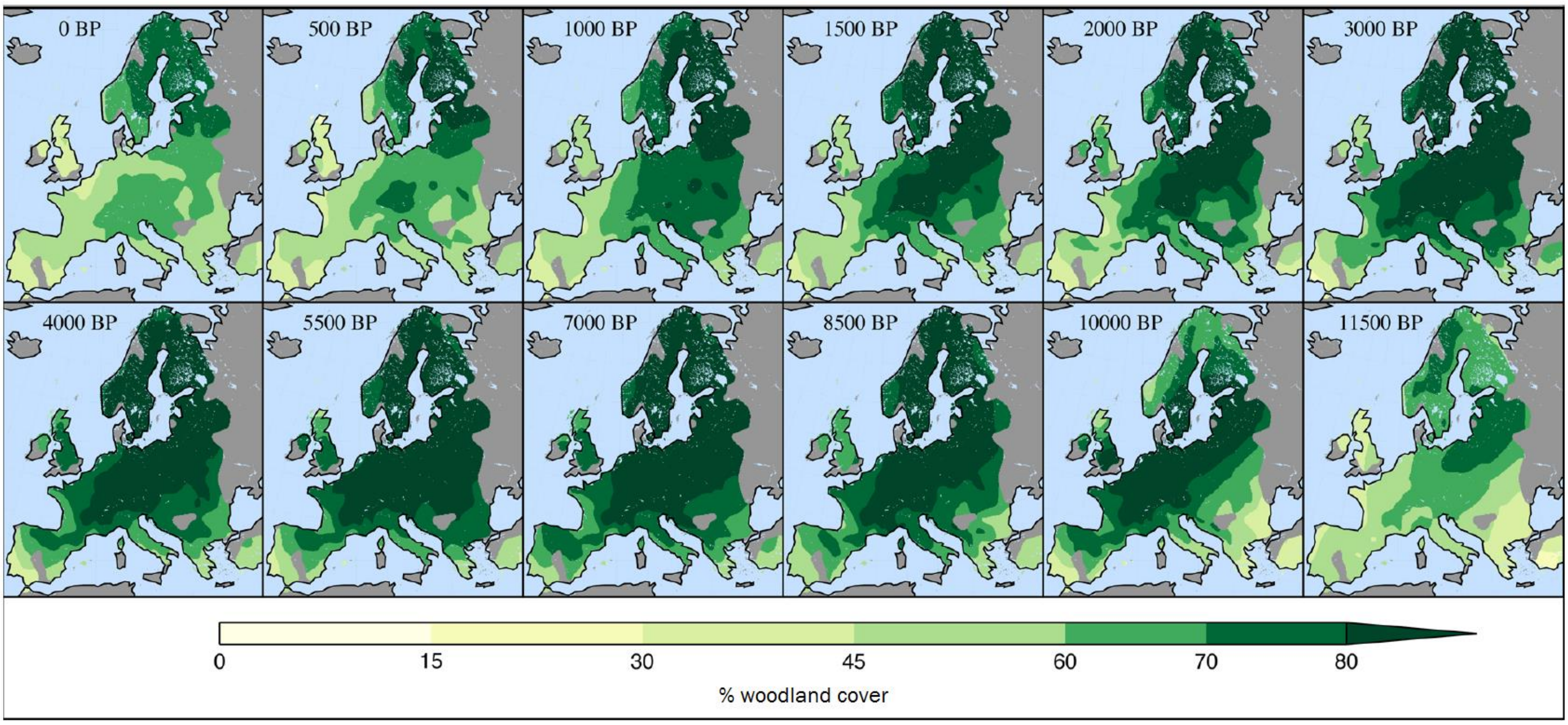
# How can reconstructions of Holocene land-use changes be improved?

## A review of the value of pollen-based vegetation reconstruction models



Woodland cover in Europe and its change over time. Using a pollen-based reconstruction method, the Plant Functional Trait approach (Davis *et al*. 2015).

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## Abstract

Humans have altered their surrounding landscape since before the start of agriculture. The notion that anthropogenic land use changes were harmful did not arise until the latter half of the 17th century (Evelyn 1662). Although the influence of humans on the landscape was small at first, this influence has expanded greatly since the urbanisation revolution of the high middle ages (van Bavel 2010) Today, 37% of ice-free land is used for agricultural purposes, and another 30% is directly under the influence of humans. This has great impacts on global greenhouse gas emissions. To understand the current and future effect of land use on GHG emissions, it is vital to understand the role of past land use in this process (Kaplan *et al*. 2017). The Historical Database of the Global Environment, HYDE, has been developed to investigate past anthropogenic land cover changes, in a way that incorporates past population estimates and assumptions of per capita land use. Because data for the past is scarce, this method becomes more unreliable the further back in time it goes. The use of pollen-based reconstructions (PBRs) can improve the accuracy of HYDE. PBRs are methods that attempt to quantitatively reconstruct the past landscape, mostly using pollen assemblages from lake sediments.

The main question this paper will answer is: **which PBRs can improve global land use models (i.e. HYDE), and in what way do they make an improvement to HYDE?** A framework with a set of standard questions about each PBR method has been developed, intended to objectively review different PBR methods. Some methodological issues regarding PBR methods will also be discussed. First, each PBR method will be introduced, and its methodology will be explained. Second, the methodology of different PBRs will be reviewed, and last, the applicability of the method is evaluated, as well as the usefulness of the method to HYDE. Six methods will be discussed: the LRA (Sugita 2007a, 2007b), the MSA (Bunting and Middleton 2009), the EDA (Theuerkauff and Couwenberg 2017), the PFT approach (Davis *et al*. 2015), the pseudobiomisation approach (Fyfe *et al*. 2010), and Bayesian models (Paciorek and McLachlan 2009 and Dawson *et al*. 2016).

There are some methodological issues associated with the use of PBR methods, and PBRs must not be seen as the final solution for answering questions about the past landscape. They must be continually re-evaluated, but even in the state they are now, these methods still provide HYDE with necessary improvements to make predictions about past land use more accurate. Most recommended is the use of REVEALS for large scale reconstructions of land cover, in combination with a PFT (Plant Functional Trait, Davis *et al.* 2015) or pseudobiomisation approach (Fyfe *et al*. 2010). For disputed areas, the MSA (Bunting and Middleton 2009) poses a good alternative for resolving these uncertainties, especially if it can use REVEALS reconstructions as its background vegetation. Other methods such as the EDA (Theuerkauff and Couwenberg 2017), the Bayesian models are less useful as of now, the EDA because it has not yet been evaluated in the field, and the Bayesian models because they rely on self-learning algorithms that need data about pristine woodlands, which is simply not available for most of the world.

