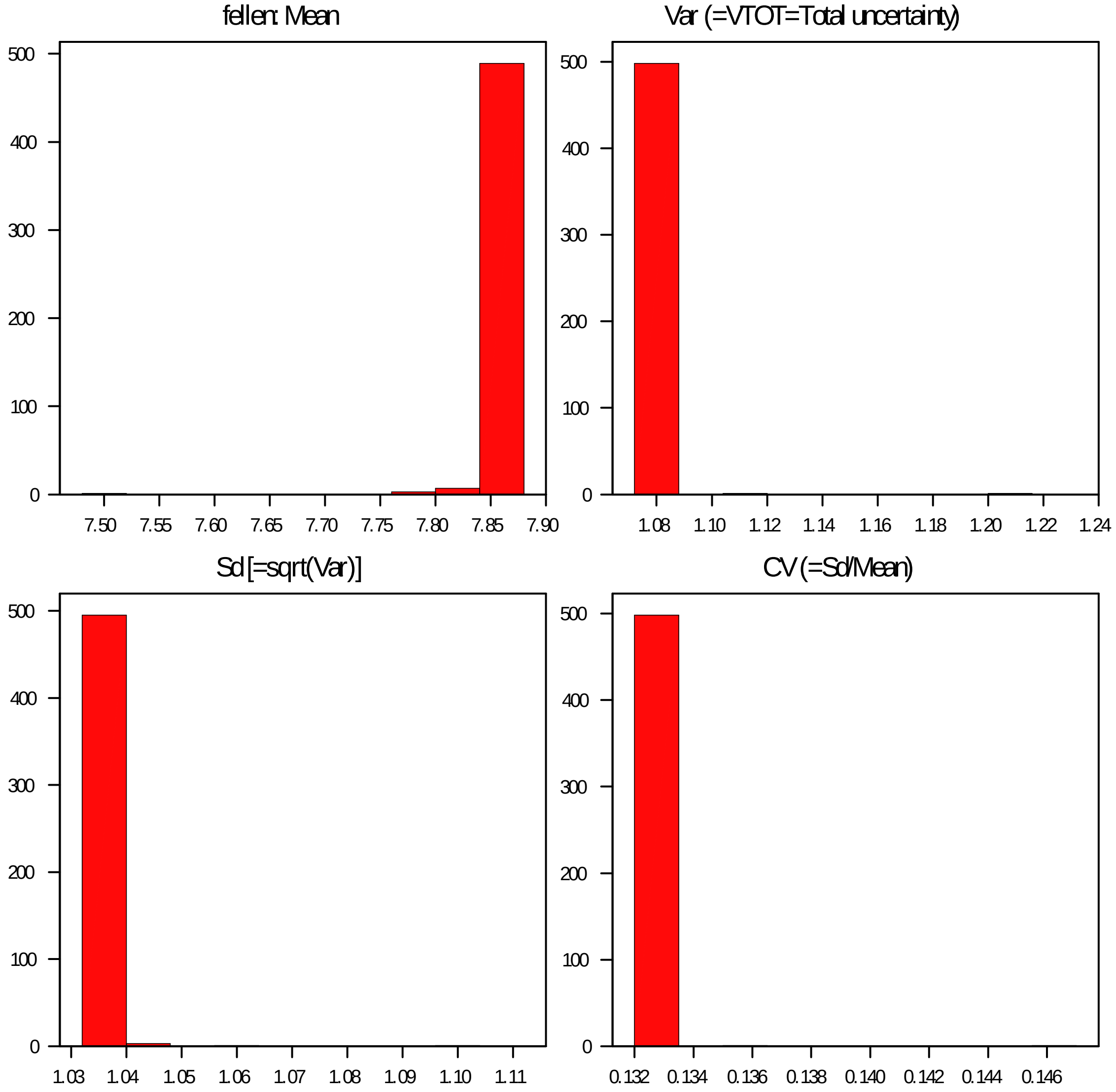


Tabulation of the number of sites of mean nitrogen availability (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean for grassland as fraction.

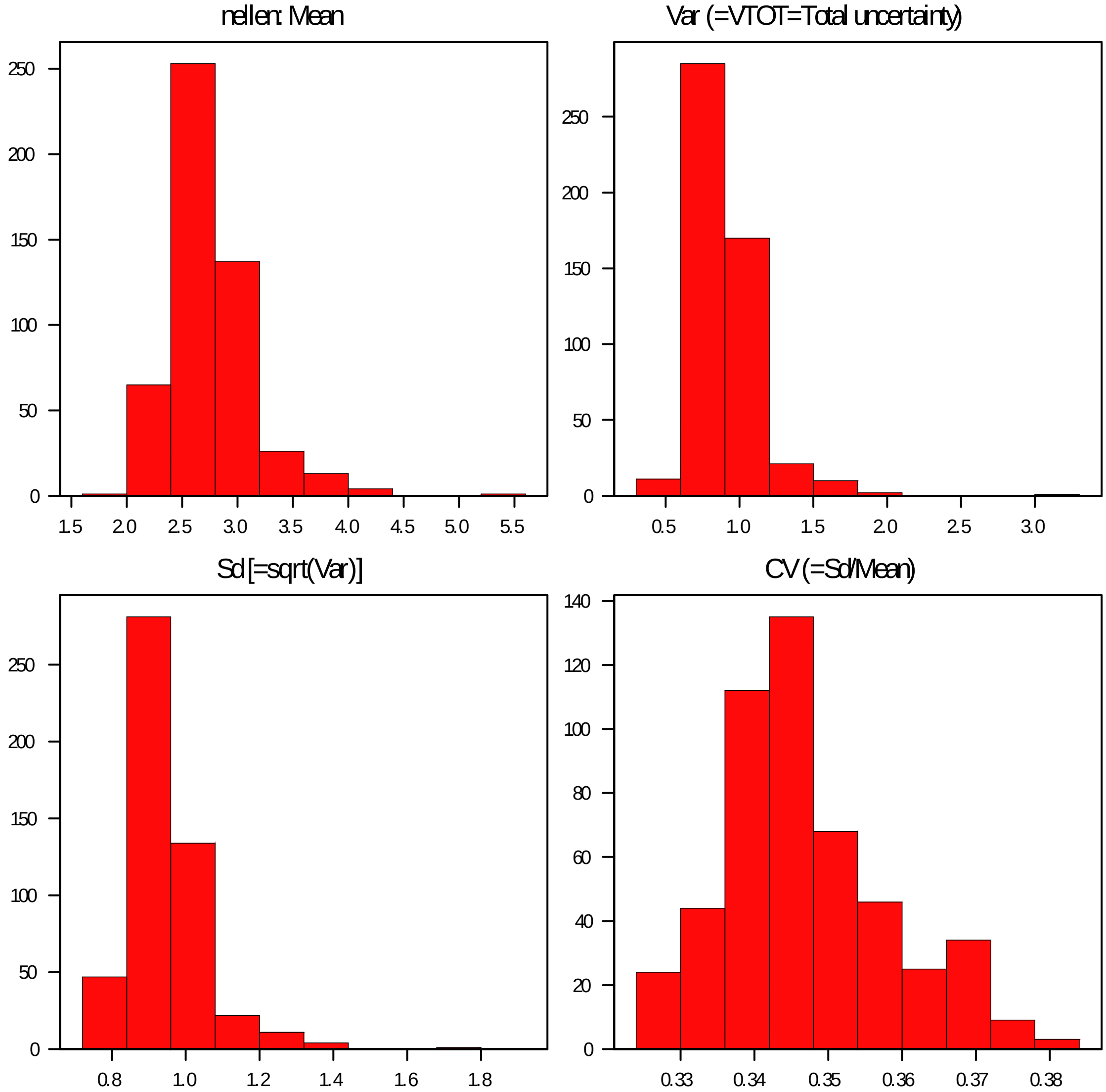


Tabulation of the number of sites of mean total biomass (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean total biomass for grassland as fraction.

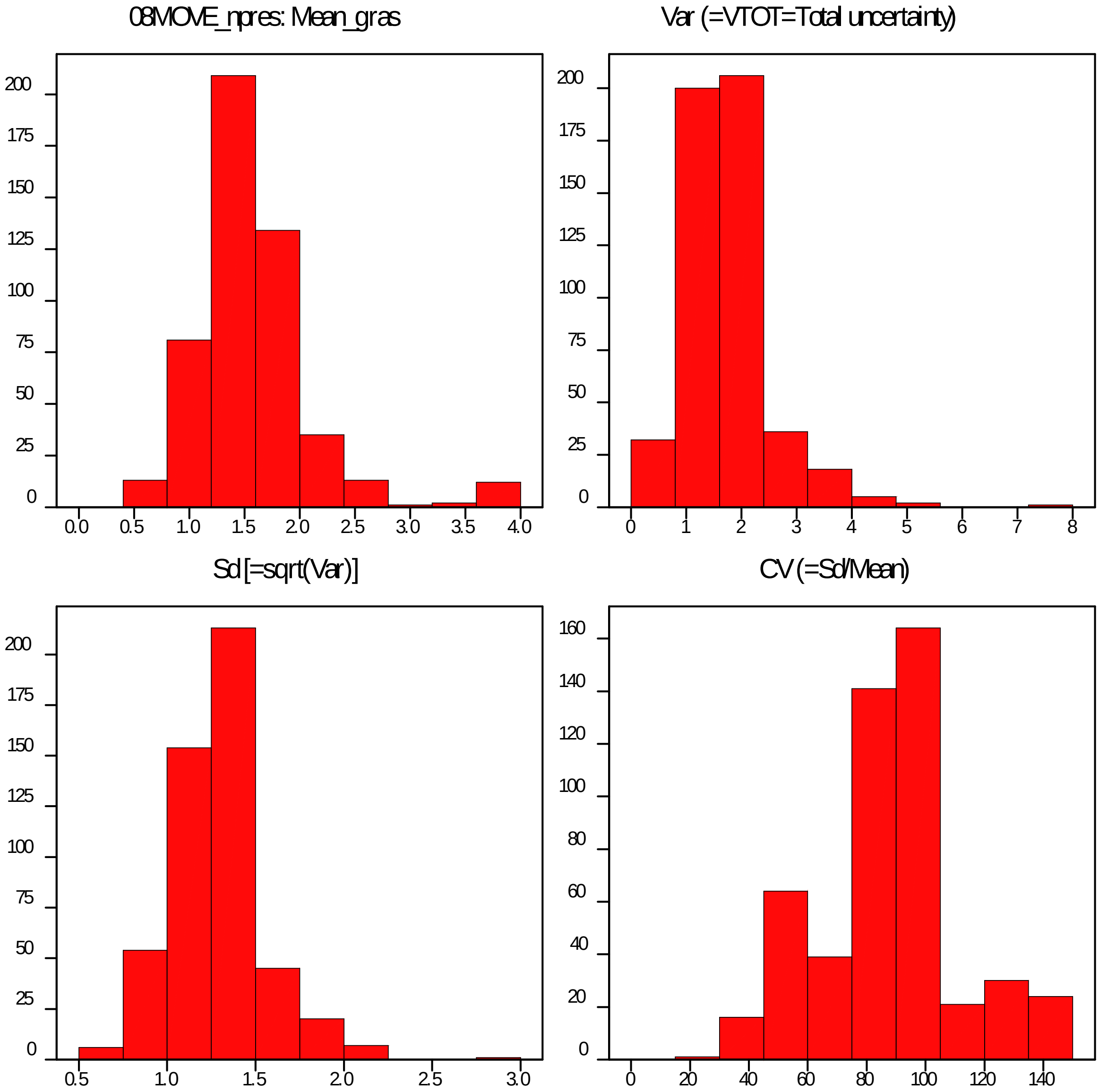

rellen: Mean
Var (=VTOT=Total uncertainty)
Sd [=sqrt(Var)]
CV (=Sd/Mean)



Tabulation of the number of sites of mean F (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean F. In the mean F figure (top left) one site was left out because it contains an outlier in one of the 15,000 drawings causing the site to be an outlier as well (F=1.8, mean F = 7.5, for location 33) for grassland as fraction.

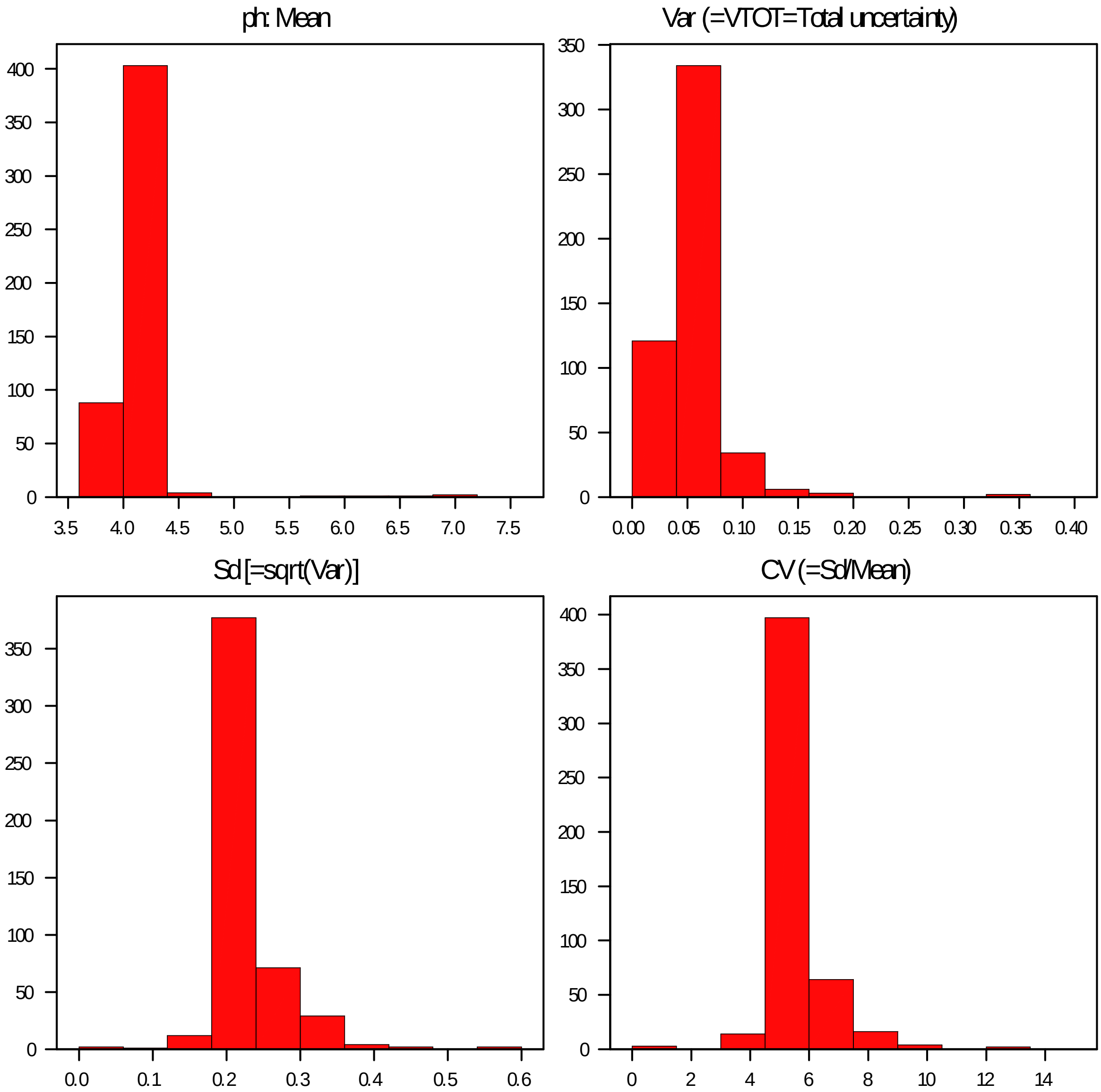


Tabulation of the number of sites of mean N (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for grassland as fraction.

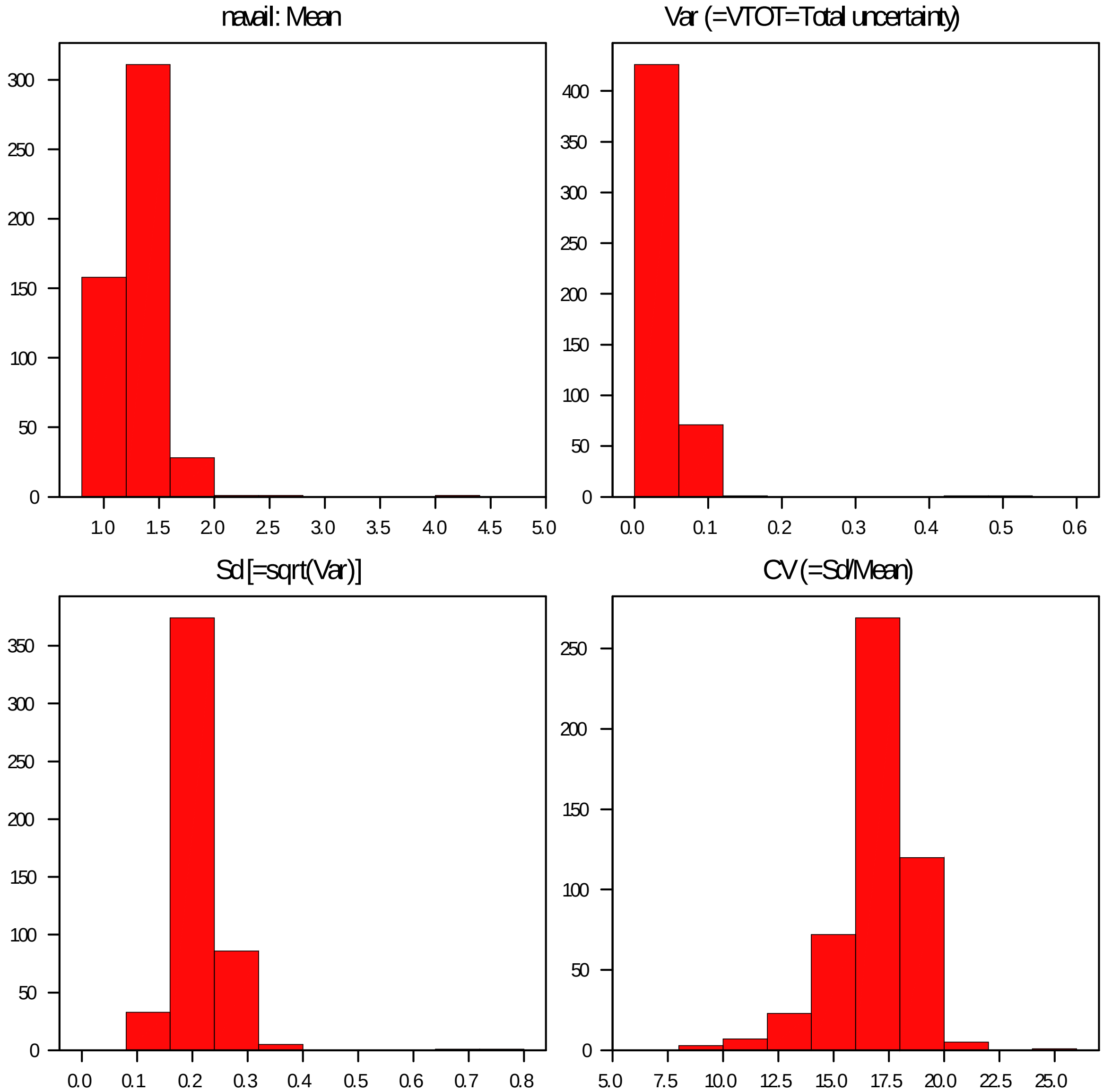


Tabulation of the number of sites of mean presences of species for MOVE4 (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for grassland as percentage.