**Key words**:
HYDE – Global land use models – Pollen-based reconstructions – LRA – MSA – EDA – PFT – Pseudobiomisation – Bayesian modelling – Review

## Layman summary

De mens heeft sinds lange tijd het landschap om zich heen vernaderd. Dit gebeurde al voor de start van landbouwactiviteiten. Pas in de tweede helft van de 17e eeuw begon men door te krijgen dat er ook negatieve effecten hingen aan het omzetten van de natuur in voor de mens bruikbaar land (Evelyn 1662). De invloed van de mens was gering voor de middeleeuwen, maar nam enorm toe met de opkomst van steden rond de 12e eeuw (van Bavel 2010). Nu is 37% van het land in gebruik voor landbouw of veeteelt, en is nog eens 30% onder directe inlvoed van de mens. Dit heeft een grote uitstoot van broeikasgassen tot gevolg, en om grip te krijgen op huidige en toekomstige uitstoot van broeikasgassen is het belangrijk om een idee te hebben wat er in het verleden al uitgestoten is. Om dit laatste te onderzoeken zijn er globale landgebruik modellen bedacht die inzicht geven in landgebruik en vernadering in landgebruik in het verleden. HYDE is een van deze modellen en gebruikt schattingingen van vroegere populaties en aannames over landgebruik per individu om een beeld te schetsen van het totale landgebruik in het verleden. Deze data wordt schaarser naarmate je verder terug gaat in de tijd, en dus is het nodig om verbeteringen aan te brengen in het HYDE model. Landschapsreconstructies op basis van pollen (PBRs) kunnen dit bereiken omdat ze zijn gebaseerd op emprische data.

De hoofdvraag luidt: welke PBR kunnen HYDE verbeteren en op wat voor manier kunnen ze HYDE verbeteren? Deze vraag wordt beantwoord aan de hand van een reeks objectieve deelvragen. Ook wordt stilgestaan bij de problemen die nog kleven aan het gebruik van PBRs. Dan wordt eerst elke PBR methode kort geïntroduceerd, vervolgens wordt de methodologie kritisch bekeken en als laatste wordt de toepasbaarheid van de methode in het algemeen, en voor HYDE in het bijzonder bekeken. In totaal komen zes PBRs aan bod: de LRA (Sugita 2007a, 2007b), de MSA (Bunting and Middleton 2009), the EDA (Theuerkauff and Couwenberg 2017), de PFT methode (Davis *et al*. 2015), de pseudobiomisatie methode (Fyfe *et al*. 2010), en de Bayesiaanse modellen (Paciorek and McLachlan 2009 en Dawson *et al*. 2016).

Er kleven tot op heden nog wel wat nadelen aan het gebruik van PBRs, en zij mogen dus niet gezien worden als 'de' oplossing voor het beantwoorden van vragen over de vroegere landschappen. De methoden moeten blijvend onderzocht en verbeterd worden, maar zelfs in hun huidige staat dragen ze bij aan een verbetering van HYDE. De meest waarschijnlijke methode om HYDE op grote schaal te verbeteren is een combinatie van het gebruik van REVEALS om pollen data om te zetten in landbedekking data en dit vervolgens met de PFT/pseudobiomisatie methode om te zetten in landgebruik data. In gebieden waar onzekerheid bestaat over de juistheid van de REVEALS reconstructie kan de MSA worden ingezet om dit op te lossen, helemaal als er gebruik wordt gemaakt van de REVEALS reconstructie als achtergrondvegetatie. De andere methodes, zoals de EDA en de Bayesiaanse modellen zijn ongeschikt in hun huidige format. The EDA is nog niet toegepast in realistische scenarios, en de Bayesiaanse modellen hebben input nodig die niet beschikbaar is (data over onaangetaste bossen). Om een beter inzicht te krijgen in landgebruik in het verleden moeten de PBR methoden blijvend verbeterd worden.

## Contents

## 1. Introduction

*"Whereas [others] think the earth made man, man in fact made the earth"*

---George Perkins Marsh, 1864

The notion that alterations to, and exploitation of, the landscape by humans had a profound effect on biodiversity and could lead to the destruction of the earth is not new. In 1864, Marsh published *Man and Nature*, one of the first books addressing the effect of human interference on the environment (Marsh 1864). More than 200 years before that, in 1662, John Evelyn warned against the overexploitation of forests in England (Evelyn 1662). Throughout history, humans have transformed the landscape in which they live, and now, humans have become the most influential actors on the landscape. This period, known as the Anthropocene, starts somewhere between the start of the Neolithic revolution and the Industrial Revolution at the end of the 18th century, although to date, much debate exists on the start date for the Anthropocene (Steffen *et al*. 2007, 2011, Lewis and Maslin 2015). Others argue for the inclusion of a pre-Anthropocene era, a Palaeoanthropocene, to mark a period in which humans influence their surroundings, but before the burning of fossil fuels caused a large increase in anthropogenic affects (Foley *et al*. 2013). Humans are the largest actors in the process of land alterations, creating their own niches for their survival (Ellis 2015). In prehistory, hunter-gatherer societies have caused megafaunal extinctions in North America, although in places, the extinctions coincide with climate change (Boulanger and Lyman 2014; Gill *et al.* 2009; Grayson and Meltzer 2003, 2015). On other continents, Australia (Miller *et al*. 2005; Saltre *et al*. 2016), Eurasia (MacPhee *et al*. 2002; Stuart *et al*. 2002) the same process took place, although evidence for Africa and South America is lacking (Barnowski *et al*. 2004; Koch and Barnowski 2006). Whereas hunter-gatherers may have altered their surroundings locally and on a small scale, the onset of farming is the start of large-scale alterations to the landscape. The Neolithic Revolution (around 12000 years ago in the Fertile Crescent), caused farmers to alter their natural surroundings drastically (Ellis *et al*. 2013; Kaplan *et al*., 2009). This is a clear example of far-reaching niche construction by humans, and in the present, the associated land use changes account for 24% of the global $CO_2$ emissions from economic activities (agriculture is just second, after $CO_2$ emissions from energy production, 25%) (IPCC 2014, p. 47).

The most far-reaching transformations of the natural landscape happened in more recent times, for Europe for example since the widespread emergence of cities in the 10-12th century (van Bavel 2010). European populations had risen since the 9th century, both as a result of the decentralisation of power, as well as agricultural innovations (Hoffmann 2014, 116; van Bavel 2010). The growing urban population meant an increased demand for agricultural products. This demand could be met by agricultural innovation and land use intensification. Traditionally, European farmers used a two-course alternating crop system (one year the land is used for crop growing, the other year it lies fallow) but a three-course rotation system was developed in northern Europe, leading to a 17% increase in yields (Hoffman 2014, p. 125; van Bavel 2010). Around the eleventh century, production shifted from dairy and meat farming to the cultivation of cereals, to meet the demands of the city population. As a result of epidemics or unsuccessful harvests due to bad weather, the natural vegetation could recover for a short time at the expense of farmland or grazing land. The Black Death (~1346-1353 CE), the plague that caused a population decline of 30-60% in Europe, led to significant agricultural regression for 50 years after the plague in Ireland (Yeloff and van Geel 2007). Furthermore, the agricultural regression lasted 90 years in the southern Netherlands, 100 years in northwest England, and even 125 years in central France (van Hoof *et al*. 2006, Mackay and Tallis 1994, Stebich *et al*. 2005).

The massive conversion of natural systems to cropland, grazing land for livestock and built-up areas has led to the domination of humans in the ecosystem. Today, 37% of the ice-free land is used for agricultural purposes, and another 30% of the land is influenced by human actions (Klein Goldewijk *et al*. 2017). The human-driven transformations have also led to geomorphological changes, changes in sediment budgets, and has impacted both freshwater, marine and terrestrial environments (Kaplan *et al*., 2017). Lastly, anthropogenic land cover changes (ALCCs) have contributed to an increase of $CO_2$ in the atmosphere, thereby contributing to climate change (Klein Goldewijk *et al*. 2017). To monitor current and future land use, global land use models have been developed. However, in order to model past global ALCCs it is necessary to understand the role the past has played in the creation of the current (changing) climate (Kaplan *et al*. 2017). Three global land use model approaches have tried uncovering past ALCCs: the HYDE model (Historical Database of the Global Environment; Klein Goldewijk *et al.* 2010, Klein Goldewijk *et al*. 2011), the KK10 model (Kaplan and Krumhardt model; Kaplan *et al*. 2010), and the ML08 model (Millenium Landcover Reconstruction; Pongratz *et al*. 2008). In their current state, the three models derive their input mostly from historical data (demographics) and on assumptions of the physical properties of the land (i.e. suitability for agriculture and distance to water, climate, and slope). This way of reconstructing past landscape changes uses estimations and assumptions and is therefore prone to (calculation) errors. Improving the model approaches is necessary for a better understanding of past land cover changes. A possible proxy for landcover changes in the past is the use of pollen in vegetation reconstructions, one of the key pillars in the study of palynology (Birks and Berglund 2018). Pollen is abundantly present in the sediment archives, and relative abundance of certain plant species through time gives information about land cover and changes in plant abundance in the past.

Quantitative reconstructions of landscapes have always been a main goal in palynology (Sugita 2007a; Bunting and Middleton 2009; Mrotzek *et al*. 2017). Since the 70s, and especially after the computer revolution of the early 80s, numerous multivariate numerical models have been developed to aid in the correct reconstruction of the landscape. Pollen production/dispersal models have gained great attention, because one of the main problems in the palynological record are those of the difference in pollen production and pollen dispersal between plant species, but even between individuals of the same species. As a result, there are many methods for translating a pollen record into a reconstruction of past landcover available today (Birks and Berglund 2018). Pollen-based reconstructions of past landcover will from hereon be referred to as PBRs (**P**ollen-**b**ased **r**econstructions). This modelling approach is mostly used in palaeo-ecological case studies, and only since recently has it been implemented in global land use models. Kaplan *et al*. (2017) have implemented a PBR-method (i.e. REVEALS, Sugita 2007a) to improve the KK10 model. However, other global land use models that use demographic estimates and per capita land use (e.g. HYDE, ML08) could also benefit from using palaeoecological data and the subsequent implementation of this data in PBRs. More details on the usefulness of PBR for the improvement of the HYDE database can be found in section 2.1.

In this review, I will analyse the strengths and weaknesses of different PBRs, used in the field of palaeoecology. Most importantly, I will analyse the usefulness of PBRs for the HYDE database. Therefore, the main question I hope to answer in this review is: **which PBRs can improve global land use models (i.e. HYDE), and in what way do they make an improvement to HYDE?** Before answering this question, I will shortly discuss what the current use of HYDE entails, and which improvements can be made to HYDE. Then, I will review several PBR methods and their usefulness in a global land use model. For this purpose, I will use a systematic framework of questions. This framework is used to discuss the practicality of the method, its assumptions, its validity, the applicability of the method to global land use models and the applicability of the models in other research fields that could benefit from reconstructions of the past landscape (see table 1). This framework is also helpful in the search for literature, as it will clearly define what questions need to be answered for each method. In doing so, I hope to be able to make a well-founded recommendation for the improvement of HYDE. This framework of questions should lead to an equal comparison of all methods, where the same criteria are used for each method, and thus to maximised objectivity.

**Table 1.** Schematic approach to reviewing PBRs and their usefulness to the HYDE database.

| **Systematic framework for reviewing the methodology of PBRs** |
|---|
| **Background** |
| Who developed the method? |
| What does the method entail? |
| What is the theoretical background of the method? |
| |
| **Analysis of the method** |
| Which assumptions does the model make? |
| Which assumptions/variables are left out in the model, and how should it not be used? |
| What is the spatial scale of the results coming from the model? |
| What is the sensitivity of the model to small changes in input-data? |
| How does the model produce its output? |
| |
| **Applicability of the model** |
| Can the model be used in practice by non-palaeoecologists (e.g. archaeologists, conservation biologists), and if so, in what way can it be used? |
| To what degree does the method incorporate the influence of humans on their natural surroundings? |
| What output does the model produce? (maps, % coverage per cell). |

In this paper, I will review the methodology of the following PBRs:

- The Landscape Reconstruction Algorithm: REVEALS and LOVE (Sugita 2007a; 2007b)
- The Multiple Scenario Approach (Bunting and Middleton 2009)
- The Extended Downscaling Approach (Theuerkauff and Couwenberg 2017)
- The Plant Functional Types Approach (Davis *et al*. 2015)
- The Pseudobiomization Method (Fyfe *et al*. 2010)
- The Paciorek and McLachlan Bayesian model (Paciorek and McLachlan 2009)
- Spatio-Temporal Empirical Prediction from Pollen in Sediments: STEPPS (Dawson *et al*. 2016)

## 2. Global land use models – HYDE version 3.2

Vegetation cover and land use are an ingrained characteristic of the climate system (Gaillard *et al*., 2010). There are many natural drivers of changes in land cover, such as: radiative forcing, weather changes, or abrupt climate change (Klein Goldewijk *et al*. 2017). Today however, humans are the most important driving factor behind land cover changes, mainly through the development of agricultural societies and the subsequent conversion of natural land to cropland or grazing land (Ellis 2015, Klein Goldewijk *et al*. 2017). This has led to an increased emission of GHGs which contribute to the increase in $CO_2$ concentration in the atmosphere. Land use changes have led to changes in the biogeochemical and biophysical cycles, but the role of anthropogenic GHGs in the global carbon budget is poorly understood for the past (Gaillard *et al*. 2010, Klein Goldewijk *et al*. 2017). These feedback mechanisms are an uncertainty in the modelling of future climate change. A global land use model can address this uncertainty by quantifying changes in landcover in the past (Gaillard *et al*. 2010).