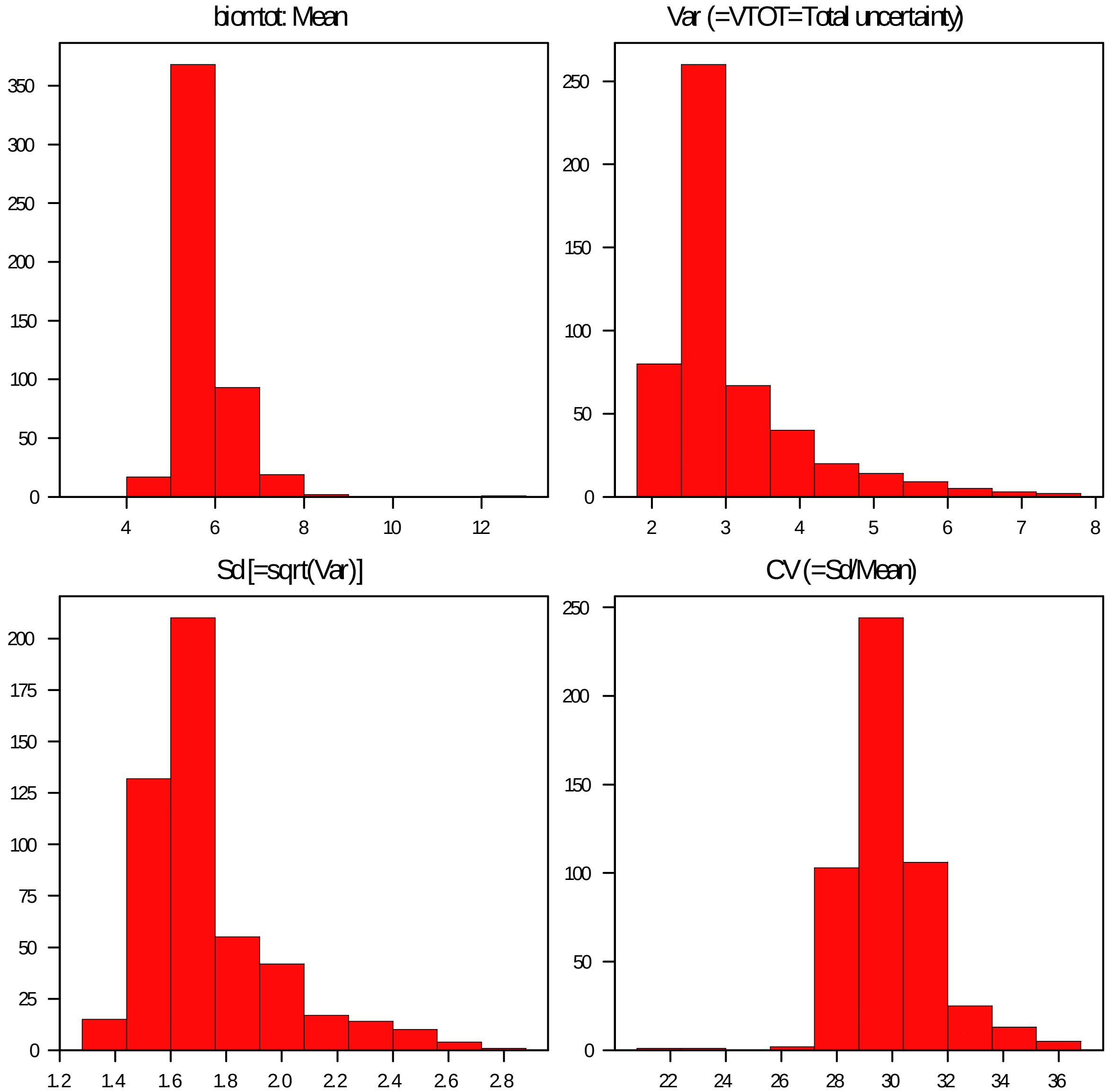
Heathland



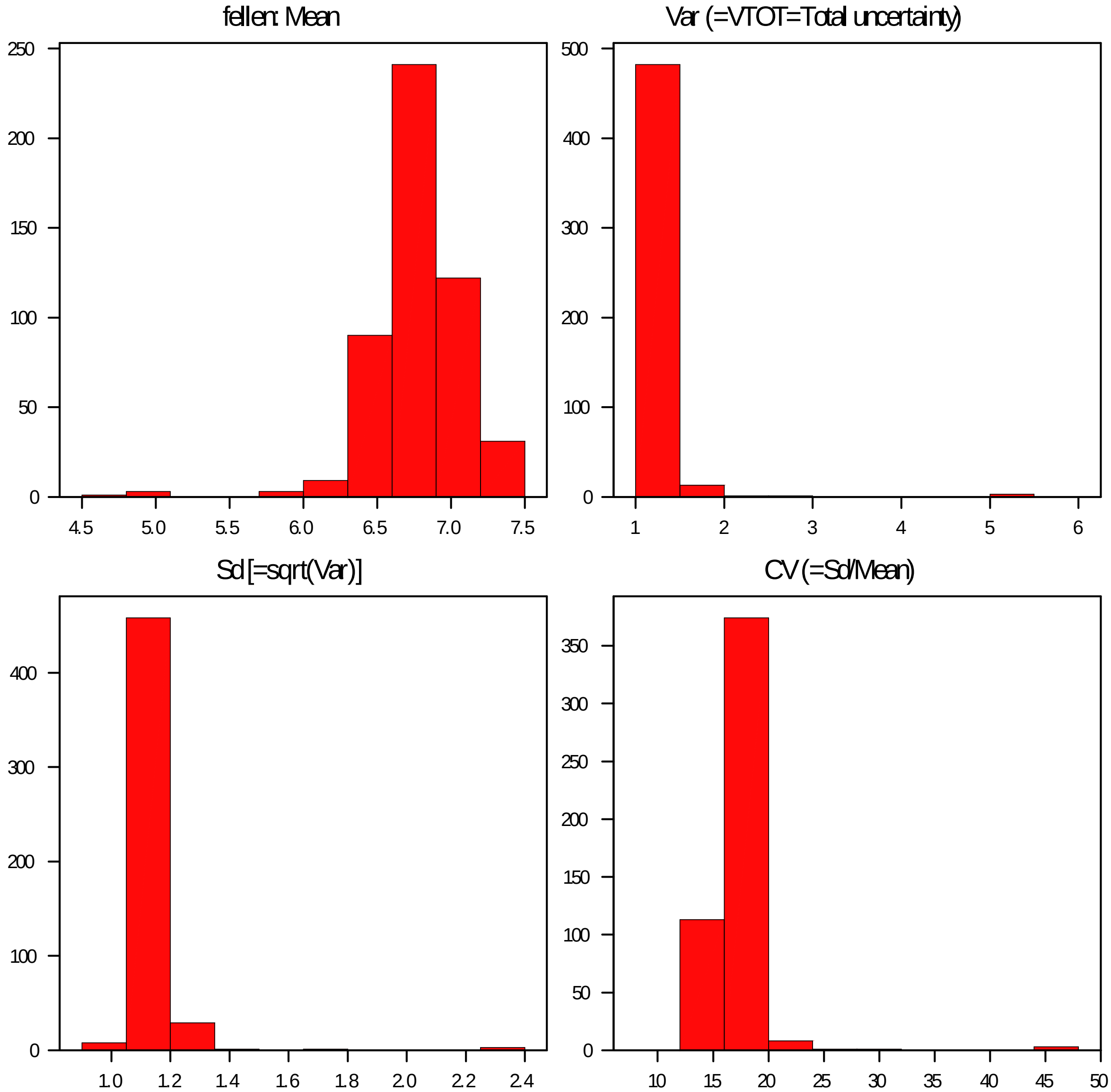
Tabulation of the number of sites of mean pH (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean pH for heathland as percentage.



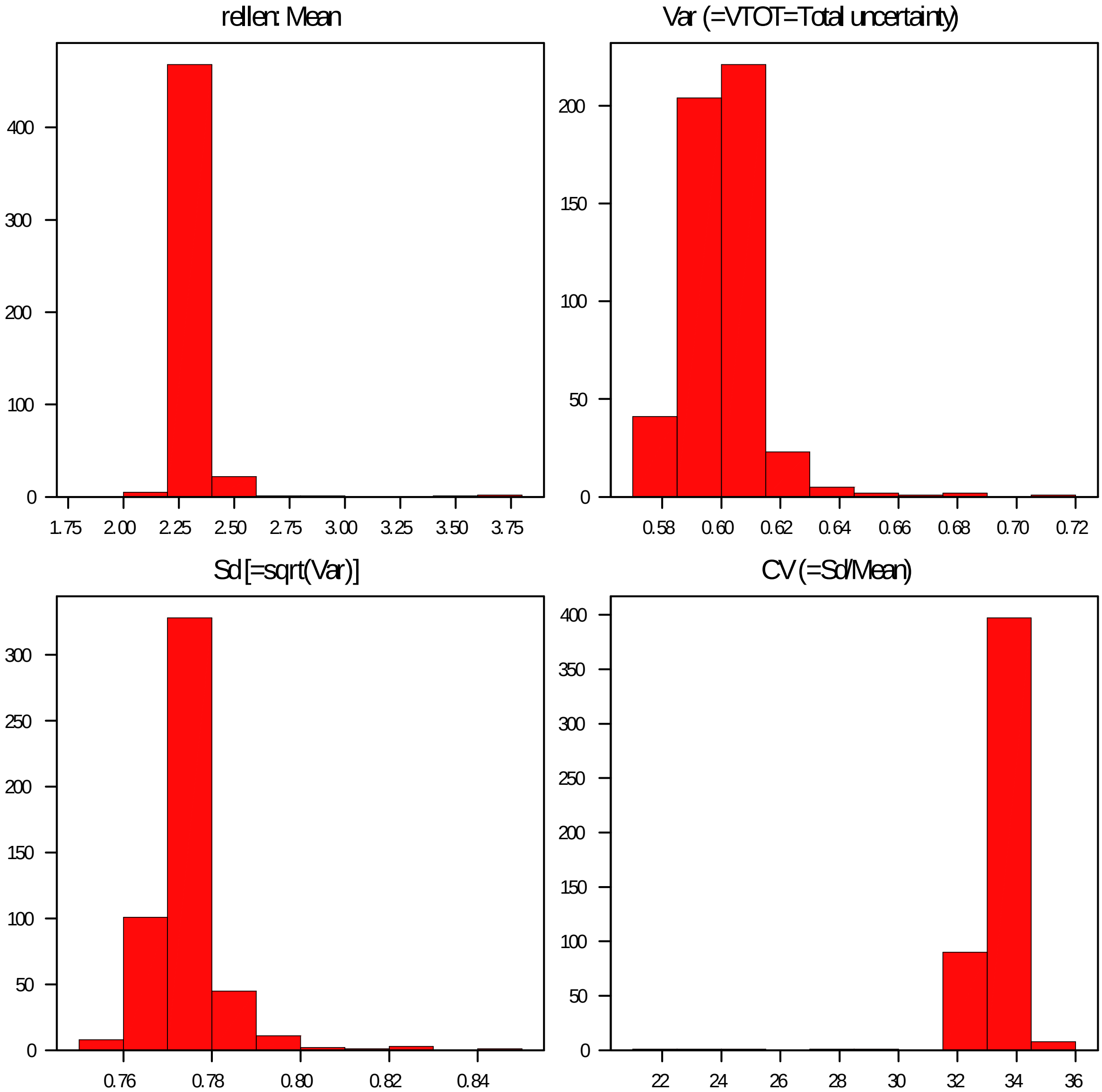
Tabulation of the number of sites of mean nitrogen availability (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean pH for heathland as percentage.



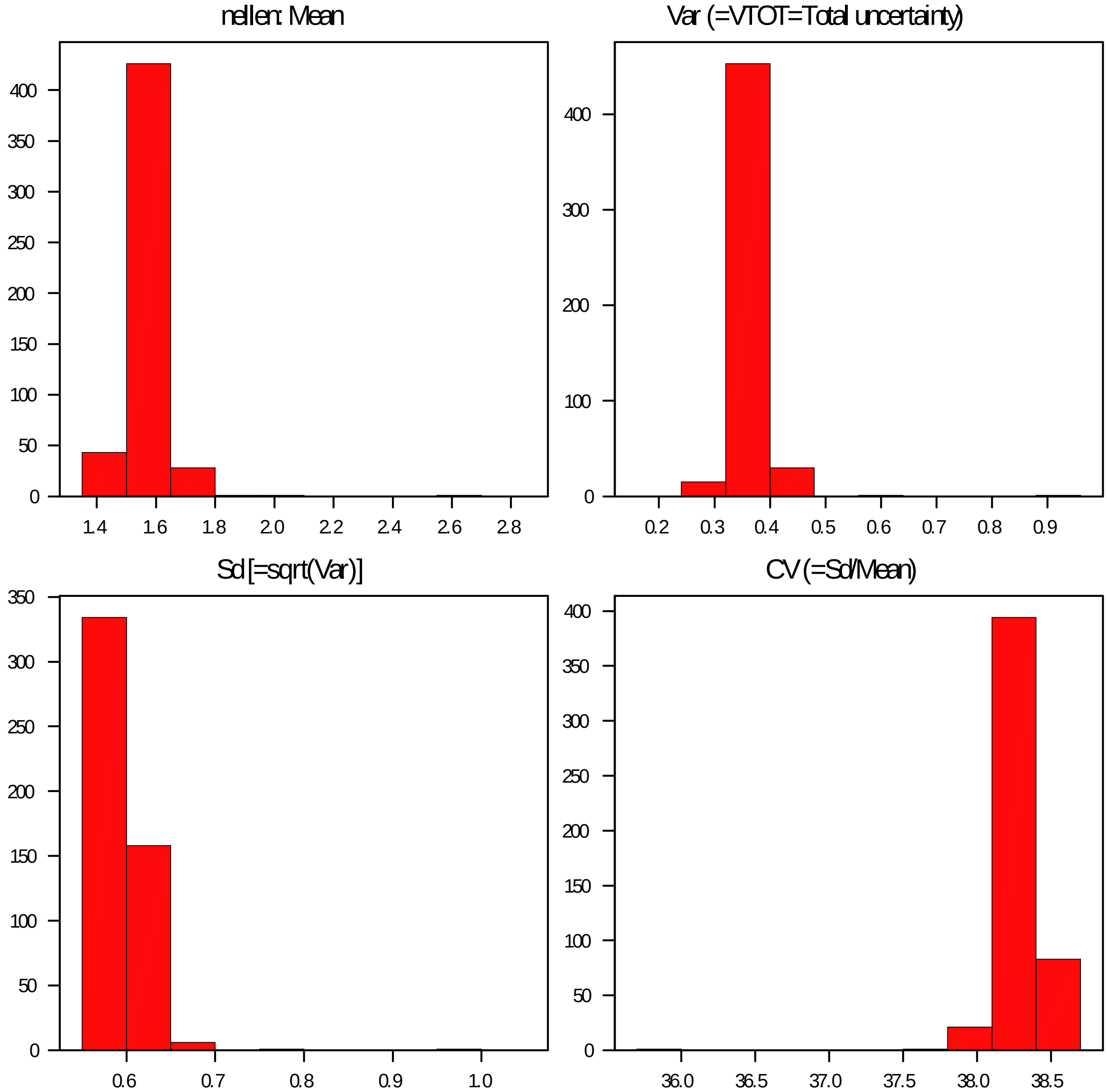
Tabulation of the number of sites of mean total biomass (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean total biomass for heathland as percentage.



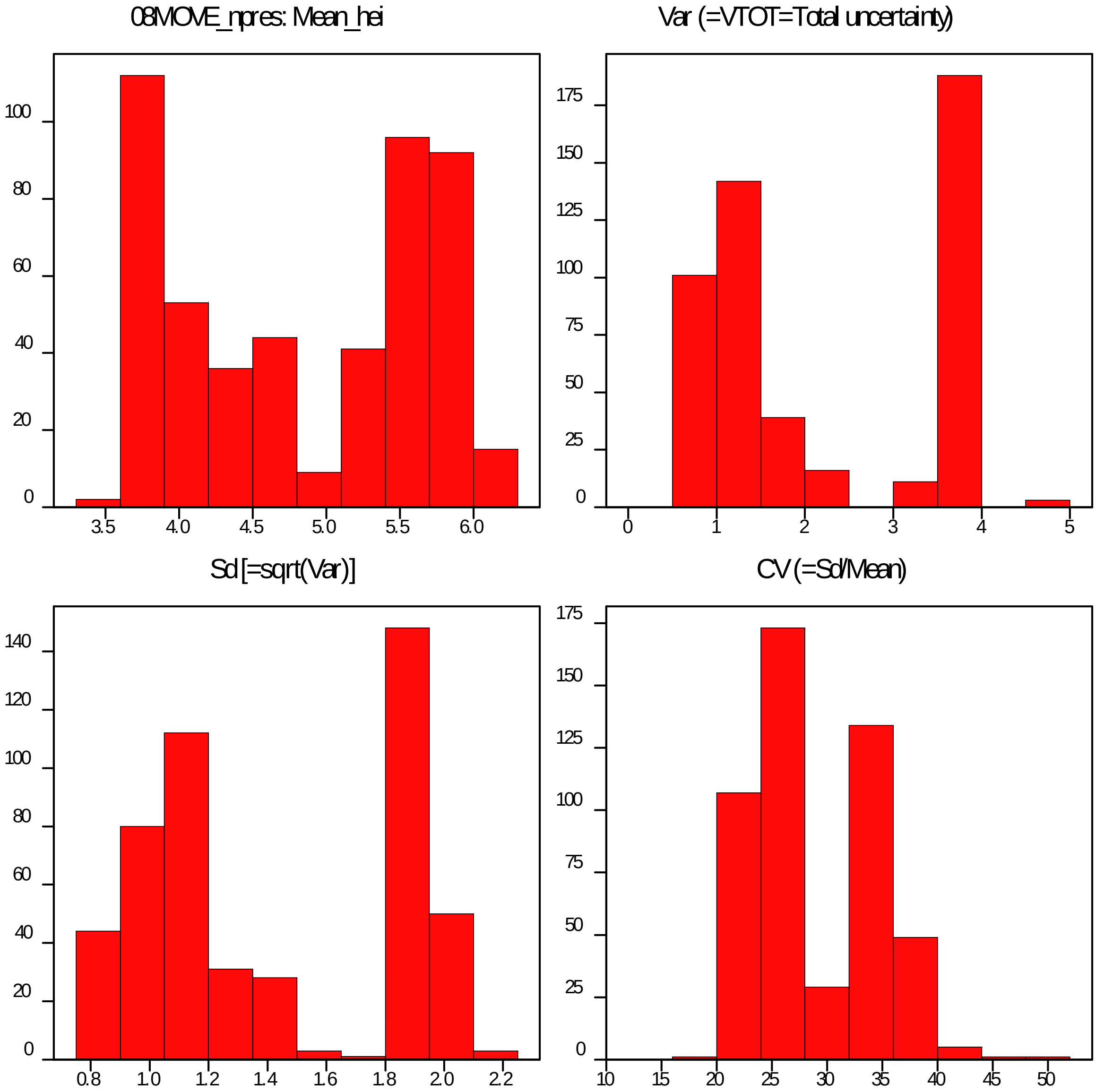
Tabulation of the number of sites of mean F (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean F for heathland as percentage.



Tabulation of the number of sites of mean R (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean R for heathland as percentage.

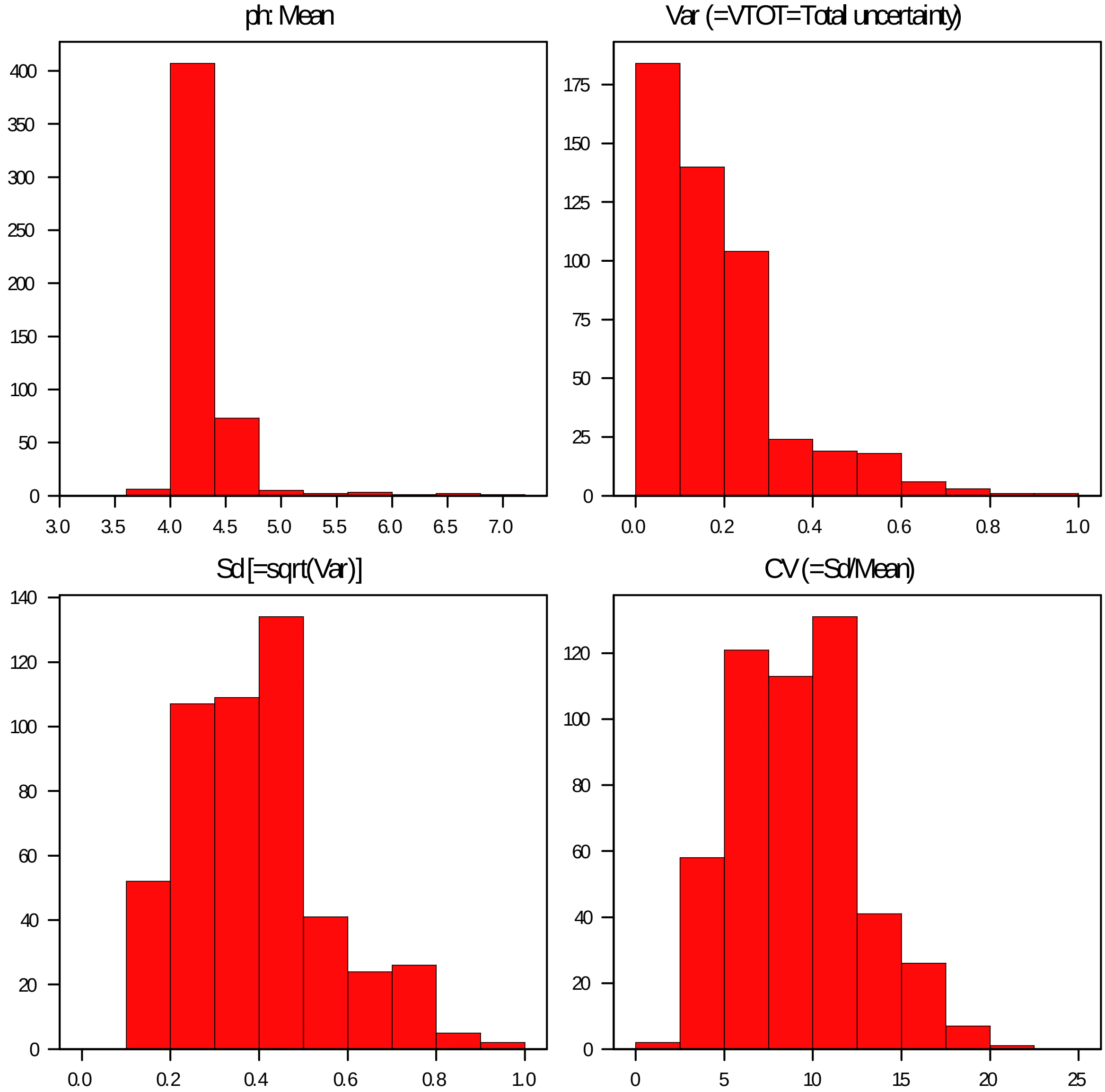


Tabulation of the number of sites of mean N (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for heathland as percentage.

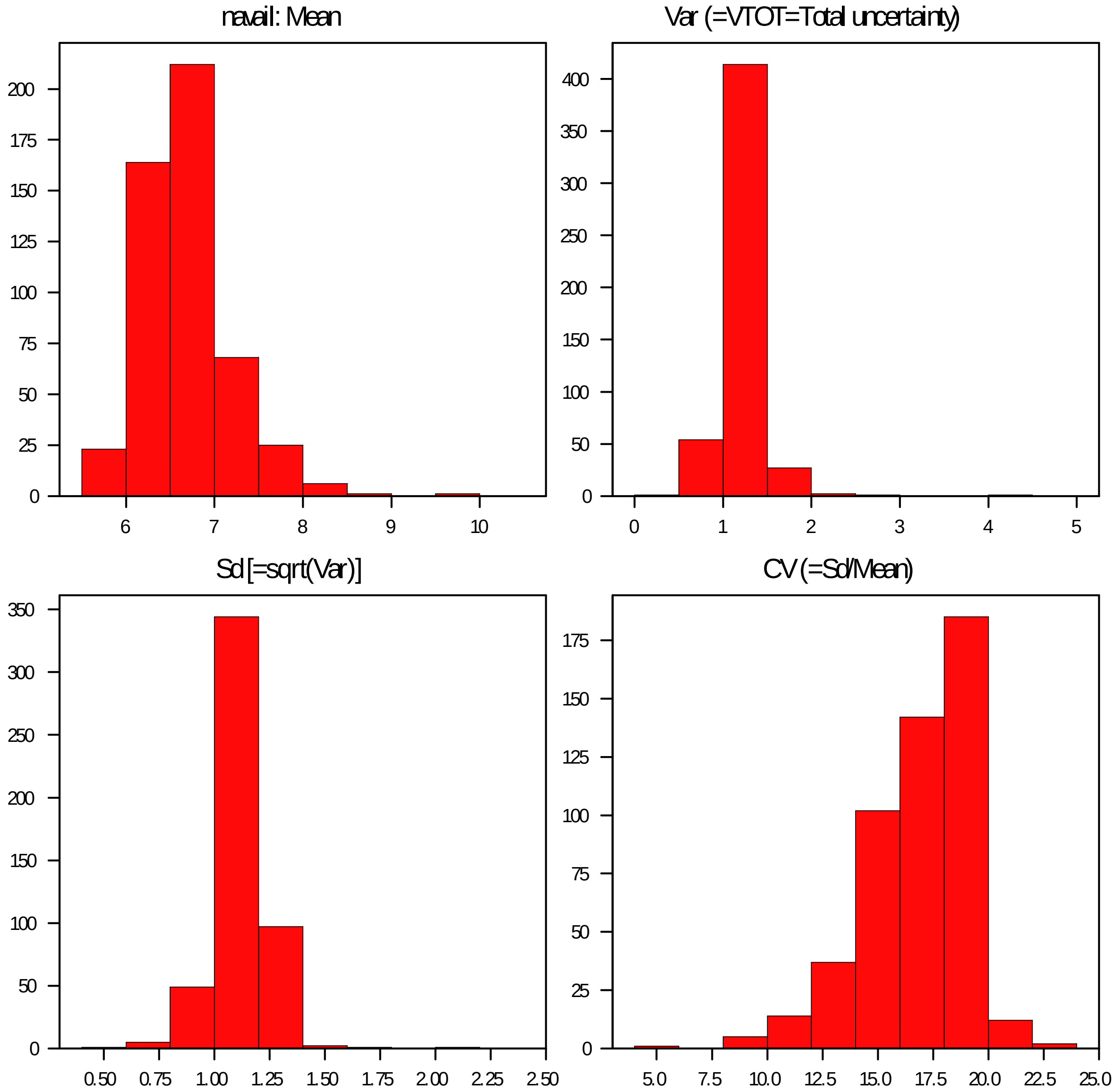


Tabulation of the number of sites of mean presences of species for MOVE4 (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for heathland as percentage.

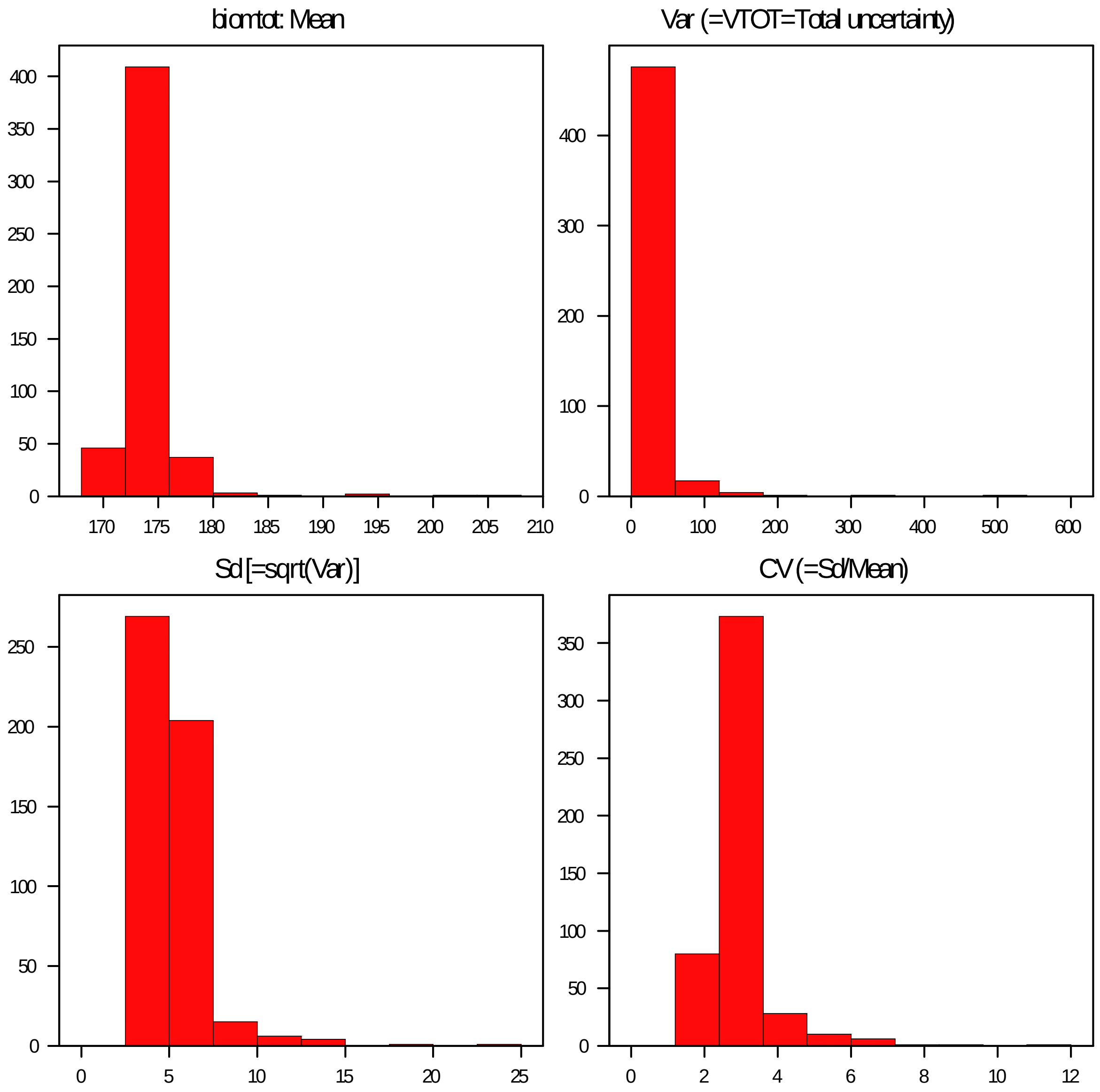
Forest



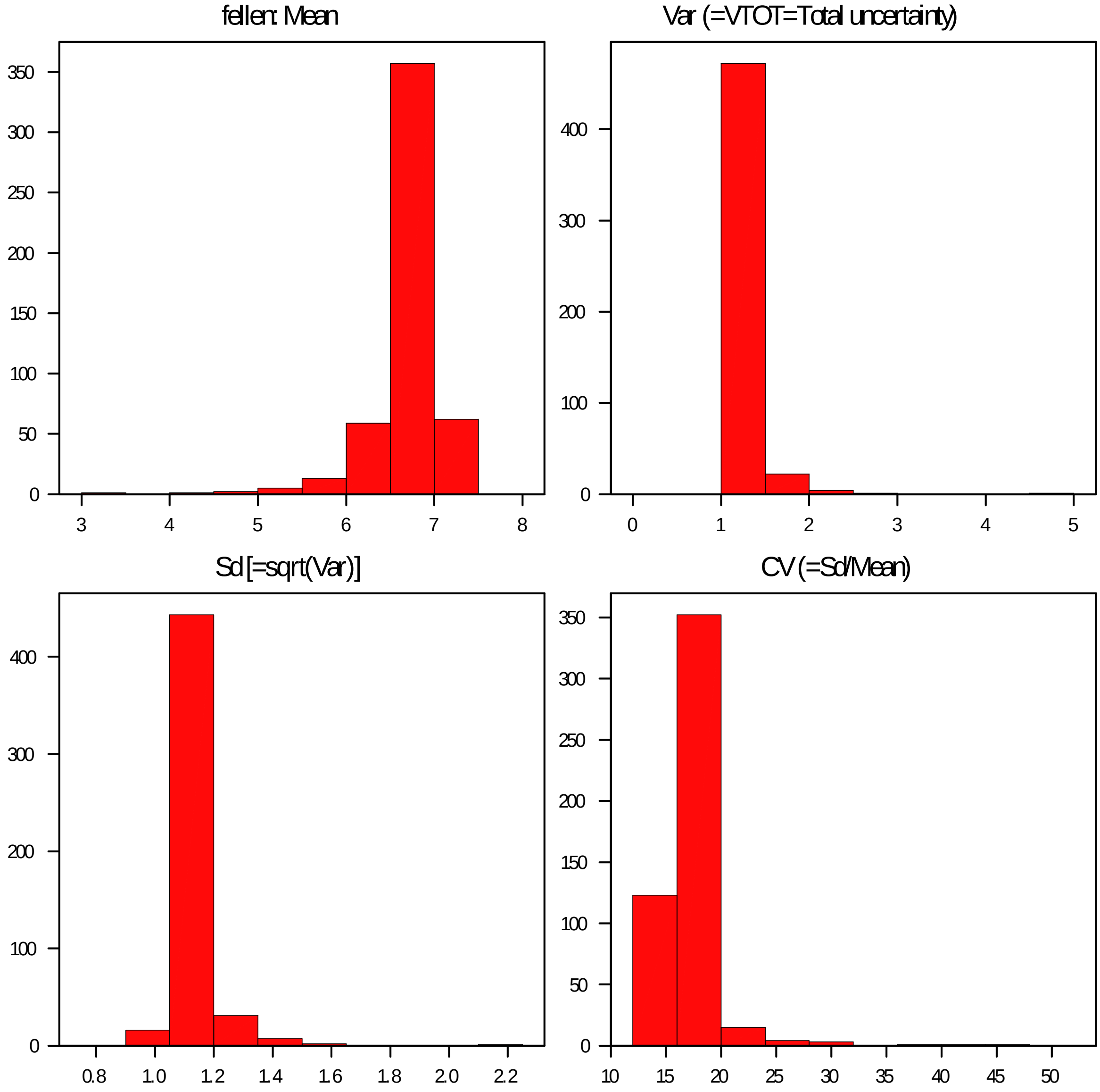
Tabulation of the number of sites of mean pH (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean pH for forest as percentage.



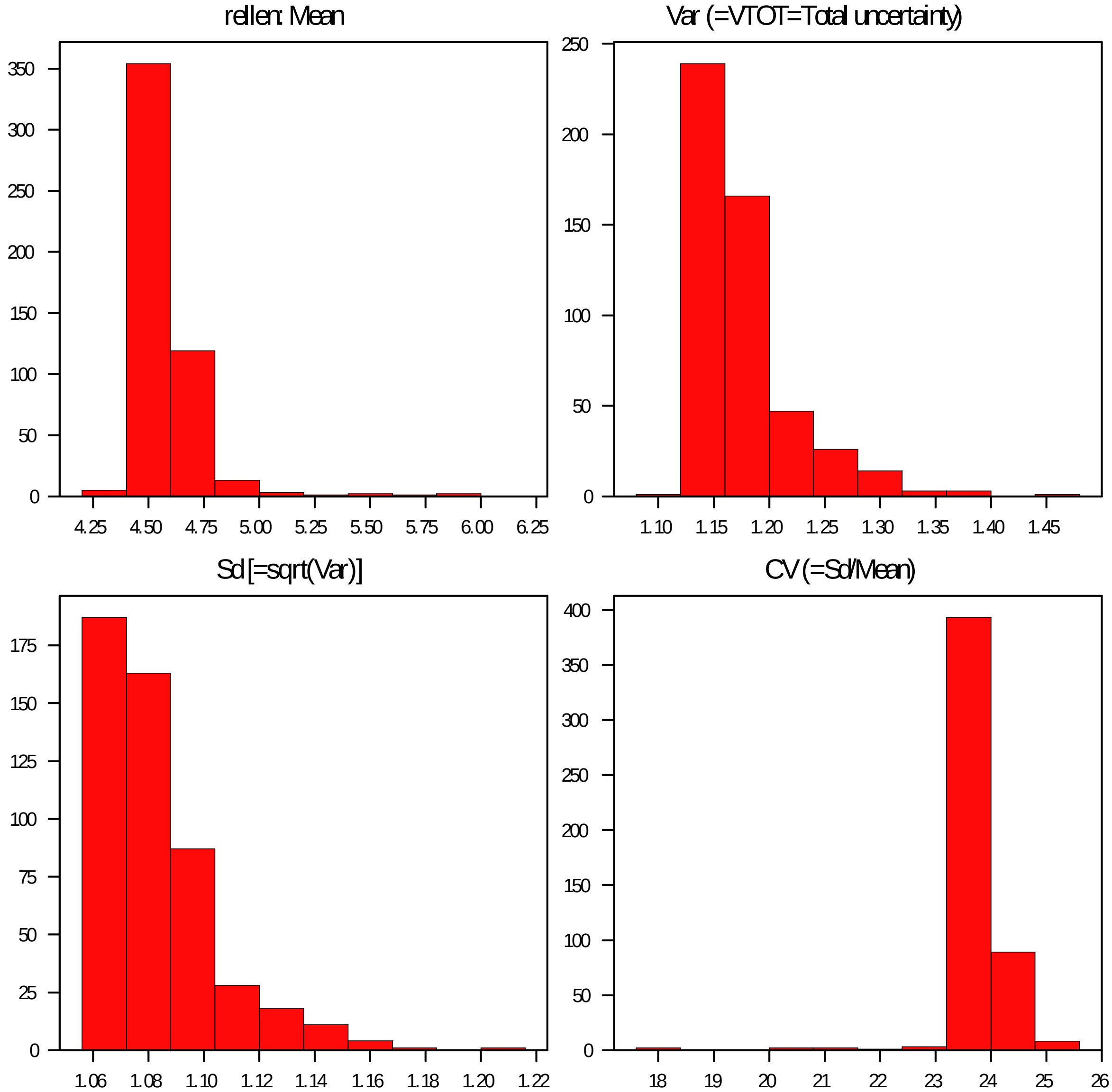
Tabulation of the number of sites of mean nitrogen availability (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean for forest as percentage.