The most recent version of HYDE (version 3.2) attempts to quantify past land use, covering the period 10000 BCE to 2015 CE (Klein Goldewijk *et al*. 2017). The HYDE model combines historical population estimates and population allocation algorithms with time-depended weighting maps for land use. The United Nations World Populations Prospects were used for population data after 1950 CE for all regions in the world. For the period before this, population data was gathered from country-specific databases of historical populations, as well as data from literature. When this data was unavailable, the population for a certain region was estimated. A time series of population development was made for every region in the world (Klein Goldewijk *et al*. 2010). Gathering reliable population evidence is crucial because humans have emerged as an important driving force of change (IPCC 2007, in: Klein Goldewijk *et al*. 2010). The spatial coverage of the world population was obtained from the LandScan database, which shows the total population at a 1km resolution (LandScan 2014). LandScan, however, can only be used for allocation of population in the present. Therefore, increasingly more weight is given to weighting maps that allocate the population based on soil suitability, distance to water, and historical and archaeological case studies (Klein Goldewijk *et al*., 2017).

HYDE divides land use in the following categories: cropland, rice-producing area, irrigated area, and grazing land. Data about land use for the period after 1960 was obtained from the FAO, which produced land cover maps at a 5' grid resolution. Remote sensing was used to produce maps about land use data (FAO, 2015). Pre-1961 data needs to be estimated, with the assumption that the per capita land use is not constant in time, but either increase or decrease with time (Klein Goldewijk *et al*. 2010; Klein Goldewijk *et al*. 2017). For each country, the per capita land use was estimated for the entire period in which the model runs by modelling backwards using a unique curve for each region. Multiplying the total population with the per capita land use at a certain time, would result in the total amount of land used at that time. The allocation of land use follows a standard procedure. First, cropland is allocated, and it is assumed that the most fertile soil will be used first, although the model does not take into account the technical limitations in prehistory that withheld early farmers to cultivate heavy compacted, but fertile, clay soils. After cropland, rice fields are allocated, then the irrigated areas, and lastly, pasture land. For pasture land, there is a distinction between intensely managed lands (pastures, created and managed by humans) and the more extensively used lands (rangelands, existing in a more natural setting, without human management) (Klein Goldewijk *et al*. 2017).

### 2.1 Uncertainties of HYDE and usefulness of PBRs

There are still some problems associated with the use of the model. Especially the hindcasting methods are problematic. The further back in time the model for land use goes, the more uncertain the estimate becomes. Since population serves as the basis for estimating per capita land use and the total amount of land used in each country, it is possible these results are unreliable. Gaillard *et al*. (2010) compare the results of the HYDE model and other global land use models with historical records of certain land use developments. They state that HYDE underestimates the impact of early humans, because HYDE shows a smaller deforested area than Kaplan *et al.* (2009). The difference is due to differing methodologies between HYDE and KK10: KK10 bases its reconstruction of ALCC on an inverse relationship between human population counts and forest cover (Kaplan *et al.* 2009, 2010). The relationship between these two is expressed by a normalised function that takes agricultural intensification and technological advancement into account. Another discrepancy is the fact that HYDE's estimate of deforestation in Europe around 1800 AD does not equal the estimate based on historical accounts, whereas the estimate from the Kaplan *et al.* (2009) model does (Gaillard *et al.*, 2010). HYDE, furthermore, underestimates the total cropland area: the GLUES (Global Land Use and technological Evolution Simulator) model (Lemmen 2009) shows areas where agriculture would have taken place, but which do not show up in the HYDE simulation. The GLUES model attempts to estimate the required land for growing crops, where subsistence style is being kept into account too (Lemmen 2009). Population data from the GLUES model did compare well to the estimates from the Kaplan *et al.* (2009) model, but not to the HYDE model (Gaillard *et al.* 2010). However, since it is difficult to quantify which method approaches reality best, it is not possible to discuss these methods in terms of 'best', or 'most accurate', as is done in Gaillard *et al.* 2010.

Klein Goldewijk and Verburg (2013) have addressed some of the uncertainties inherent in the HYDE data set. The use of historical data is problematic. Population data for the pre-1950 are is scarce, and do not cover the entire world, nor the entire period, and this is even more so the case with historical land use data (Klein Goldewijk *et al.* 2017). Furthermore, the relation between population and land use might not be as straight forward as is assumed by Klein Goldewijk *et al.* (2017), as factors like urbanisation and technological advancements might also affect the land use (Klein Goldewijk and Verburg 2013). Further uncertainty comes from the model parameters and assumptions used: such as what defines a city area, and how the per capita agricultural land use has changed over time (Klein Goldewijk and Verburg 2013). The structure of the HYDE model can also be the cause of uncertainty: land use allocation is based on different local factors (e.g. population, soil suitability, slope, distance to water, and climate), but it is uncertain which of these factors is the most important driver behind where people grow their crops. Therefore, the model assumes an equal weight for all these factors (Klein Goldewijk and Verburg 2013). The uncertainties are not spread evenly in time and location but do increase as the model goes backwards in time. Uncertainties in input data are stacked upon other uncertainties, which may lead to large calculation errors.

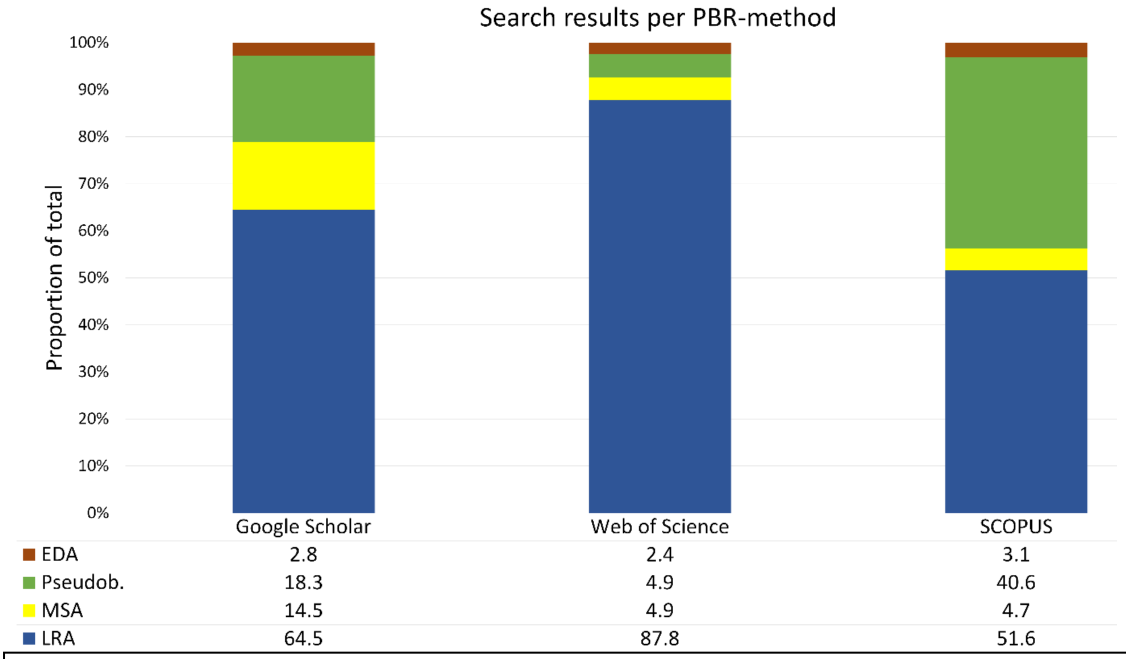
Since the base line version of HYDE is used in many studies on the global carbon cycle, it is important to address and reduce these uncertainties for better use in future assessments of the global carbon cycle (Klein Goldewijk and Verburg 2013). Besides model improvements, interdisciplinary studies might help in addressing some of the uncertainties. Data from historical ecology might help address the uncertainties of per capita land use, and palaeoecological data (pollen records, tree-ring analysis), together with archaeological data, might provide an insight in the spatial differences in land use for crops, and to show evidence of historical land use. Both Klein Goldewijk and Verburg (2013) and Gaillard *et al.* 2010 propose the use of landcover models using pollen data as a probable method to lower some of the uncertainties associated with the HYDE model.

Pollen data is a useful proxy for reconstructing the landscape: despite of many taphonomic processes in the soil that can degrade the pollen record, and despite the differences in pollen production and dispersal between different plant species, pollen richness can provide a baseline for floristic diversity (Odgaard 1999). The differences in production and dispersal of pollen can account for inaccuracies when using just the pollen percentages as a representation of the past vegetation, but in recent times, methods have been developed that correct for these factors (Gaillard *et al.* 2010, Marquer *et al.* 2014). Later studies showed that pollen richness and evenness reflect the vegetation richness and evenness, if the study site is appropriately chosen, and the local vegetation component is disregarded (Giesecke *et* al. 2014, Matthias *et al.* 2015). Giesecke *et al.* (2014) investigated the palynological richness and evenness of three different landscapes using a a taxa accumulation curve. This curve takes the differences in count size between samples into account, which makes it possible to utilise the complete taxonomic differentiation per sample (Giesecke *et al.* 2014). Catchment of pollen with low is still poor using this method (Birks *et al.* 2016b), which means that taxa such as *Tilia* and *Fraxinus* are still underrepresented in this research. Despite this, Giesecke *et al.* (2014) have shown that palynological richness reflects past floristic richness. So, if the appropriate method is used, pollen diversity is a good proxy for the structure of past vegetation and the diversity of the landscape (Matthias *et* al. 2015). Differences in pollen richness and floristic richness can be explained by the landscape structure (pollen diversity in open landscapes are good representations of the vegetation diversity, whereas changing pollen production and pollen dispersal do not reflect pollen and floristic richness (Meltsov *et al.* 2011, Meltsov *et al.* 2013). Despite challenges, e.g. difficulties with pollen taxonomy, and pollen-plant richness relationships (which is not a 1:1 translation), pollen record richness does reflect floristic differences in most studies that were reviewed by Birks *et al*. (2016b), which named other factors of influence: landscape structure, openness of the landscape, and diversity within the Absolute Pollen Source Area or Relative Pollen Source Area. Numerical or other PBR methods can provide improvements to global land use models, because they will provide empirical data about vegetation changes in the past (and thus also land use) that can be used in the global land use models, supplementing the historical data and replacing backwards modelled estimations of land use. The use of numerical PBR methods has increased enormously since the founding of the POLLANDCAL network in 2001 (Gaillard *et al*. 2008), which adopted the POLLANDSCAPE approach of Sugita (1994; in Gaillard *et al*. 2008).

In the next section, I will review PBR methods, using the framework outlined in the introduction (table 1). Then, I will determine how and precisely what each of the PBR methods can contribute to the HYDE database. It goes beyond the scope of this paper to discuss the possible improvements to other global land use models, such as the KK10 (Kaplan *et al.* 2010), GLUES (Lemmen 2009), and ML08 (Pongratz *et al.* 2008).

## 3. Results / Analysis of PBRs

In recent years, many new methods to quantitatively reconstruct the landscape of the past have been published, with all varied methods of usage. Some models were specifically designed for smaller scale reconstructions (e.g. MARCO POLO, Mrotzek *et al.* 2017), whereas other methods have already been applied to continental or even global scale (e.g. REVEALS, Sugita 2007a). A comparison of the amount of references each new method has, learns that the LRA, and especially REVEALS, has gained most traction in the research field (see figure 1). Three databases for scientific journals were used to find papers mentioning the following methods: the LRA (keyword: “landscape reconstruction algorithm”), the MSA (keyword: “multiple scenario approach” AND “pollen”, which was done because multiple scenario approach is not unique to palynology), the Pseudobiomisation approach (keywords: “pseudobiomisation” OR “pseudobiomization”), and lastly the EDA (keywords: “extended downscaling approach” AND “pollen”, similar reasoning as for the MSA). The results were updated until 24th of April 2018. The plant functional type approach was excluded because this method is not exclusive to the field of palaeoecology, and is mostly used in modern day vegetation studies. Bayesian modelling is a very common practice in ecology, and other biological disciplines and is therefore excluded from the search as well. The amount of papers on a certain method show how widely known the method is, but also that the method is being applied most widely in research. The LRA has been extensively used in applied research and has been described as “perhaps the most significant [advancement] in the analysis of pollen data in recent decades” (Edwards *et al*. 2015, p. 123).



| | Google Scholar | Web of Science | SCOPUS |
|---|---|---|---|
| 🟫 EDA | 2.8 | 2.4 | 3.1 |
| 🟩 Pseudob. | 18.3 | 4.9 | 40.6 |
| 🟨 MSA | 14.5 | 4.9 | 4.7 |
| 🟦 LRA | 64.5 | 87.8 | 51.6 |

**Figure 1**. Search results per PBR method (in percentages. Below, the proportion (in %) of each method to the total is displayed, for clarity. n=394 Google Scholar, n=41 Web of Science, n=64 Scopus.

### 3.1. The Landscape Reconstruction Algorithm (LRA): REVEALS and LOVE (Sugita 2007a, 2007b)

#### 3.1.1. Background of the model (from Sugita 2007a, 2007b)

The LRA was developed by Sugita (2007a, 2007b) and consists of two parts. The first part is a model to reconstruct the composition of the regional vegetation for large areas ($10^5$ – $10^7$ ha), called REVEALS (Regional Estimates of VEgetation Abundance from Large Sites). Secondly, smaller areas ($<10^4$ ha) can be reconstructed too, using the LOVE (Local Vegetation Estimate) method (Sugita 2007b). Sugita evaluates his LRA model by comparing the results to an older modelling approach (POLLSCAPE). The basic assumption in the model is that large lakes or bogs in an area have a similar pollen composition, and thus a regional vegetation that is homogenous. Within the large study site obtained from a REVEALS reconstruction, the pollen assemblage is constant, so at each individual smaller site for the LOVE reconstruction, a pollen assemblage will be obtained that represents the entire area. This is evidenced by theoretical and empirical studies (Sugita 1994, and references therein). These lakes can be selected and analysed for pollen content, and together with estimations of pollen production, a model for pollen dispersal (Prentice-Sugita model), and determining the relationship between pollen loading (pollen grains/$m^2$) in an area and plant abundance in that same area, it provides a reconstruction of the regional vegetation composition of past landscapes. The REVEALS method is similar to the R-value model (Davis 1963), with the addition of pollen dispersal-deposition coefficients. These reduce biases regarding differences in the dispersal of pollen. Another improvement with regard to older methods is the exclusion of local background pollen using the LOVE method (Sugita 2007b).