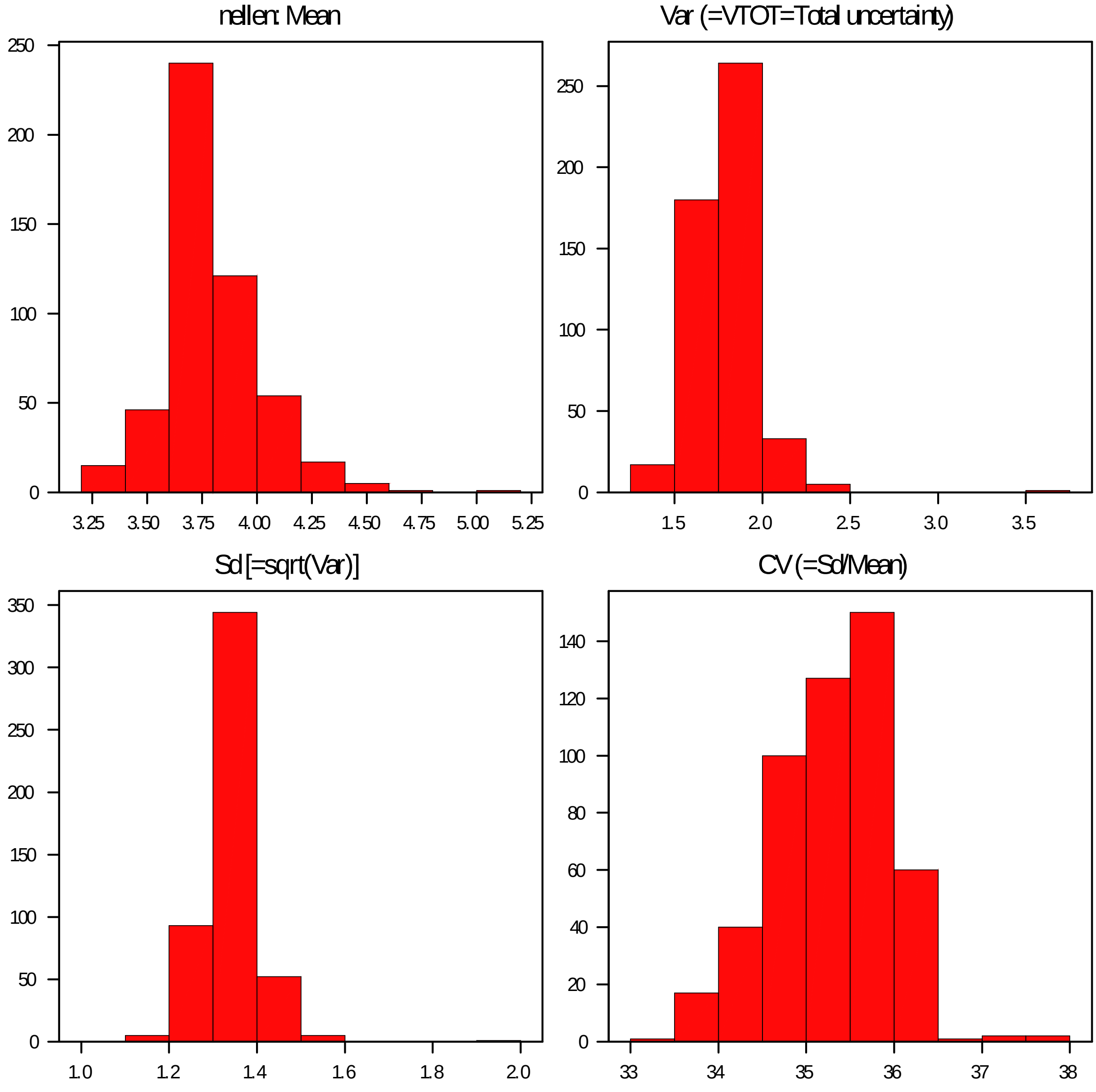
Tabulation of the number of sites of mean total biomass (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean total biomass for forest as percentage.



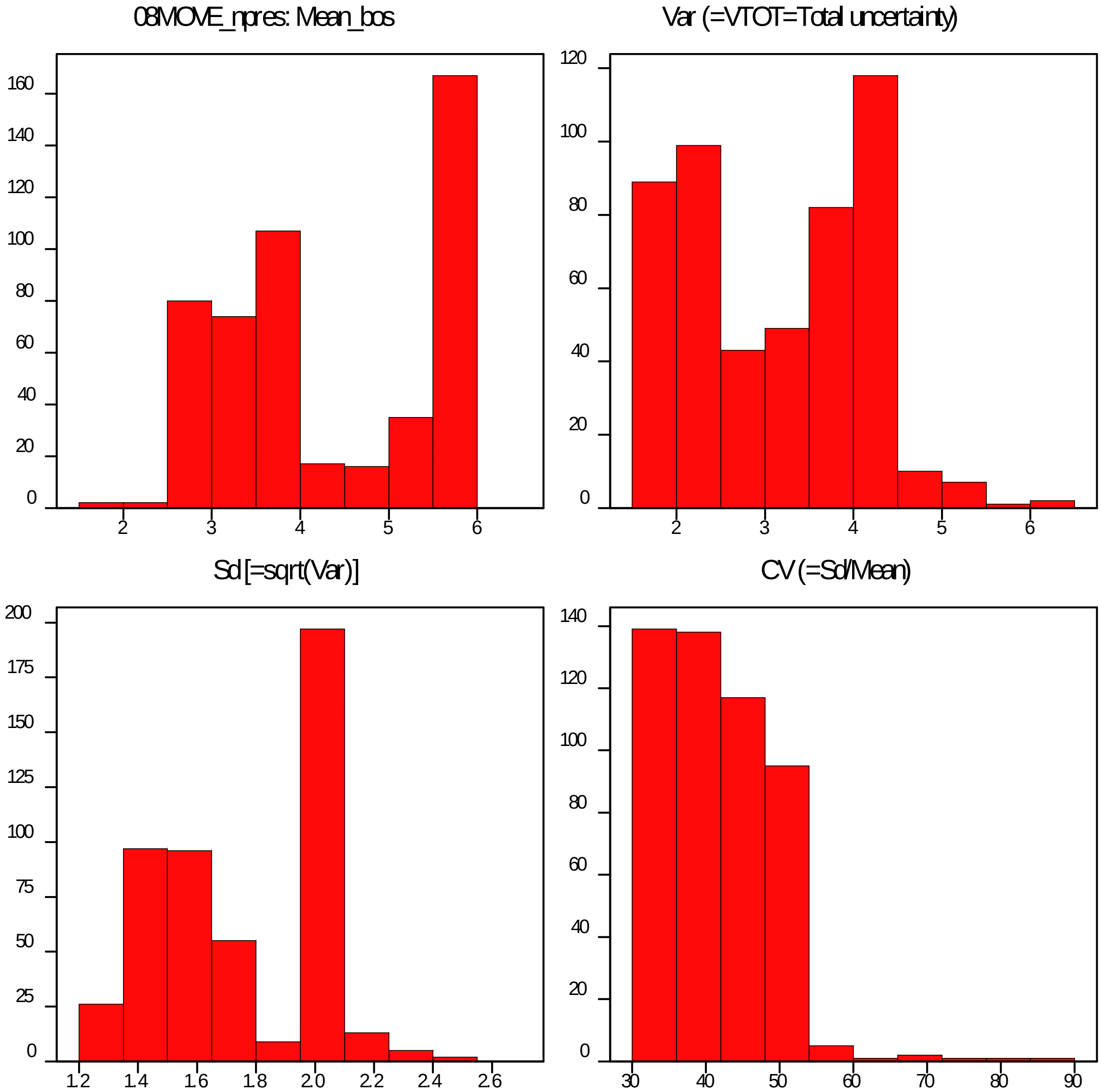
Tabulation of the number of sites of mean F (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean F for forest as percentage.



Tabulation of the number of sites of mean R (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean R for forest as percentage.



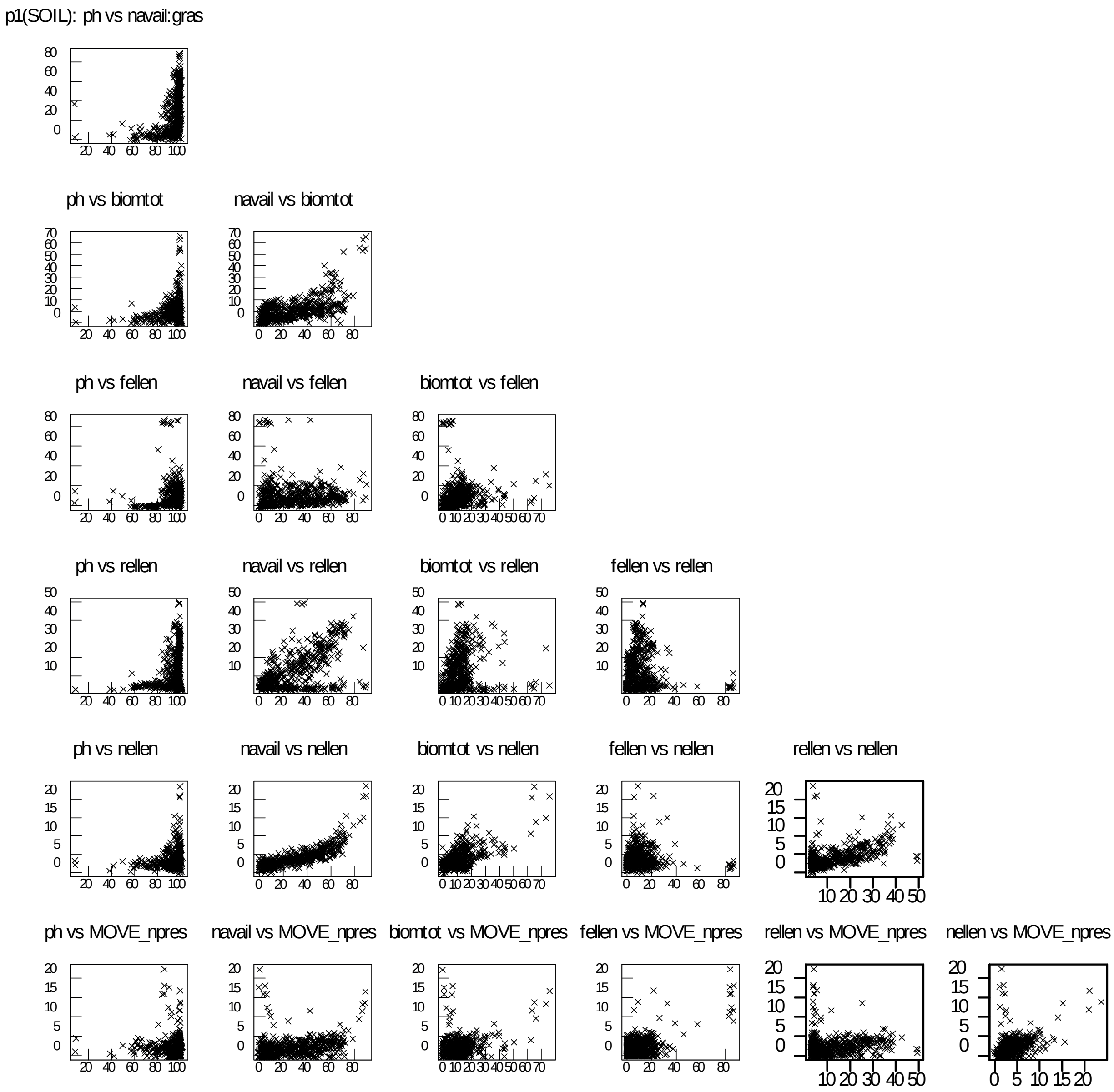
Tabulation of the number of sites of mean N (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for forest as percentage.

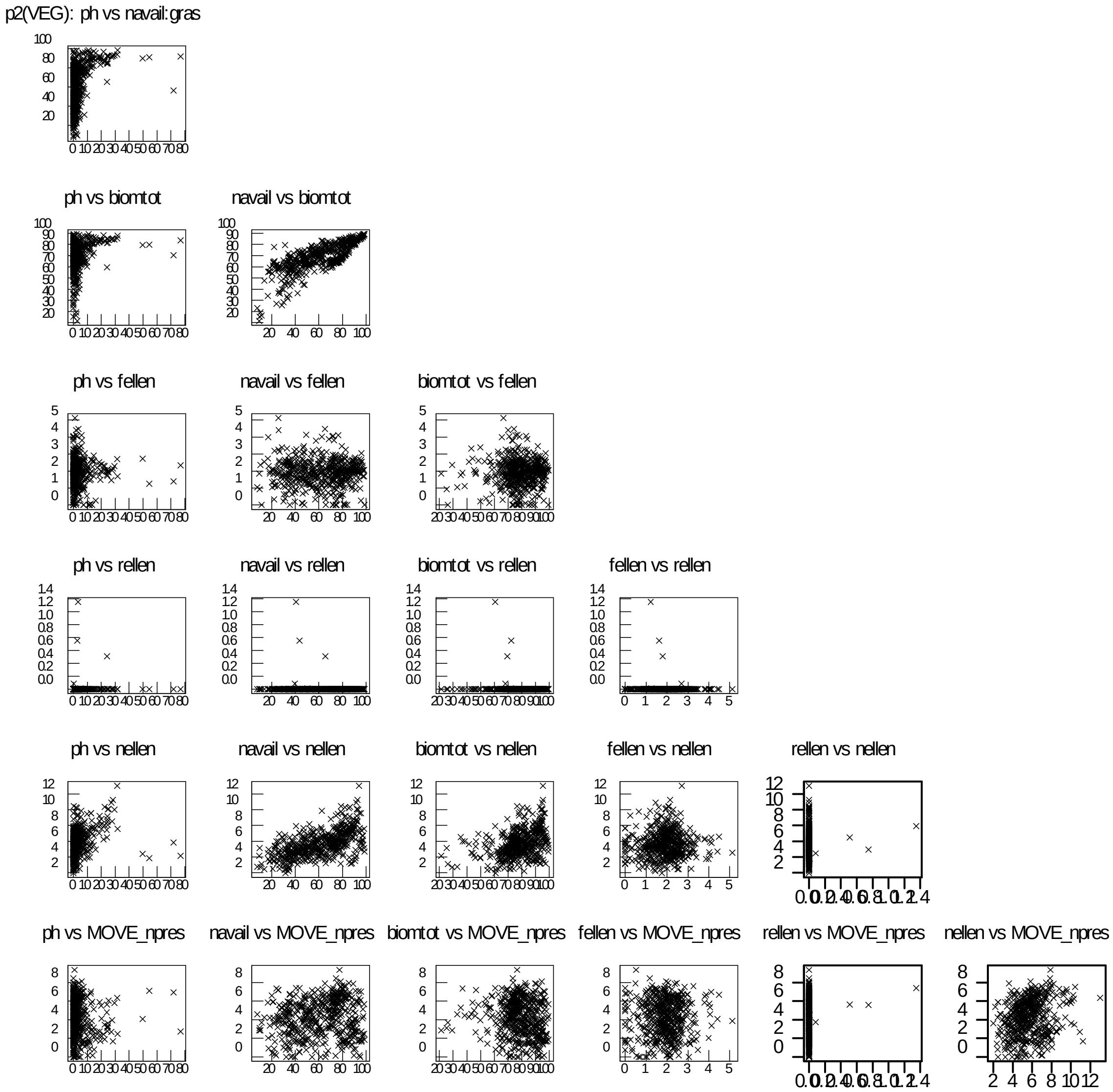


Tabulation of the number of sites of mean presences of species for MOVE4 (n=15,000), the variance, the standard deviation and the ratio of standard deviation/mean N for forest as percentage.