Reconstructing the regional vegetation, and thus excluding local background pollen means that pollen from outside the relevant source area of pollen needs to be estimated or modelled to distinguish between local and regional vegetation (which is assumed to represent how the landscape looked like, whereas local vegetation is highly variable depending on (a)-biotic factors). This method, LOVE, uses the results from the REVEALS reconstruction, the pollen counts from smaller sized sites, and pollen productivity estimates, to reconstruct the vegetation within the relevant source area of pollen (RSAP). RSAP is defined as the distance beyond which the correlation pollen-vegetation abundance does not change (Sugita 2007b). The biggest flaw in this method is determining the RSAP, because it is only possible to estimate these values for modern day landscapes where the locations of plants are known and registered. RSAP, as evidenced by simulation studies in the past, is mainly influenced by spatial patterns (topography) and species composition of vegetation (Sugita 1994, 2007a, Bunting *et al*. 2004). For past landscapes, Sugita (2007b) proposed to obtain the RSAP by backward modelling of the LOVE approach. To estimate past vegetation in the RSAP, all parameters can be filled in, which makes it possible to approach the likely true value of RSAP by doing multiple iterations (Sugita 2007b). An advantage of the LRA is that the spatial scale of all the reconstructions are expressed: namely in the form of the RSAP (which is $>10^4$ ha for REVEALS estimates, and $<10^4$ ha for LOVE, Sugita 2007a, 2007b). REVEALS estimates the abundance of taxa at a large region around the site, and the output is used for the LOVE method, which gives a reconstruction that is more representative of local plant communities (Edwards *et al.* 2015). Local plant communities can also be reconstructed without the use of pollen dispersal models using the MARCO POLO (MAnipulating pollen sums to ReCOnstruct POllen of Local Origin) approach (Mrotzek *et al*. 2016). Both LOVE and MARCO POLO are unsuitable for HYDE, as the scale of these reconstructions is very local (and thus small). They will therefore not be discussed any further.

#### 3.1.2. Critical analysis of the method

The LRA makes a few basic assumptions. Firstly, the sampling site (a large lake) is assumed to be circular and to have no connection to flowing water (inlets or outlets). Furthermore, all pollen is considered to be dispersed by wind. However, in reality, the larger the lake, the more likely it is to have incoming or outgoing streams (Pennington 1973: in Sugita 2007a). These assumptions make it necessary to carefully select sites, because otherwise, stream-borne pollen will affect the assemblage in the lake (Peck 1973, Bonny 1978; in Sugita 2007a). In the LRA, pollen is dispersed by wind, and the model uses the pollen dispersal-deposition function of the Ring-Source model for lakes (Sugita *et al*. 1999), and the model of Prentice (1985, 1988) in the case of bogs or mires. Wind direction is not considered in the LRA. However, Theuerkauf *et al*. (2013, 2014, 2016) showed that the Prentice model has its shortcomings and that it might be better to use a Lagrangian stochastic model, and a case study of the Tasmanian cultural landscape also suggests that Langrangian stochastic models perform better than the Prentice-Sugita model (Mariani *et al*. 2017). The Prentice-Sugita model, a Gaussian plume model, estimates the entire dispersal pattern at once, whereas the Lagrangian stochastic model simulates the trajectory of a single pollen grain, after which the overall pattern is obtained from a large number of simulated trajectories

(Theuerkauf *et* al. 2013). Height differences in the pollen sources are not considered, meaning that arboreal pollen will have the same trajectory as pollen of herbaceous and flowering plants. This implies that the LRA does not work well in mountainous areas. The pollen assemblage obtained represents the entire area, which implies that the region around the site (with a 100-200 km radius) has uniform vegetation distribution (Sugita 2007a). This is problematic because there are many areas in the world where the composition of the vegetation can change significantly at small distances, because of abrupt changes in topography, hydrology, or even because of human influences.

Sugita (2007a, 2007b) states that pollen production is constant through time, and species specific. Assuming pollen production is species specific is unproblematic, but assuming it is constant over time is not. A study by van der Knaap and van Leeuwen (2003) has shown that pollen production is affected by temperature and precipitation, and that some taxa benefit from certain weather changes, whereas others do not. Repeated investigations have shown similar results for tree and shrub taxa (Huusko and Hicks 2009, van der Knaap *et al.* 2010; Donders et al. 2014). Lastly, Sugita states that there is no preservation bias for individual certain taxa, which is an oversimplification. Taphonomy, the way individual pollen grains are subject to weathering and degradation after dispersal, has a large influence on pollen preservation (Hunt and Faccioni 2018). Besides taphonomic factors, there are statistical factors that influence pollen preservation, and pollen preservation can vary greatly within and between sites (Tweddle and Edwards 2010 and references therein), and it is difficult to determine the specific taphonomic processes occurring in the sediment (Campbell 1999). An experimental study by Twiddle and Bunting (2010) also showed difference in degradation occurring to different pollen types, where pollen that indicate human activity (in this case *Secale*, rye) are less resistant to degradation. As pollen taphonomy is a universal factor that is ignored in almost all vegetation studies, this factor will not be discussed for the other PBR methods, but it is a factor that should be improved in new PBRs.

It is important to count an appropriate amount of pollen per sample: if this is 300-500 per sample, as is common in palynology, the standard error of the LRA is around 10-20% higher than when 1000 pollen grains are counted (Sugita 2007a). Further uncertainty stems from the estimates of pollen production, which are highly dependent of geographic location. This means that the LRA only works for those areas for which Pollen Production Estimates (PPEs) are known. These studies mainly limit the application of the LRA to Europe and North America, although there is slow improvement for areas on the southern hemisphere (Mariani *et al.* 2016), and China (Li *et al*. 2017). Sugita (2007a, p. 237) presents a list of papers that have estimated pollen productivity for certain regions. However, these PPEs are obtained from cultural landscapes, and research from the Bialowieza forest, Poland, shows that low pollen-producing taxa (i.e. *Corylus* and Poaceae) are six times underrepresented in the forested landscape (Baker *et al*. 2016). Furthermore, PPEs are assumed to be constant through time, their (modern) values being obtained from experimental set-ups (surface-sample experiments), and this assumption is questionable (Theuerkauf and Couwenberg 2018). Theuerkauf and Couwenberg developed a model-based approach to the reconstruction of past PPEs and past plant abundance (ROPES, REVEALS without PPEs), which uses a single pollen record (2018). This method provides a possibility to produce PPEs for areas where no surface-sample studies have been carried out, and these values can subsequently be used for the LRA reconstruction (Theuerkauf and Couwenberg 2018).