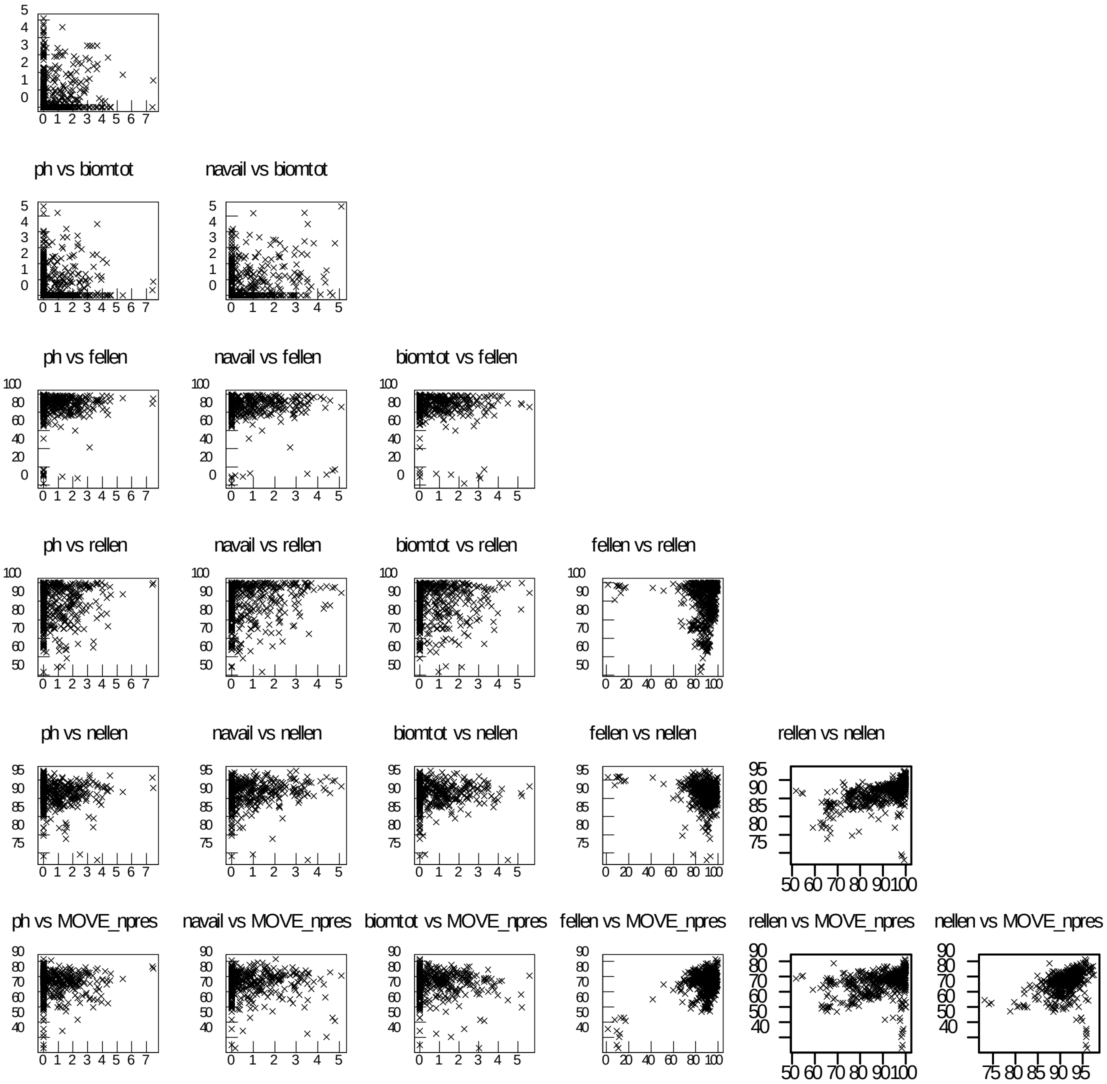
Appendix 12 Scatter plots of explained variances for the relations between output variables for the four parameter groups

Grassland

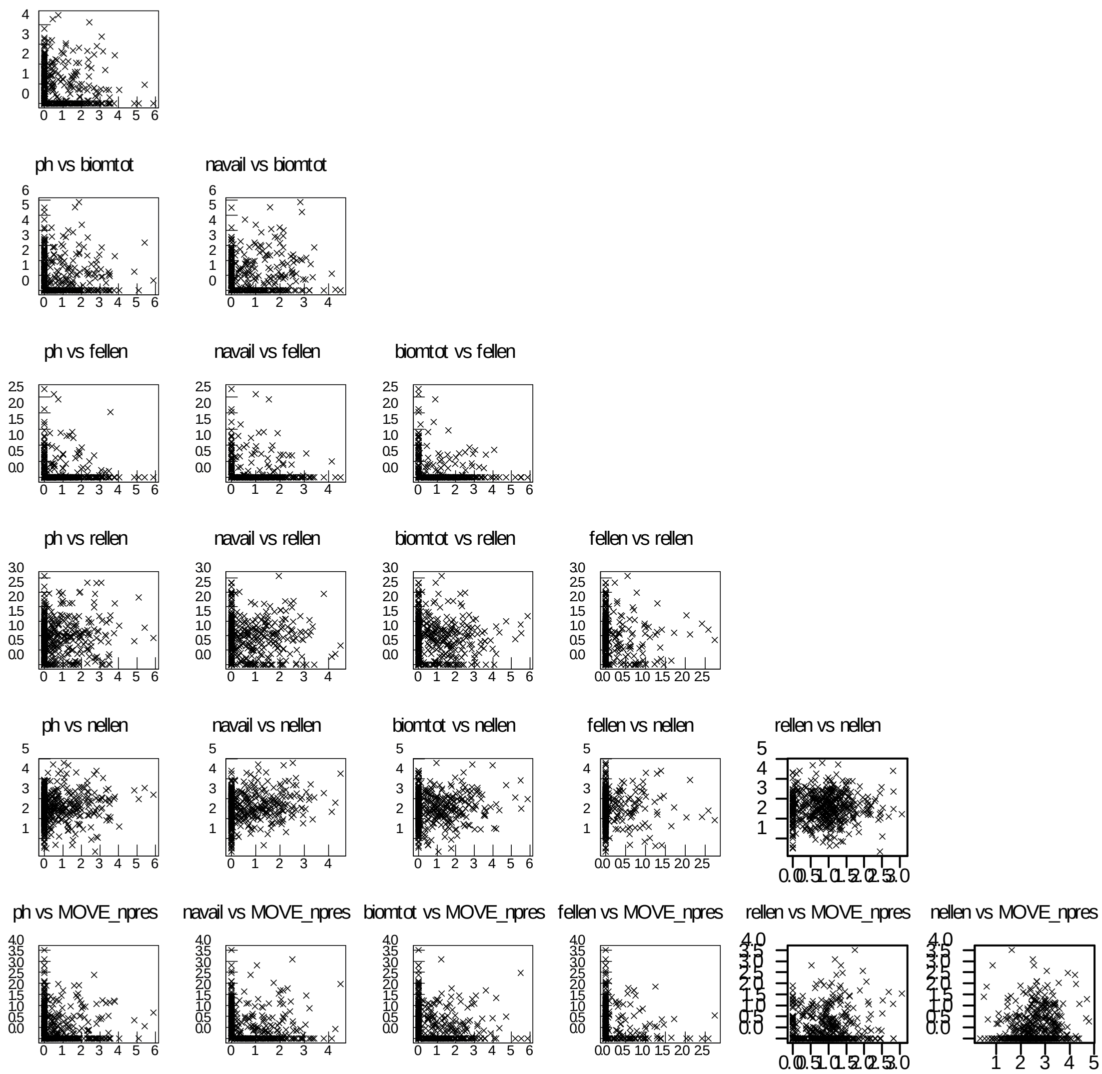



p2(VEG): ph vs navail:gras
ph vs biomtot
navail vs biomtot
ph vs fellen
navail vs fellen
biomtot vs fellen
ph vs rellen
navail vs rellen
biomtot vs rellen
fellen vs rellen
ph vs nellen
navail vs nellen
biomtot vs nellen
fellen vs nellen
rellen vs nellen
ph vs MOVE_npres
navail vs MOVE_npres
biomtot vs MOVE_npres
fellen vs MOVE_npres
rellen vs MOVE_npres
nellen vs MOVE_npres