Besides the underrepresentation of low-pollen producing taxa in densely wooded areas, there is also the effect of forest composition (flowering age and understory position) on the pollen production of plants (Matthias *et al*. 2012). Lake biomass linearly relates to the pollen accumulation ratios, meaning that, especially for small lakes, the vegetation around the lake largely determines the pollen assemblage (Matthias and Giesecke 2014), which means that pollen records from small lakes mostly represent the local vegetation. Land management, and changes in land use lead to changes in pollen production too, specifically in the case of grasses and crop plants (Theuerkauf *et al*. 2015). Woodland management practices such pollarding or coppicing (the periodic cutting of trees and shrubs for wood and fodder) also affect pollen production in individual trees. Waller *et al*. (2012) show that *Tilia cordata* (lime) and *Carpinus betulus* (beech) are “palynologically invisible” when being under a coppicing regime, whereas *Corylus avellana* (Hazel) produces more pollen being coppiced. Thus, site selection and knowledge of historical landuse is very important if the reconstruction needs to be representative of the entire region. This may become easier when PPEs are modelled using the ROPES method (Theuerkauf and Couwenberg 2018).

REVEALS is shown to work better than previously developed methods that attempt to quantitatively reconstruct vegetation cover in the case of open landscapes, wooded landscapes, conifers and broad-leaf trees, grasses, and cereals in flat areas (Hellman *et* al. 2008a), especially in the case of landscapes dominated by herbs (Gaillard *et al*. 2010). Differences in basin size, basin type, number of dates per sample, and the PPEs have no effect on the output of the model, except when entomophilous plants are included in the analysis (Mazier *et al*. 2012). The use of pollen percentages instead of REVEALS estimates is discouraged as the latter gives a better insight into changes in the vegetation through time and space (Marquer *et al*. 2014), and the application of REVEALS can be applied from regional scenes to a sub-continental scale (Marquer *et al*. 2017). Kaplan *et al*. (2017) show that REVEALS estimates for the last 100 years are good: they compare well to the land use observations obtained from satellites. Furthermore, HYDE has a low uncertainty of around 11% for this period, and REVEALS has a good correspondence with that.

The method works best with the use of multiple large sites, and uncertainty increases with decreasing numbers of lakes and decreasing size of the lakes used in the analysis (Hellman *et al*. 2008b, Trondman *et al*. 2015). It becomes unreliable to use small bogs in the REVEALS model, as these do not fit the assumptions made by the model (Trondman *et al*. 2015). Small sites can be used but then the standard errors are larger than when large sites are used (Trondman *et al*. 2016), as was already shown by Sugita (2007a) and by Mazier *et al*. (2012). When using REVEALS, it is essential to have a larger number of sampling sites that can represent the regional average of vegetation cover, but this is problematic since there are few regions that possess such a network of sites, even in Europe where most sites are available (Edwards *et al*. 2015). Lastly, it is important to note that different vegetation patterns may result in the same pollen assemblage, which means that there is the problem of equifinality (Bunting and Middleton 2009, Edwards *et al*. 2015). The problem of equifinality will be discussed more in detail in part 3.2, because the Multiple Scenario Approach (MSA) uses this as the basis of the method (Bunting and Middleton 2009), but it is evident that the omission of equifinality in the LRA provides a major source of uncertainty in these reconstructions.

### 3.1.3. Applicability of the model

As stated before, the LRA is the PBR method that has gained the most attention in literature today, and is widely used by palaeoecologists, although in most cases, only REVEALS is used. Studies have been published for Sweden (Hellman *et al*. 2008a, Cui *et al*. 2013, Hultberg *et al*. 2015), Denmark (Overballe-Petersen *et al*. 2013), Norway (Hjelle *et al*. 2015, Mehl and Hjelle 2016), the Czech Republic (Mazier *et al*. 2012, Abraham *et al*. 2017), France (van Beek *et al*. 2018), northern Europe (Nielsen *et al*. 2012, Marquer *et al*. 2014, 2017), even for all of Europe (Trondman *et al*. 2015, Kaplan *et al.* 2017, Roberts *et al.* 2018), and the Tibetan Plateau, southwestern China (Wang and Herzschuh 2011). These studies all have evaluated the LRA. REVEALS has also been used to evaluate the global land use model of Kaplan *et al*. (2017). The one limitation that now exists for the use of the LRA is the availability of PPEs, which needs improvement for South America, Africa, and large parts of Asia. However, this approach has considerable potential when it deals with questions on a continental or global scale (Bunting and Middleton 2009).

The method produces the percentage cover of each taxon used in the reconstruction for the entire area (figure 2, next page). It produces land cover estimates per pollen sample, and thus extra steps need to be taken to convert these estimates into land cover percentages at certain points in time, which will depend strongly upon the strength of the time-depth model available. Kaplan *et al*. (2017) placed 25 individual plant taxa in 10 plant functional type (PFT) categories (e.g. grazing land, cropland or woodland), and calculated the percentage cover for each PFT category for $1^{o}$ grids (~$10^4$ $km^2$). With some adjustments, the data from REVEALS reconstructions can thus be reconverted to land cover data useful for HYDE reconstructions. However, converting land cover per individual taxon to land use categories will introduce additional errors, because assigning taxa to one PFT means excluding it for other PFT categories. Furthermore, due to difficulties with pollen identification, where sometimes a single pollen grain can be identified up to the family level, and thus a lot of ecological information is lost. This leads to certain pollen types being ascribed to PFT categories that they might not belong to, or that multiple PFT categories might be fitting for one pollen type (Trondman *et al*. 2015). More about PFT approaches will follow in chapter 3.4.

Pollen analysis is a time-consuming process, especially when the required 1000 pollen grains are counted for each sample. It requires the attention of an expert, because it is important to get as much detail about the pollen types as possible. In some cases, determination of pollen grains can be done to the family level (in the case of grasses for example), and sometimes to a species level. The more accurate this is done, the more information it will give about the vegetation cover of the past. Furthermore, determination to the species level gives more ecological information, than when only the genus or family is known. These factors make it difficult for non-palynologists to use LRA, but this will be the case with each method based on pollen analysis. This does, however, promote interdisciplinary research. Despite these difficulties, model improvements have been proposed, as well as ways to make the use of the LRA easier

(Birks and Berglund 2018). Theuerkauf *et al*. (2016) have made REVEALS available in R, but instead of using the Ring-Source model (Sugita *et al*. 1999) or the Prentice models (1985, 1988), it uses a Langrangrian stochastic dispersal. This new R-function is freely available within the DISQOVER package in R. It offers an opportunity to experiment with and analyse model sensitivities.