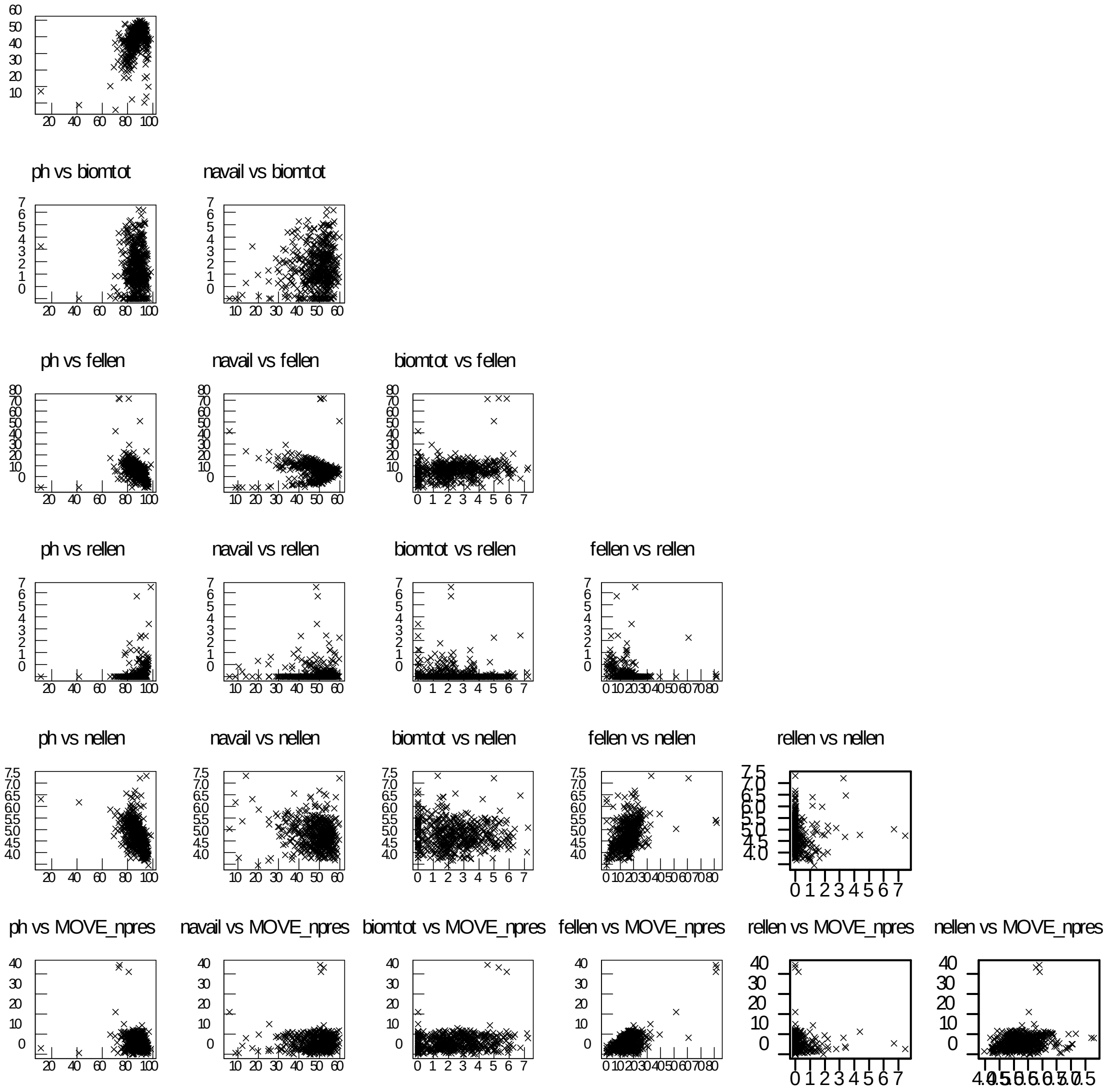
p3(P2E): ph vs navail:gras

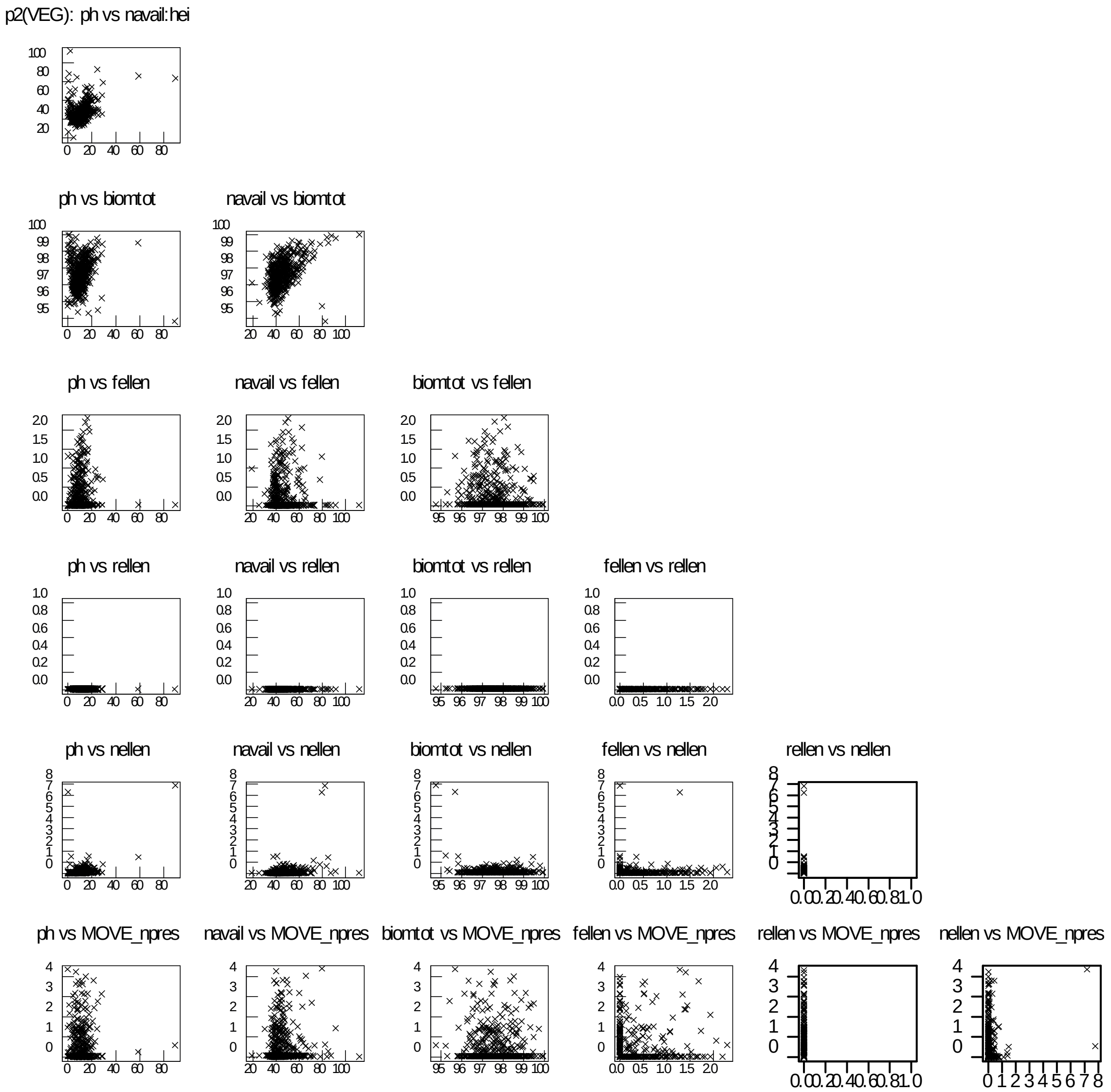


p4(MOVE): ph vs navail:gras

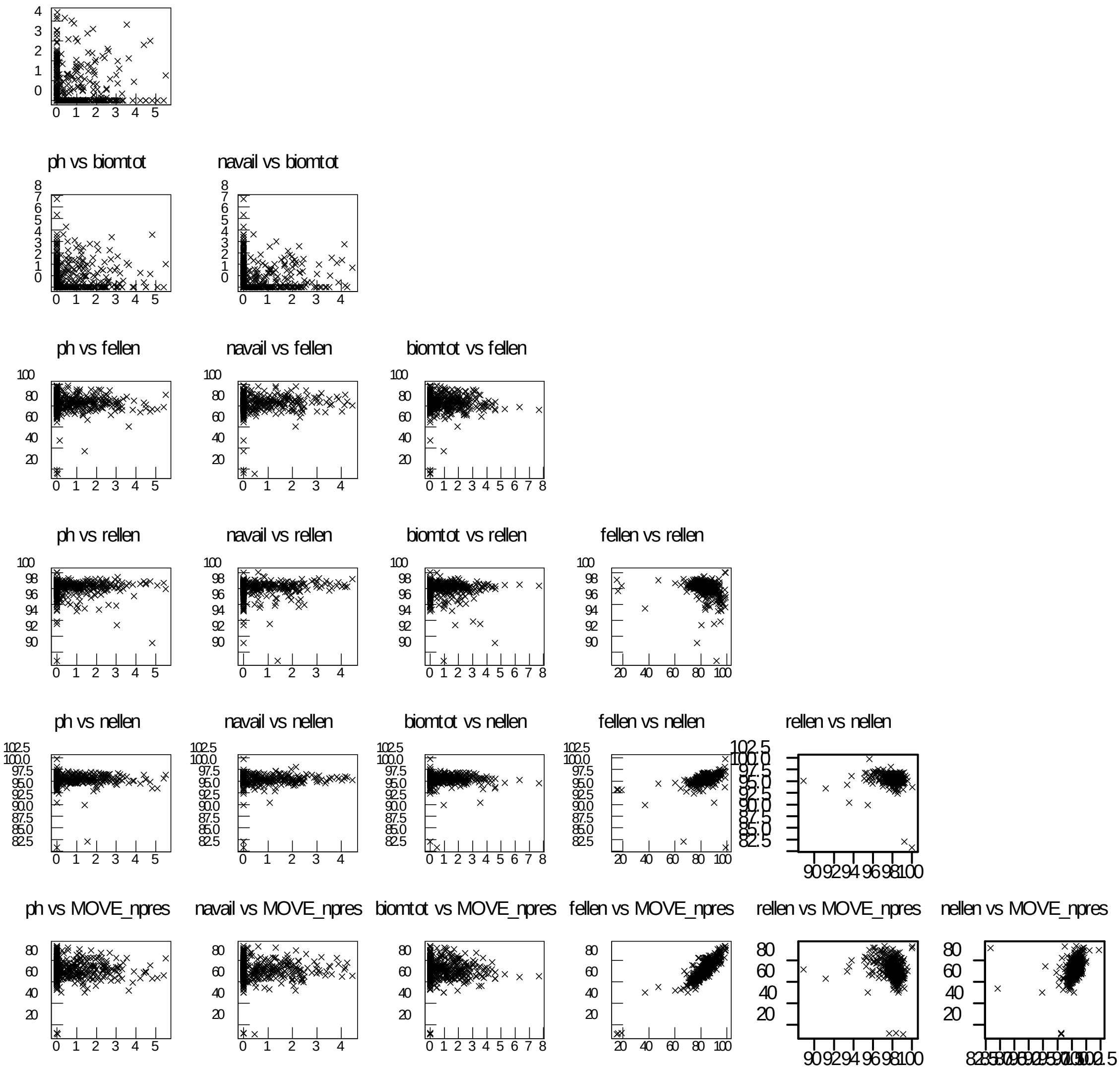


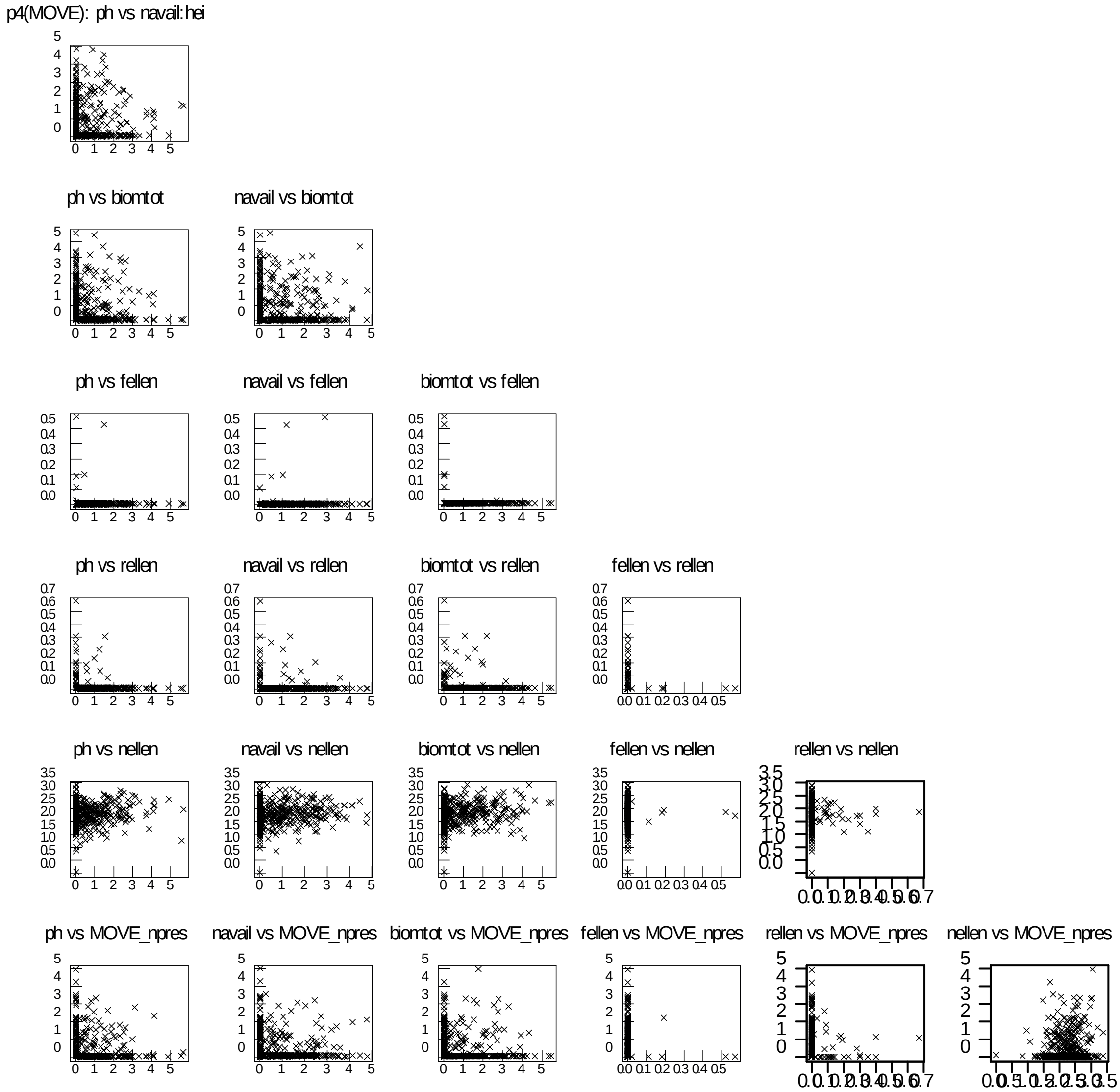
p1(SOIL): ph vs navail:hei



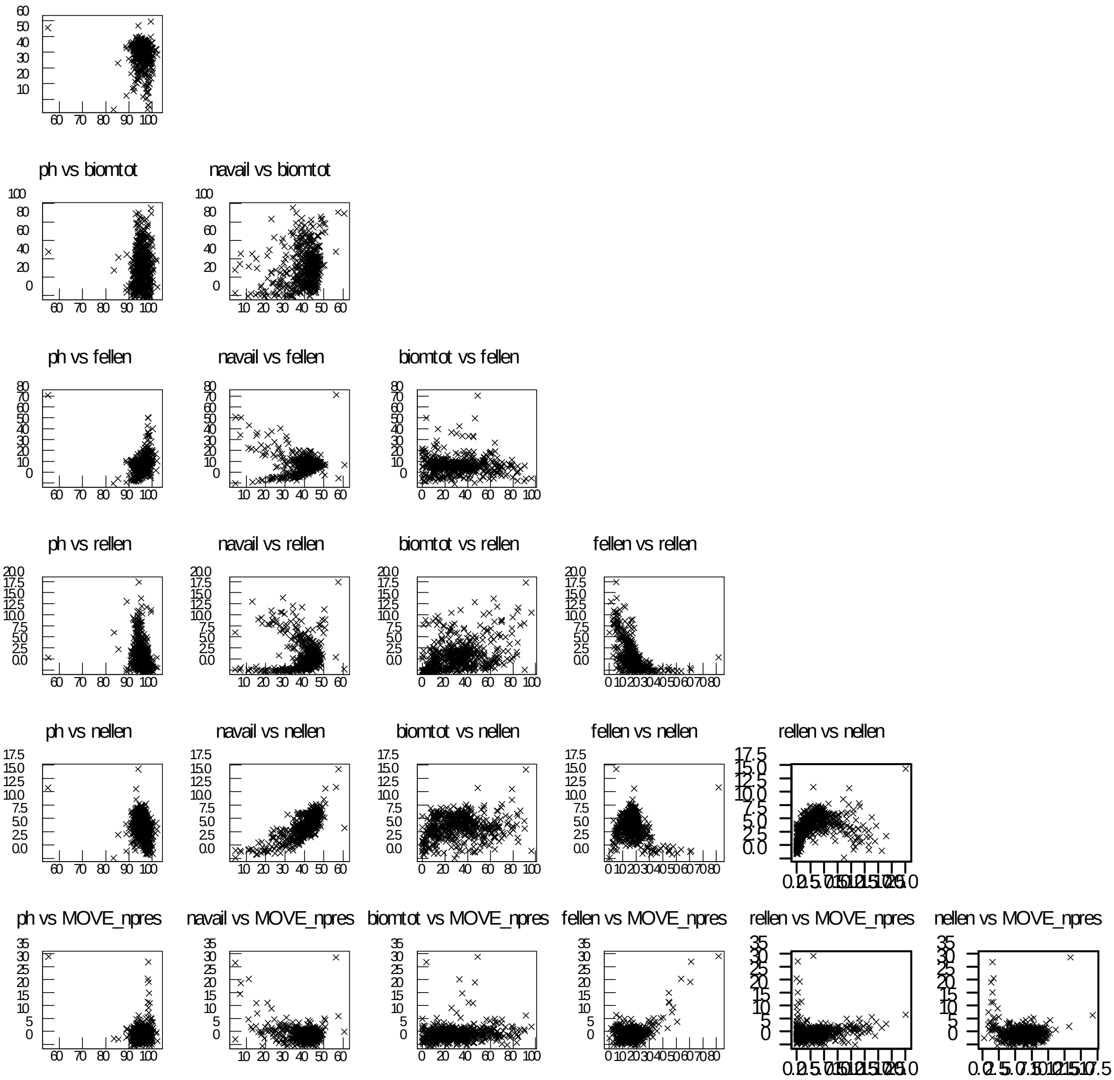

p2(VEG): ph vs navail:hei
ph vs biomtot
navail vs biomtot
ph vs fellen
navail vs fellen
biomtot vs fellen
ph vs rellen
navail vs rellen
biomtot vs rellen
fellen vs rellen
ph vs nellen
navail vs nellen
biomtot vs nellen
fellen vs nellen
rellen vs nellen
ph vs MOVE_npres
navail vs MOVE_npres
biomtot vs MOVE_npres
fellen vs MOVE_npres
rellen vs MOVE_npres
nellen vs MOVE_npres

p3(P2E): ph vs navail:hei

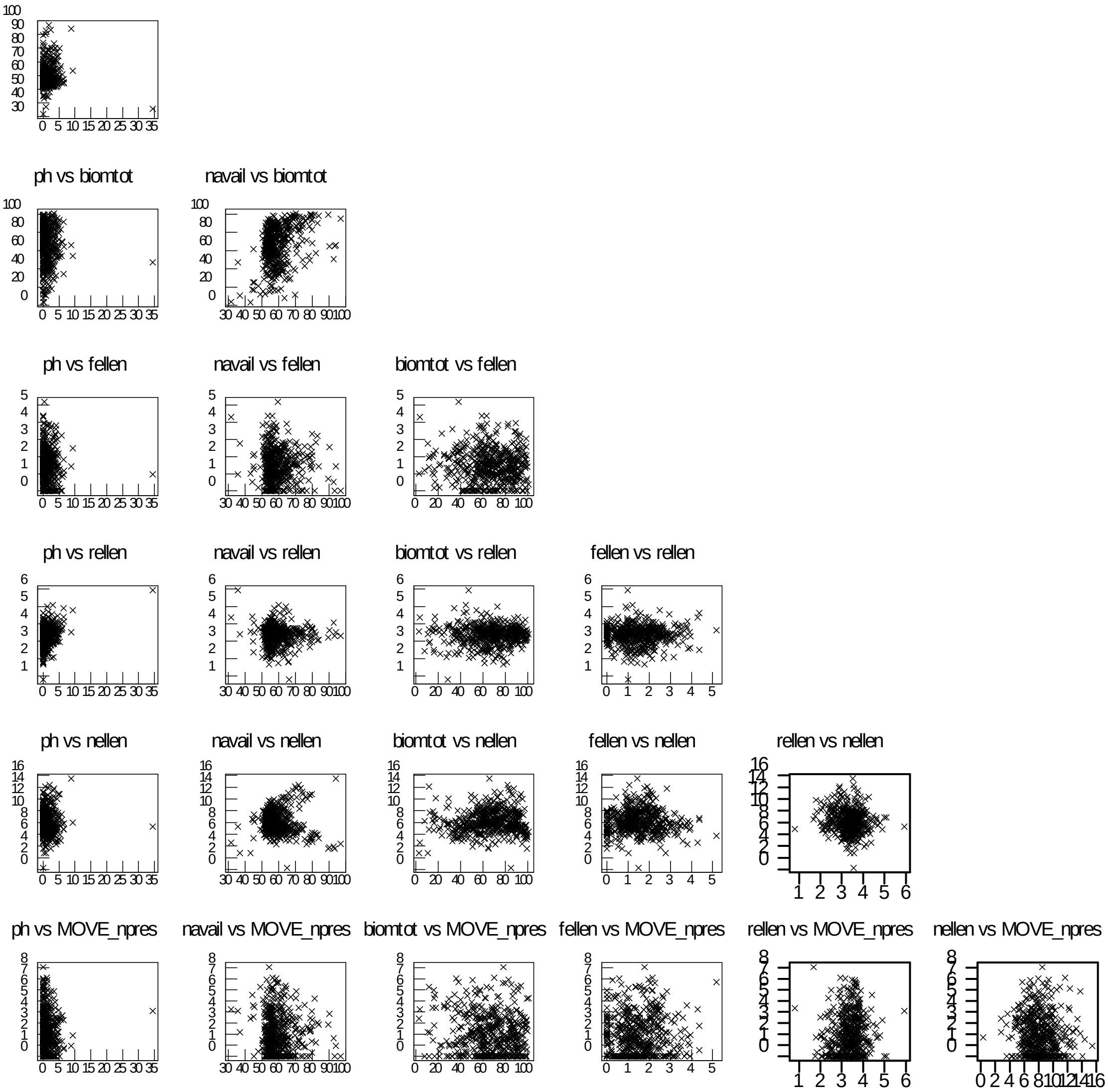



p4(MOVE): ph vs navail:hei
ph vs biomtot
navail vs biomtot
ph vs fellen
navail vs fellen
biomtot vs fellen
ph vs rellen
navail vs rellen
biomtot vs rellen
fellen vs rellen
ph vs nellen
navail vs nellen
biomtot vs nellen
fellen vs nellen
rellen vs nellen
ph vs MOVE_npres
navail vs MOVE_npres
biomtot vs MOVE_npres
fellen vs MOVE_npres
rellen vs MOVE_npres
nellen vs MOVE_npres

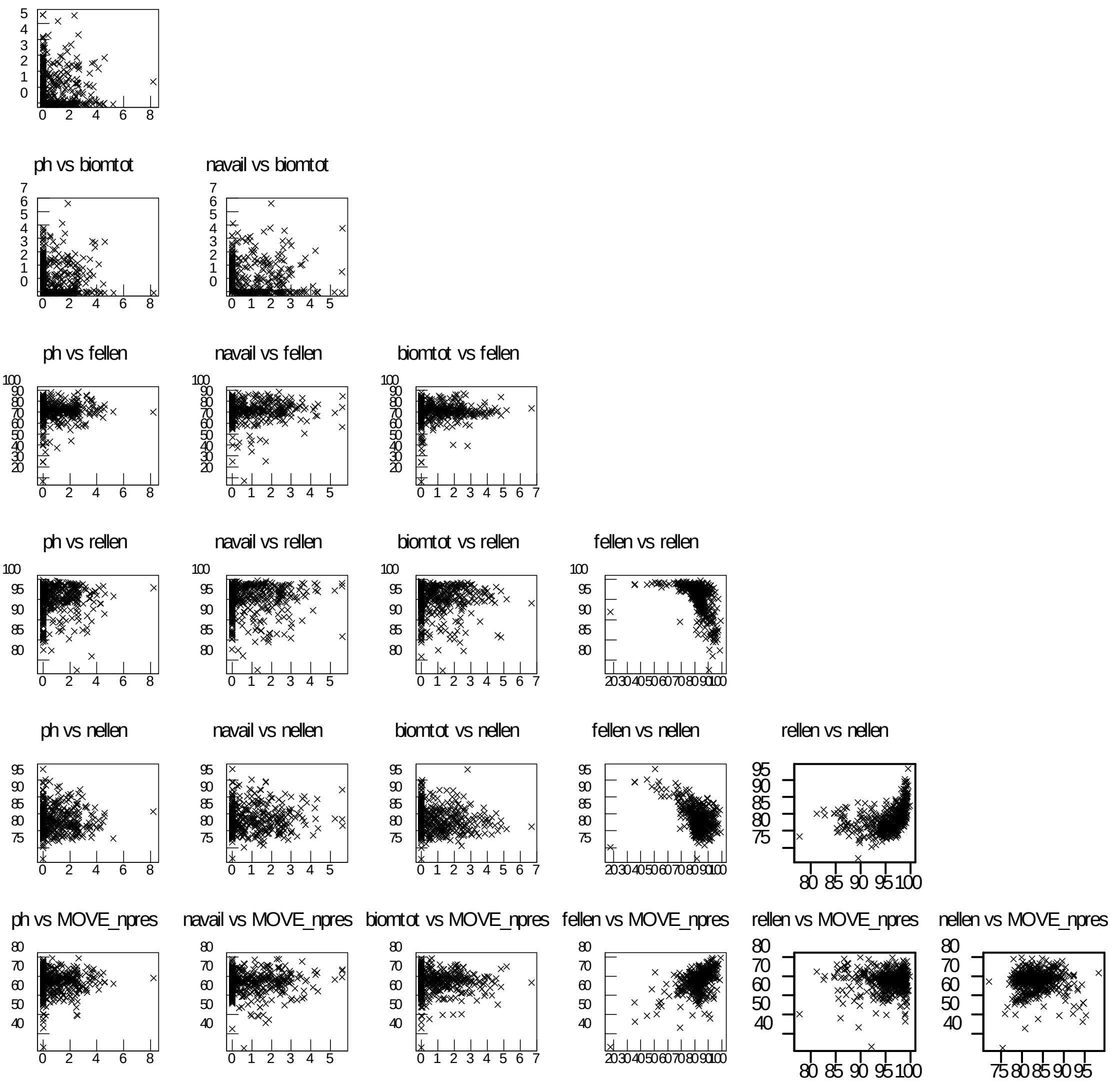
p1(SOIL): ph vs navail:bos



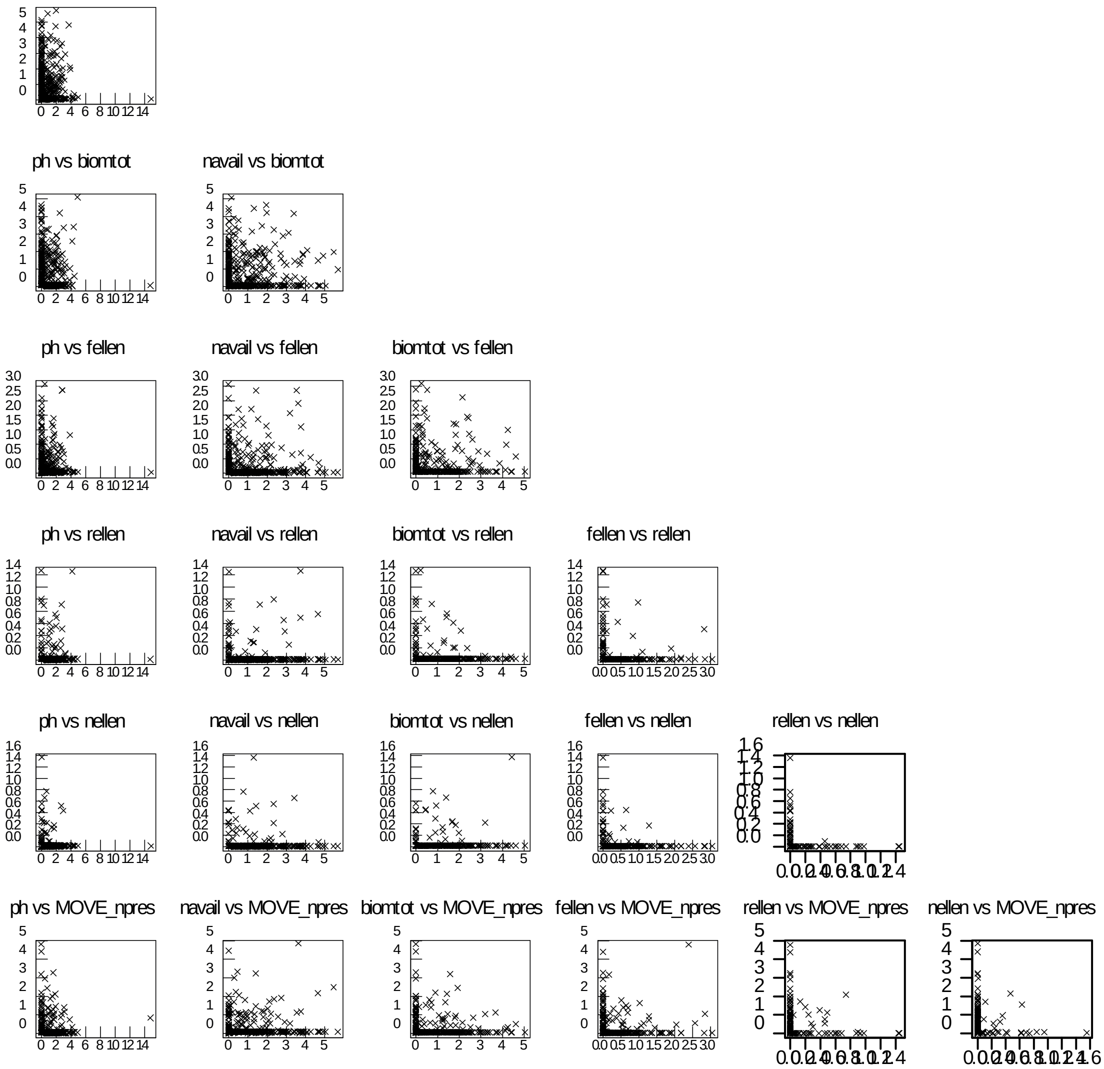
p2(VEG): ph vs navail:bos



p3(P2E): ph vs navail:bos



p4(MOVE): ph vs navail:bos



Appendix 13 Reviews

	Wettelijke Onderzoekstaken Natuur & Milieu		
F-0009	**Beoordelingsformulier WOt-publicaties (studies, en, papers)**	Versie	1.8
		Gewijzigd	05-01-2010
Eigenaar	Hoofd WOT Natuur & Milieu		
Beheerde	Kwaliteitsfunctionaris	Pagina	1 van 5

Betreft manuscript in de reeks WOt-*studies* / WOt-*rapporten* / WOt-*papers*
Studie / Rapport / Paper nr. ***Titel:*** **Uncertainty analysis of SMART2-SUMO2-MOVE4, the soil and vegetation model chain of the Nature Planner**

Referent: Peter Janssen
Datum beoordeling: 15-07-2010 ***Handtekening:***

Nr.	Onderdeel	Ja	Nee	Toelichting door beoordelaar	Verwerking commentaar door auteur
Algemeen (alleen bij WOt-studie)					
S1	Is het onderwerp origineel en integrerend van karakter?	ja		Met name is het onderwerp integrerend omdat het de onzekerheid bekijkt van een hele modelketen, en daarbij probeert aan te geven welke onderdelen van de keten daar het meest toe bijdragen.	-
S2	Hebben opiniërende passages een duidelijke relatie tot de probleemstelling van het manuscript?	ja		Ik had wel verwacht dat in de conclusies nog concreter naar voren werd gebracht wat de beperkingen (wb. het wel/niet meenemen van bepaalde onzekerheden, o.a. wb MOVE4) en mogelijke consequenties van de resultaten van de studie waren (met name aanbevelingen betreffende vervangen van P2E-module en belang van validiteits-studie naar MOVE4-resultaten over mate van voor-komen van soorten).	Al deze punten werden al aangestipt in de conclusies. Er is een kleine uitbreiding gedaan m.b.t. de toepas-baarheid van de resultaten van MOVE en een aan-beveling om MOVE te valideren. Er is echter niet uitgewerkt hoe dat zou moeten gebeuren, dat past niet binnen het kader van deze opdracht.

Structuur van het manuscript		Ja	Nee	Toelichting door beoordelaar	Verwerking commentaar door auteur
1	Is het manuscript helder van gedachtegang en opbouw?	ja			-
2	Bestaat het manuscript uit de volgende onderdelen (*naast de standaardonderdelen Inhoud, Woord vooraf, Referaat, Samenvatting, Literatuur*): Inleiding, Methode, Resultaten, Discussie, Conclusie? Zo nee, zijn er dwingende redenen om hiervan af te wijken?	ja			-
3	Zijn alle figuren en tabellen noodzakelijk?	Ja/ nee		Omdat in de hoofdtekst toch een tamelijk brede beschrij-ving van de resultaten gegeven is, zijn de bijbe-horende figuren ook daar vermeld. Eventueel was een keuze mogelijk geweest waarbij enkele figuren werden uitgelicht, terwijl het restant in de bijlagen was verschenen. Bij de figuren uit hoofdstuk 8 ware het beter geweest als de figuren over de standaard deviaties vervan-gen zouden zijn door figuren over de CV (coeffi-cient of variation), die directer inzicht leveren over de relatieve grootte van de onzekerheid. Ook is de keuze van de onderscheiden klassen in de legenda nog weinig uniform hetgeen de vergelijkbaarheid van de figuren niet ten goede komt. Daarnaast is het opschrift van sommige figuren nog in het Nederlands en moet dit nog worden omgezet naar Engels. In appendix 11 wordt trouwens wel de CV in de figuren getoond, maar niet overal op dezelfde wijze (1/3 van de figuren laat de CV als fracvtie zien, de rest de CV als percentage).	Er is lang over gedacht al door de projectgroep wat wel en niet in de hoofdtekst zou moeten, op basis van die discussie was al een deel naar de bijlage verplaatst. Er is nu besloten om nu niet nog meer te verplaatsen. Over hoodstuk 8 (zie ook hieronder) dat had inderdaad gekund, maar nu besloten om dit niet meer te veranderen. Er is bewust gekozen om de klasse-grenzen niet hetzelfde te houden omdat er dan veel figuren zouden zijn met geen kleuronderscheid en je ook zeer veel nietszeggende plaatjes krijgt. De opschriften zijn ver-dwenen Appendix 11. klopt en is erg slordig van ons, het zou echter veel werk vergen dat te veranderen, dus daarom de onderschriften aangepast zodat het in ieder geval duidelijk is dat er verschil-lende eenheden zijn ge-bruikt in de figuren.
4	Dekt de titel de lading van het manuscript?	Ja		De enige omissie is het ontbreken van een verwij-zing naar de P2E module in de titel, maar deze maakt een integraal bestanddeel uit van de SMART2-SUMO2-MOVE4 keten dat deze omissie niet relevant is.	Toegevoegd aan de titel

Inleiding		Ja	Nee	Toelichting door beoordelaar	Verwerking commentaar door auteur
5	Is het probleem helder omschreven? Geeft de inleiding een goed overzicht van eerder onderzoek?	Ja			-
6	Zijn de doelstelling en de maatschappelijke en/of wetenschappelijke relevantie helder omschreven?	Ja			-
7	Zijn de vraagstelling en deelvragen helder beschreven?	Ja			-
8	Zijn de vooronderstellingen (hypothesen) voldoende expliciet?	Ja			-
9	Is er een evenwichtige keuze uit de literatuur gemaakt bij de afbakening van het onderwerp ten opzichte van eerder onderzoek? En is daarbij voldoende gebruik gemaakt van recente (internationale) literatuur?	ja			-
10	Is het gebruik van vaktermen juist en begrijpelijk?	Ja			-
11	Is het overzicht van het onderzoek duidelijk? Is er een leeswijzer opgenomen?	Ja; Nee			-
Methode					
12	Zijn de gebruikte aanpak en methoden helder uiteengezet?	Ja			-
13	Zijn de aanpak en methoden adequaat om de gestelde vragen te beantwoorden, en is de keuze goed verantwoord?	Ja			-
Resultaten					
14	Is er duidelijk onderscheid gemaakt tussen eigen onderzoeksgegevens en gegevens uit overige bronnen?	Ja			-
15	Zijn de onderzoeksresultaten goed onderscheiden van de interpretatie en discussie?	Ja			-

Discussie en Conclusies					
16	Worden de resultaten voldoende kritisch besproken?	Ja/ nee		Jammer is alleen dat niet geprobeerd wordt om een verklaring te geven waarom voor bepaalde sites wel de bodem- en/of vegetatie-parameters een substantiëlere onzekerheidsbijdrage leveren bij de Ellenberg- en MOVE resultaten.	Terechte opmerking. Het zou echter een nieuwe analyse vergen om dit uit te zoeken en kan mogelijk worden gedaan wanneer besloten wordt ook MOVE4 nog aan onzekerheid te onderwerpen.
17	Vindt in de discussie een terugkoppeling plaats naar de hoofdvraag/deelvragen?	Ja/ nee		Uiteindelijk zou ik met name ook geïnteresseerd zijn in de belangrijke vraag wat de resultaten betekenen voor de inzet van de Natuurplanner bij toekomstige beleidsanalyses en verkenningen, en welke toekomstige activiteiten/ ontwikkelingen tav de Natuurplanner gewenst zijn om e.e.a. ook in de toekomst met succes en vertrouwen te kunnen blijven inzetten.	Staat wel in de discussie en in de conclusies, de conclusies zijn aangescherpt
18	Worden de bevindingen afgezet tegen resultaten van vergelijkbaar onderzoek?	Ja			-
19	Geeft de discussie aanknopingspunten voor verder onderzoek? (welk deel van de hoofdvraag/ deelvragen is niet beantwoord?)	Ja		Maar dit is nog niet maximaal aangestipt of uitgewerkt, met name wat betreft: (a) P2E-module vervanging en potentiele effecten op onzekerheid van de uitspraken; (b) validiteit van Natuurplanner voor het doen van uitspraken over het 'voorkomen van soorten'	(a) aangescherpt met verwijzing naar eerder onderzoek (Wamelink *et al.* 2005) waarin werd aangetoond dat R meer dan tweemaal zo grootte onzekerheid geeft dan pH. (b) dit onderzoek doet geen uitspraken over de validiteit van MOVE (voorkomen van soorten), temeer daar MOVE zelf niet is meegenomen in de onzekerheidsanalyse. Het zou ongepast zijn daar nu wel uitspraken over te doen.
20	Worden in de discussie de beperkingen en /of toepassingsmogelijkheden voldoende besproken?	Ja/ nee		Er had wat explicieter ingegaan kunnen worden op de onderliggende aannamen, beperkingen, en de mogelijke gevolgen voor de conclusies van het niet volledig meenemen van de MOVE4 onzekerheden.	Tekst over MOVE4 iets aangescherpt, echter er was al een stuk geweid in de discussie hierover.
Samenvatting					
21	Geeft de samenvatting een goede dekking van het manuscript?	Ja/ nee		Vooral de Nederlandse samenvatting; de engelse zou daar nog mee gelijk getrokken moeten worden	Samenvatting aangepast
22	Bevat de samenvatting de belangrijkste antwoorden op de hoofdvraag of hoofdvragen?	Ja			-

Advies
Het manuscript kan worden opgenomen in de reeks **Studies / Rapporten / Papers** van de WOT Natuur & Milieu
(vink item aan).

☐ met geringe aanpassingen	☑ met veel aanpassingen	☐ kan niet worden opgenomen

Aanvullende opmerkingen

Omvangrijke, gedegen en zorgvuldig beschreven studie, uitgevoerd met adequate (state-of-the-art) technieken, en met relevante resultaten!! *Dank!*

Het wordt echter nog onvoldoende duidelijk gemaakt wat de bevindingen van deze studie betekenen voor de toekomstige inzet van de Natuurplanner bij beleidsanalyses en verkenningen, en welke verbeterpunten gewenst zijn om een verantwoorde en succesvolle inzet van dit instrument te blijven garanderen.

Ww: ik heb alle opmerkingen in het document met track changes aangegeven aangepast, behalve de onderstaand. Eerst wordt de opmerking gegeven en dan ons commentaar waarom er niets mee is gedaan.

Bij een paar figuren wordt gevraagd om de Nederlandse tekst weg te halen.
WW uiteindelijk gedaan, was veel werk

P43 Jammer dat geen expliciete info gegeven wordt over de R^2 die voor de lezer een beeld geeft van de fit van dit achterliggende regessiemodel.
WW Er wordt al wel veel info gegeven, de rest is te vinden in het artikel naar waar wordt verwezen (Wamelink et al. 2002)

Hstd 7. p 52. Maar kun je toch een tentatieve uitspraak doen over hoe belangrijk deze omissie is voor de OZ-resultaten?
WW Dit gaat over het niet meenemen van de onzekerheid in MOVE4, daarop wordt in de discussie terug gekomen.

P58 e.v. Algemene opmerkingen bij dit soort plotjes (nu en in de rest van dit hoofdstuk). Let op: svp engelse titels van legenda. Keuze van klasse grenzen in legenda's is niet altijd uniform en lijkt soms tamelijk sterk ad hoc. Bovendien had ikzelf de voorkeur gegeven aan plotjes van de CV (variatiecoeficient)in plaats van de stdev, want de eerstgenoemde geeft meer informatie over de relatieve onzekerheid in de site-waarden dan de laatsgenoemde.
WW. Zie ook hierboven, Engelse legenda's niet gemaakt, ook niet echt nodig. Keuze van de klassegrenzen is bewust zo gedaan, omdat er anders niets te zien valt voor veel kaartjes. Plotjes van CV had ook gekunt. Gaan we nu echter niet meer toevoegen.

WAGENINGEN UR
For quality of life
Wettelijke Onderzoekstaken Natuur & Milieu

F-0009	**Beoordelingsformulier WOt-publicaties (studies, en, papers)**	Versie	1.8
		Gewijzigd	05-01-2010
Eigenaar	Hoofd WOT Natuur & Milieu		
Beheerde	Kwaliteitsfunctionaris	Pagina	1 van 10

Betreft manuscript in de reeks WOt-*studies* / WOt-*rapporten* / WOt-*papers*
Rapport met Titel: ***Uncertainty analysis of SMART2-SUMO2-MOVE4, the soil and vegetation model chain of the Nature Planner***
Referent: Paul Goedhart (Biometris)
Datum beoordeling: 11 juni 2010
Handtekening:

Nr.	**Onderdeel**	**Ja**	**Nee**	**Toelichting door beoordelaar**	**Verwerking commentaar door auteur**
Algemeen (alleen bij WOt-studie)					
S1	Is het onderwerp origineel en integrerend van karakter?	X			
S2	Hebben opiniërende passages een duidelijke relatie tot de probleem-stelling van het manuscript?	X		Maar zie main critisisn	
Structuur van het manuscript					
1	Is het manuscript helder van gedachtegang en opbouw?		X	Het rapport is vrij breed-sprakig en met 90 pagina's hoofdtekst wel erg lang.	Klopt, het is al ingekort en de andere reviewer vroeg om nog meer uitleg wat mondjesmaat is gedaan. Standaard statistiek uitleg is niet toegevoegd.
2	Bestaat het manuscript uit de volgende onderdelen (*naast de standaardonderdelen Inhoud, Woord vooraf, Referaat, Samen-vatting, Literatuur*): Inleiding, Methode, Resultaten, Discussie, Conclusie? Zo nee, zijn er dwingende redenen om hiervan af te wijken?		X	De Methode wordt uitge-legd in verschillende hoofd-stukken. Er is geen dwingende reden om af te wijken van het hiernaast genoemde sjabloon	
3	Zijn alle figuren en tabellen noodzakelijk?		X	Zie gedetailleerd commen-taar	
4	Dekt de titel de lading van het manuscript?		X	P2E opnemen in titel	Gedaan

Inleiding					
5	Is het probleem helder omschreven? Geeft de inleiding een goed overzicht van eerder onderzoek?	X		Overzicht over eerder onderzoek kan ik niet beoordelen	
6	Zijn de doelstelling en de maatschappelijke en/of wetenschappelijke relevantie helder omschreven?	X		Voor zover ik kan beoordelen	
7	Zijn de vraagstelling en deelvragen helder beschreven?		X		
8	Zijn de vooronderstellingen (hypothesen) voldoende expliciet?		X	Zie main criticism hieronder	
9	Is er een evenwichtige keuze uit de literatuur gemaakt bij de afbakening van het onderwerp ten opzichte van eerder onderzoek? En is daarbij voldoende gebruik gemaakt van recente (internationale) literatuur?			Kan ik niet beoordelen	
10	Is het gebruik van vaktermen juist en begrijpelijk?	X`			
11	Is het overzicht van het onderzoek duidelijk? Is er een leeswijzer opgenomen?	X		Er is geen leeswijzer opgenomen	Er is een samenvatting van de methode dat als zodanig kan worden beschouwd.
Methode					
12	Zijn de gebruikte aanpak en methoden helder uiteengezet?	X		Maar zie gedetailleerd commentaar hieronder.	
13	Zijn de aanpak en methoden adequaat om de gestelde vragen te beantwoorden, en is de keuze goed verantwoord?		X	Zie main critisism	
Resultaten					
14	Is er duidelijk onderscheid gemaakt tussen eigen onderzoeksgegevens en gegevens uit overige bronnen?	X			
15	Zijn de onderzoeksresultaten goed onderscheiden van de interpretatie en discussie?	X			
Discussie en Conclusies					
16	Worden de resultaten voldoende kritisch besproken?		X	Zie main critisism	
17	Vindt in de discussie een terugkoppeling plaats naar de hoofdvraag/deelvragen?	X			
18	Worden de bevindingen afgezet tegen resultaten van vergelijkbaar onderzoek?	X			
19	Geeft de discussie aanknopingspunten voor verder onderzoek? (welk deel van de hoofdvraag/ deelvragen is niet beantwoord?)	X			

20	Worden in de discussie de beperkingen en /of toepassings-mogelijkheden voldoende besproken?		X	Zie main critisism	
Samenvatting					
21	Geeft de samenvatting een goede dekking van het manuscript?		X	NL samenvatting is prima (maar main criticism opnemen), UK samenvatting schiet tekort	Samenvatting aangepast
22	Bevat de samenvatting de belangrijkste antwoorden op de hoofdvraag of hoofdvragen?	X		UK samenvatting aanpassen	Samenvatting aangepast

Advies
Het manuscript kan worden opgenomen in de reeks **Studies / Rapporten / Papers** van de WOT Natuur & Milieu
(vink item aan).

☐ met geringe aanpassingen	☑ met veel aanpassingen	☐ kan niet worden opgenomen

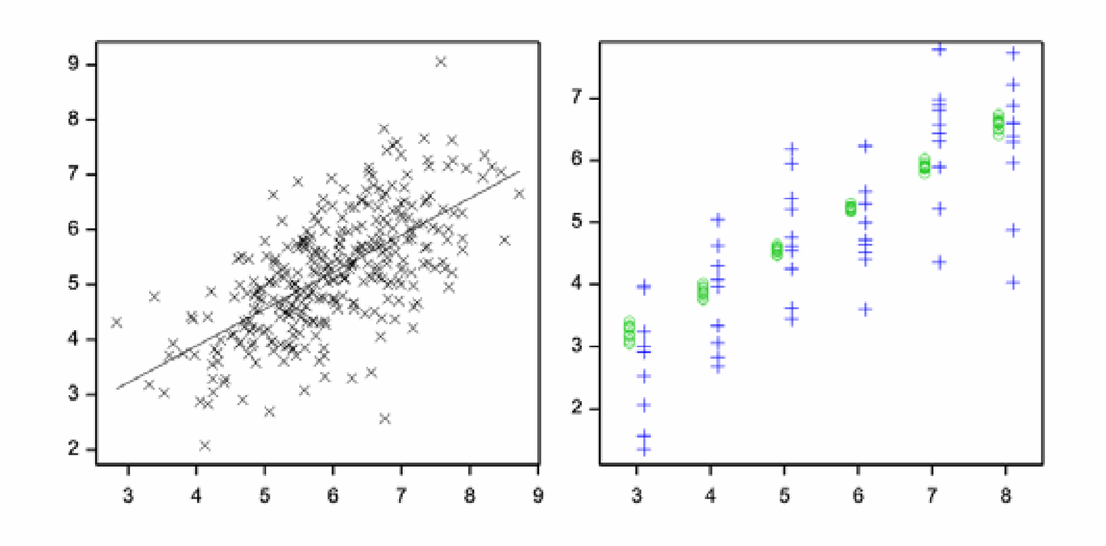
Note

The detailed comments in file “Concept WOt-rapport Comments PGO.doc“ are an integral part of this review.

WW, comments reaction etc are incorporated after the comments in italics and always starts with WW

Main Critisism
The model chain SMART-SUMO-P2E-MOVE predicts the number of species at a site. The model chain is an important part of the Natuurplanner. The Natuurplanner is used as follows *“Hiermee kan op basis van simulaties van grondwater, bodem en vegetatieprocessen uitspraken gedaan worden over mogelijke gevolgen van beleid, vegetatiebeheer, klimaatverandering of depositie op het voorkomen van plantensoorten en duurzaam voorkomen van diersoorten. De resultaten worden gebruikt voor beleidsevaluatie en adviezen aan het beleid en politiek, vooral op landelijk niveau”* .
The model chain was subjected to an uncertainty analysis. The basis of such an analysis is the variability in the model outcome, i.e. the number of predicted species, which is due to all possible sources of uncertainty. The uncertainty in the model outcome can be calculated in two fundamentally different ways which is best explained for a simple linear regression model $Y = \alpha + \beta X + e$ in which e is the model error term. We might be interested in the *mean* value of Y for a given X_0, or in a predicted value of an *individual new* observation. In both cases the predicted value equals $Y_0 = \alpha + \beta X_0$. The variance of these predictions are however different. When it come to the *mean* value only the variability in the parameter estimates for α and β is taken into account. For an *individual new* observation the variability of the model error term e is added to this. To put it another way, for the *mean* only parameter uncertainty is used while for the *individual* parameter uncertainty and model error is used.

These variances can be very different. Consider the situation of Figure 13 in the report for the Ellenberg indicator for acidity (eR) for heathland. The left panel in the graph below shows simulated data according to the fitted equation on page 44. The right panel shows 10 simulated values for pH=3, 4, 5, 6, 7 and 8. The green predictions only take parameter uncertainty into account, while the blue predictions also include model error. Note that the right graph also shows that the variability in the *individual* values is largely due to the model error. This implies that for the uncertainty in the *individual* values the size of the dataset is of very little importance since the model error contributes most to the uncertainty.



Now what is the implication of this for the uncertainty analysis of the model chain SMART-SUMO-P2E-MOVE? Note that the uncertainty analysis is done for 500 sites which were selected using stratified random sampling.

- SMART and SUMO result in a predicted value for pH and N. The model error of these predictions is not taken into account. So the uncertainty due to SMART and SUMO is mainly parameter uncertainty . Note that also uncertainty in the input of SMART (such as soil type and MSW) are taken into account
- P2E contains simple linear regression models which can be used to predict *mean* values and *individual* values. The uncertainty analysis carried out in this report uses prediction of *individual* values. Hence both the parameter uncertainty and the model error of P2E is taken into account.

This unevenness between SMART/SUMO on the one hand and P2E on the other hand implies that the uncertainty contribution of SMART/SUMO is underestimated. The extend of this underestimation depends on the relative size of the model errors. A more even handling of the models can be achieved by not taking the model error of P2E into account, or by adding model error to SMART and SUMO. When the model error of SMART and SUMO is unknown, an educated guess can be used. Figure 16 seems to indicate that there is hardly a relationship between N as calculated by SMART and the Ellenberg indicator N. This might suggest that the model error of SMART is rather large.
In conclusion: it seems that no thought-out choice has been made between the two fundamentally different ways in which uncertainty is handled. This issue must be stated explicitly in the summary, discussion and conclusions of this report.

WW We added a remark in the summaries and discussion and conclusions. Note that the model uncertainties of SMART2 and SUMO2 are unknown and that even an educated guess is difficult to make at the moment.

A second remark is that the uncertainty analysis is focused on individual sites. The total variance and the percentage which can be ascribed to the three parameter groups are first calculated for each site separately. The tables of Results (tables 2, 3 and 4) then give the mean of these values over the 500 sites. However one of the main uses of the Natuurplanner is targeting the Netherlands as a whole ("*vooral op landelijk niveau*"), but it will also be used for provinces and larger nature areas such as De Veluwe. In that case the relevant uncertainty is some sort of spatial aggregation of the uncertainties at individual sites. This is only useful when spatial correlations are taken into account. This has already been done for soil and MSW but not for the other sources of uncertainty. This issue should also be discussed in the summary and conclusions.

WW. At the beginning of the restart of this project it was decided to look at the individual sites, because result are generated on that level and later aggregated to a local or national level. Validation when carried out will also take place on the site level and in the case of MOVE somehow aggregated to a higher level. So to stay in line with this and to simplify an already complicated analyses we did stick to the site level. Nevertheless, the remark made is valid and a part of the discussion is now dedicated on this topic. The remark on spatial correlation is not correct, also for SMART2 and SUMO2 parameters the effect of spatial correlation is included, and the correlations for this are given in Appendix 3

A third remark concerns the way in which the relationship between Ellenberg N and Nitrogen is estimated and how the uncertainty of this regression line is quantified. Figure 16 shows the relationship between nitrogen availability of SMART2 and the Ellenberg N value for 145 sites. The authors consider these data as inadequate for estimating a regression line for Ellenberg N. The reason for this is not clear, but probably has to do with the rather flat declining (green) fitted line in Figure 16. Assuming that there is a relationship between the two, as is implicit in the Nature Planner, this seems to indicate that SMART2 is doing a bad job in predicting nitrogen.

The alternative they propose for estimating a linear regression is however based on the same data and is very questionable. Their alternative, if I understand the procedure correctly, first draws a line between a min point and a max point. These points are approximately (2.8, 1) and (10.5,6.5). This gives a line which runs from left bottom to right top in Figure 16. The vertical differences between this line and the points are subsequently taken as residuals and these residuals are used (how?) to obtain standard errors of the regression coefficients. It is unclear to me why these artificial residuals are informative about the standard errors. I suggest to remove the alternative procedure and use the expert judgment instead. Expert judgment values for the parameters a_N and b_N are then also needed

WW, That we judged the relation for Ellenberg N and nitrogen availability inadequate is indeed the flat line and is that obvious that no further addition to the text are made, also to stick to the main results. The goal of this exercise is not look at model problems, but to look at the uncertainties. It could be also stated that Ellenberg N is doing a bad job, or that N availability and Ellenberg N cannot be translated in each other.
We clearly state already that the applied method is awkward, but that it is used based on the fact that in general a high N availability is correlated with a high Ellenberg N. We explored alternative methods and we believe that it is useful to keep this in the report, also to show that we tried to solve the problem in a more sophisticated than expert judgment. We believe that the results for this speak for themselves. We agree that this is a very awkward step and should be improved , but it is not the topic of this research.

General remarks

1. In my opinion this report should have been checked and scrutinized more carefully before subjecting it to an external review. Important and less important things are frequently mixed and it is left to the reader to deduce the main issues from the text. *WW, every reader differs in what he wants to know and already less important parts are moved to the appendices, which make up about half of the report. The other reviewer did ask for even extra information, part of it text book statistics, so it is very difficult to*

please everybody. The text is not changed regarding this comment also for practical (financial) reasons though the authors applaud the reviewers comment.

2. The report would greatly benefit from an English editor.
   WW, agree, but is not scheduled
3. Numerous remarks are placed in the DOC file by using track changes and by adding comments.
   WW almost all are implemented.
4. I suggest to add P2E to the title of this report.
   WW; done
5. The report frequently states that there are 4 groups of parameters. However only three groups are considered uncertainty in MOVE was not accounted for. *WW, yes correct, but for the readability we did not change this, since there are indeed four groups of parameters.*

Summary and Samenvatting

6. The Dutch Samenvatting is more informative than the English Summary.
7. It must be stated clearly that the output of MOVE, i.e. the number of species, is calculated by summing the probabilities of occurrence of individual species. *WW, this is not the case and is actually forbidden by the makers of MOVE, see the MOVE report. The chance of occurrence was transformed to 0 – 1 using kappa statistics as described in the MOVE report. Subsequently these 1's were summed. The text is changed to make this clear.*

Section 1.

8. Some minor comments.
   WW implemented

Section 2.

Quite a few minor comments.
WW implemented

Section 3.

9. Simulation of soil type (in 3.2) and water table (in 3.3) is state of the art.
   WW ok, but?
10. The simulation sites are selected from a 250 x 250 grid and Bayesian Maximum Entropy (Brus *et al*., 2008) is used to obtain simulated soil types. The case study in Brus *et al*. uses the same data but states that "The conditional pdf is estimated for the nodes of a square grid with a grid-distance of 1 km", see pp 171. Is the methodology re-applied for the 250 x 250 grid or are the results for the 1 x 1 km grid used and if so how?
    WW the results are downscaled, as it says in that section
11. A basic description of the method of Bayesian Maximum Entropy is missing. At the bottom one might add for instance "BME results in predicted probabilities of occurrence of the seven soil types for each of the selected sites. The variation in these probabilities is characterized by the entropy given in equation [1]. The predicted probabilities are used to simulate soil types.". The equation (1) of Brus *et al*. should then be added to the report.
    WW not added. As stated it is a basic description and can be found in Brus et al. We obeyed here the wish of the reviewer to keep to the main topic of the report, which is already long as also stated by the reviewer.

12. Figure 5 shows a single simulation for the three different vegetation types. It would be more informative to show three simulations for a single vegetation type as in Figure 9 for groundwater.
WW, agree, but not changed, it is also informative to show this and we made the choice to show different examples to give a maximum of info in a minimum of space.
13. There are qualitative remarks about entropy values being very high, e.g. "higher than 0.8". However most readers will not have a clue as to whether such values are large or small. A simple example with two probabilities (i.e. two soil types) could be added. For instance with probabilities (0.05, 0.95) the entropy is 0.20, for (0.10, 0.90) it is 0.33 and for (0.50, 0.50) the entropy is 0.69. This example necessitates the addition of the formula for entropy as suggested in point 3. Above
WW, example added.
14. The average entropy scale in figures 7 and 8 (right) is different from figure 6.
WW yes, done to give a meaningful legend.
15. The uncertainty in the water table (see 3.3) is not interpreted. Figures could be added with e.g. the coefficient of variation for the simulated values.
WW, not added

Section 4

16. I understand that uncertainty of the soil parameters is largely based on a Dutch forest inventory. Can this also be used for grassland and heath?
WW, yes.
17. The simulated soil parameters are rounded (I presume) to meet the minimum and maximum in Appendix 1. This poses some problems for the bsat_0 parameter. For example for CC the standard deviation 0.021 in Appendix 1 is much larger than the mean value -0.004. This implies, disregarding spatial modeling, that almost half of the draws from this uncertainty distribution are larger than zero and these are all rounded to zero. This seems to imply that for this parameter the wrong uncertainty distribution is used.
WW, when further research will be conducted this will be taken into account.
18. I can not judge whether the used geostatistical model is appropriate. However the model is well described and the hierarchical approach which incorporates the uncertainty in soil type at this stage is highly applicable.
WW -

Section 5

19. There is too little information on how the simulated values are drawn. No information, neither in Wamelink (2008), is provided on the choice of the rank correlations in Appendix 3
    a. I understand that the bio parameters are drawn from a multivariate distribution with means and variance in Appendix 2 and correlation matrix on page 114.
    b. The way the verdeling parameters are drawn is less obvious since it is not clear from the text, neither from Wamelink (2008), how the correlation parameters on page 115 are taken into account (I suspect that Genstat procedure UNITCUBE is used followed by EDCONTINUOUS, so that in effect rank correlations are used). I understand from the last line of page 115 that first the "s" parameter is drawn from a beta distribution, then the "b" parameter and that r is calculated as r = 1 – s – b. It should be noted that a different order, e.g. first "r", then "s" and then b = 1 – r – s, gives simulated values that have different distributions even when the rank correlation is zero.

c. The verlies parameters are all drawn from beta distributions, except for some which are set to 1, but I do not understand how to fill in the empty cell in the rank(?) correlation matrix on page 116. Why is there a correlation between verlieskw and verliesdw which are different functional types, and no correlation between verlieskw and verliesks which are parameters for the same functional type.
d. Unlike the verlies parameters, the correlations for the Nmin and Nmax parameters are non-zero for the same functional type and zero (or empty) for different functional types. The Nmin distributions are chosen such that some 20% of the values are larger than maximal allowed value.
e. The Gax parameters are uncorrelated.
f. The Aantal and Eten parameters are fully rank correlated. Aantal is the number of grazers, but the distribution is beta which results in a number between 0 and 1. Is this simulated number multiplied by something to give a number of grazers?
g. The last line of the paragraph states that “The used procedure was similar to the procedure used for the simulation of the soil parameters.” But the soil parameters are simulated by geostatistical methods, while the SUMO2 inputs are drawn using (simple) rank-correlated simulation, or am I mistaken.
WW The appendix 2 is changed and for each parameter is given if it is based on expert judgement or not. Most of them are based on expert judgement and therefore per definition difficult to explain why which was chosen. The File behind this is still available, but that large that it was decided not to include in the report, though it makes the values indeed difficult to interpret. In appendix 3 the spatial correlations are given, which seems not be understood, that is also why the internal correlations for a parameter with itself is not 1, which would imply that all values for the whole of The Netherlands for this parameter would be fully correlated besides the distance. Explanation is added. Most of the confusions given here above seem to be based on this.

Section 6

20. The last paragraph of each section shows that the simulated values match the parameters of the 3-variate normal distribution. This is nothing more than a check that the algorithm used to generate the random numbers is correct; this section can thus be removed.
WW we do not agree, and did not remove this. It provides important info.
21. It would be nice to add the fitted regression line to Figures 12, 13, 14 15 and 16 along with error bands for predicting individual observations.
WW, they are published before and it is not important for this analysis, so not added.
22. A combined single relationship for Ellenberg F is fitted for the three vegetation types because of “lack of data”. However Figure 15 seems to reveal that there is enough data to fit separate models to the three types. It also appears that the relationship for heather and forest is flatter than the relationship for grassland.
WW, this is a matter of judgment and we decided that there are not enough data available to split it up, also based on the distribution of the data over the ax.

Section 7

23. This is a rather technical paragraph. Maybe it is sufficient to define the TVM and the relative TVM (as in the sentence just above 7.3), say what type of design is used to estimate TVM for the separate groups and give a reference.
WW, this paragraph was already shortened; we believe that it now gives the minimum amount of info necessary to understand the analysis. It must be kept in mind that these kind of analyses are still rather unique and that even for day to day users it is difficult to understand the procedure.

24. I do not understand what is represented by S4 in Figure 17. Since there are only three parameter groups (MOVE is excluded) I would expect that only S0, S1, S2 and S3 are relevant. Does this imply that 12000 simulations are performed instead of 15000? Or does it imply that there are in fact 6000 simulations available for estimating Var(y_0)?
Fig. 17 is an example how the method works for the originally meant 4 parameter groups, of which later MOVE was skipped. S4 was relevant, but became irrelevant, which is now stated at several places. There were 150000 runs carried out, but only 12000 were used for the analysis since MOVE was left out.

Section 8

25. This section contains many qualitative words such as many, substantial, quite high, most, minor, somewhat larger, almost equally, range is reasonable, variation is moderate, etc. These qualifications can be made more specific by using numbers e.g. from Tables 2, 3 or 4.
WW, but it makes it also less readable and numbers can not give the qualifications we want to make. This is largely a matter of stile and we chose not to repeat the content of the values which can be found in the tables.
26. I suggest to move the spatial Figures to an Appendix (or an Electronic Appendix so that the Figures can be viewed at a higher resolution) and discuss the tables and the accompanying histograms (instead of the figures). The spatial configuration of the uncertainty seems of less importance than the summary statistics. Each subsection should start with the table and histogram which can be discussed briefly. *WW, we kept the tables and figures in the main text.*
27. Each percentage TVM figure has its own limits for the colours. Common limits, e.g. 10, 20 ... 90 using extra colours, would make it easier to interpret the figures.
WW, it would it also make less easy to interpret and we especially did not take the same limits because the figures would become partly without meaning.
28. It should be said somewhere that the value in S(y) in Table 2 is not the square root of the Var(y), because there is a difference between first taking the mean and then averaging, and first averaging and then taking the mean. The same holds for CV.
WW, I do not understand this.
29. The columns se1 – se3 in the Tables have generally small numbers and are not discussed in the text. I suggest to remove these columns or to move them to an Appendix.
WW, not done.
30. The correlation matrices, e.g. given in Figure 26, are calculated as follows. For each site and for each output variable the %TVM attributable to SMART can be calculated. This gives a matrix with seven columns (the variables) and 500 rows (the sites). The correlations between these columns are given in the top matrix in Figure 26. I wonder whether this is sensible because for e.g. pH only the uncertainty in SMART and SUMO is relevant, while for F also the uncertainty in P2E matters. So what is the interpretation of these correlations. Moreover, and again, since MOVE was excluded from the uncertainty analysis it is not clear what the last correlation matrix in Fig 26 represents. *WW The correlations are still useful even for MOVE4, because it shows what the influence of the three parameter groups is on the end result. Although MOVE4 uncertainty itself was not included. The latter is now frequently added to the report.*
31. Figure 27 seems unnecessary as the graphs are also given in the Appendix. Moreover for heathland and Forest no separate figure is given for large correlations. *WW, we agree, but we eventually decided to keep the figure in as an example of the matrices and how they can be interpreted.*

32. Comments in the DOC file for section 8.1 could be used to improve the text in 8.2 and 8.3.
WW, done.

33. The results for Heathland are discussed twice, starting on page 71 and starting on page 80. The same holds for soil pH in Forest, see page 84 and page 95. *WW, the first part concerns the average results, the second part is site specific.*

Section 9

34. It is suggested that the uncertainty will be reduced when Ellenberg values in MOVE4 are replaced with measured values.
WW, Yes, and there are at least good indications to support that (Wamelink, Goedhart, Van Dobben & Berendse JVS 2005).

35. MOVE4 was not included in the uncertainty analysis. MOVE4 not only has parameter uncertainty associated with it, but also model selection uncertainty. Both these elements are important and should possibly taken into account in a future study. *WW, agree.*

36. It is stated that "Whether or not a species is assumed to be actually present depends on the predicted probability of occurrence and a species specific threshold value. This automatically generated threshold value may be too high". But the occurrence probabilities are summed to get the number of species and not the rounded 0/1 data. So the threshold is not used in this study.
WW, no sorry, this is a mistake in our text and now removed, the kappa statistics are used to decide whether or not a species may occur.

37. The last line in this section stated that the relationship for Ellenberg N is rather unscientific. Why did not the authors use expert judgment for this relationship as is done for many other parameters in the model chain.
WW, but we did, but we stick to the fact that it is rather unscientific, even for expert judgment.

Section 10

38. The following could be added to the conclusions: the standard errors of the uncertainty contributions show that enough simulations have been used. They also show that in a future uncertainty analysis of this model chain possibly fewer simulations can be employed.
WW, agreed and added, thanks!

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WOt

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