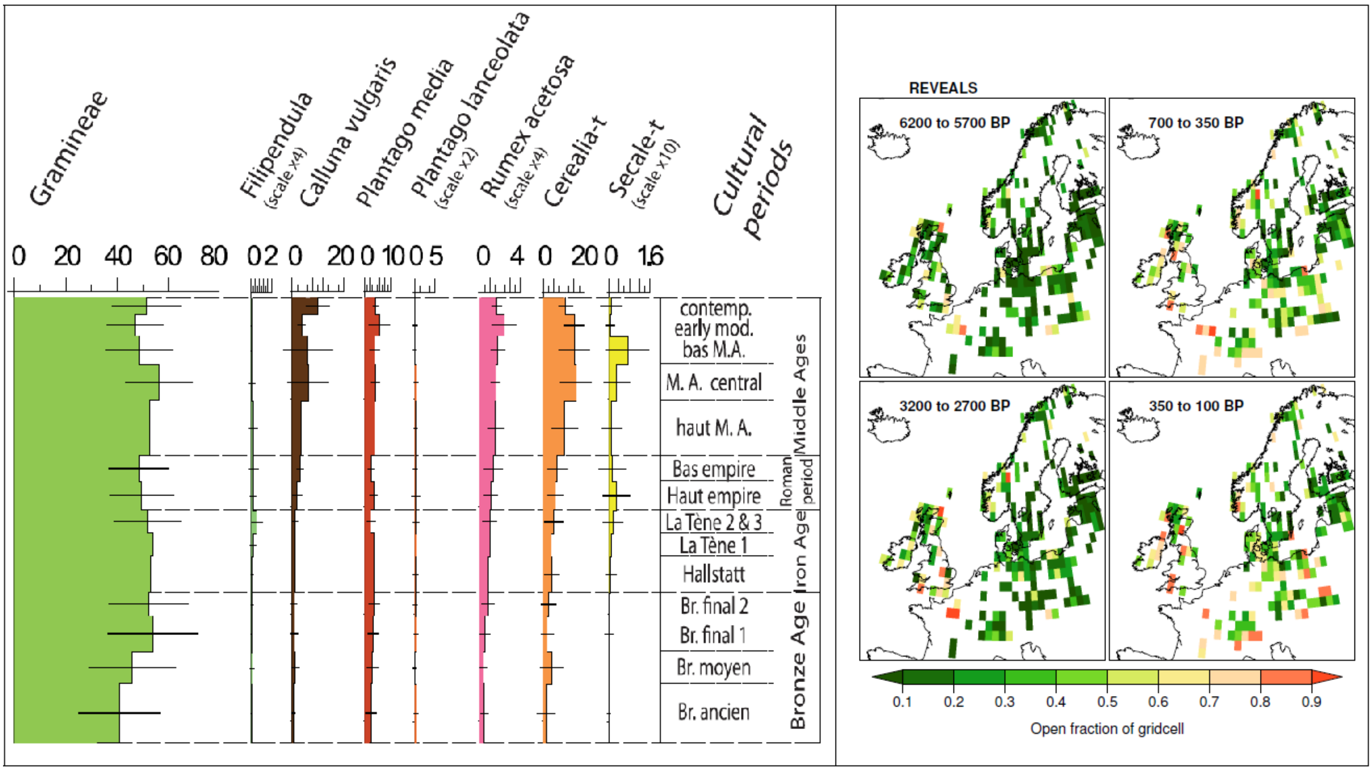


**Figure 2**. On the left, detail of a diagram with REVEALS results showing the cover (in %) of different taxa. Figure from van Beek *et al*. 2018.
On the right, detail of a map showing openness of 1° grid cells using REVEALS. From Kaplan *et al*. 2018.

The LRA was developed to quantitatively reconstruct vegetation changes in the past, but in recent years it has gotten much attention outside the field of palaeoecology as well. Especially among archaeologists, it has led to debates about the output and methodology of the LRA and other PBRs. PBRs are still very abstract and the concepts associated with the methods too. The scale of reconstructions is large, and for archaeologists, these scales do not cover the perspective of an individual in the past (Richer and Gearey 2017). It has been argued that the PBR methods provide virtual reconstructions of “plausible” or “faithful” reconstructions of the past vegetation cover, but that they do not provide an actual reconstruction of the landscape (Caseldine *et al*. 2008). Others question whether the reconstructions are just “data visualisation,” or constitute the real landscape of the past (McCoy and Ladefoged 2009). Past vegetation distribution mapping suggests some form of stability, and thus implies that these maps are ‘representative visualisations’ (McCoy and Ladefoged 2009, Richer and Gearey 2017). Edwards *et al*. (2015) argue among similar lines, stating these reconstructions constitute pseudolandscapes: “a partial and credible representation of a fraction of the lived experience of communities who had a mutual relationship with the plants around them”, p. 125). It is important to remember these considerations, because they can improve the way in which the PBRs are used and how researchers should interpret the results from PBRs. Since the LRA focuses on the large regional reconstructions, it does not represent anthropogenic activity in pre-medieval times, because the effect of humans on the landscape before this time was local-scale.

## 3.2. The Multiple Scenario Approach (Bunting and Middleton 2009)

### 3.2.1. Background of the model

The Multiple Scenario Approach, developed by Bunting and Middleton (2009), aims to tackle the problem of translating pollen data to land cover by a reverse approach, one that keeps in mind that multiple landscapes might produce a similar pollen assemblage (equifinality). The method produces hypothetical landscapes in a GIS environment that each produce a pollen assemblage (total simulated pollen records can be $10^4$-$10^5$). These hypothetical landscape maps are based on based on ecological values of individual species, soil maps, elevation, slope angles, palaeogeography (in some instances), and random factors. It also requires the use of a pollen deposition model, and uses the Prentice-Sugita model, as does the LRA. Because of the inclusion of random factors, a multitude of vegetation maps is produced that can all be compared to an actual pollen assemblage from the field to obtain the most plausible reconstructions of the past landscape, by statistically comparing the simulated pollen records to an actual pollen record from the site (Bunting and Middleton 2009). The method is highly site-specific, as it requires each site to be modelled and interpreted differently. The method produces vegetation maps, which are 'time-slices', because all reconstructions is a two-dimensional, site specific, vegetation map for a single point in time. Then, the 'time-slices' are stacked together to gain insight in the vegetation dynamics in the research area. It is possible to use areas where only one location is being sampled (Bunting *et al*. 2008), although more robust reconstructions are obtained when analysing multiple sites within one landscape that have strong chronological links that can be combined (Pratt 2006, in: Bunting and Middleton 2009). Comparison of simulated pollen assemblages to real pollen assemblages from the field is done using an approach from the modern analogue technique (MAT) which calculates the squared chord distance (Maher 2000, Wahl 2004, in: Bunting and Middleton 2009). Likely sets of plausible hypothetical maps are those that fall below a specific value, which are typically 0.15-0.25 in the MAT. All hypothetical landscapes that fit these criteria are then analysed again, with a larger number of replicates, in order to find those hypothetical landscapes that are considered to be the best-fitting scenarios. This method relies on several software packages to work. For a complete and updated list of software used, see Bunting *et al*. 2018.

### 3.2.2. Critical analysis of the method

The MSA assumes that one pollen type represents one or multiple species of which the ecological traits do not change over time (e.g. *Alnus glutinosa* for alder, and its ecological requirements are constant through time). Furthermore, each pollen morphotype has a definable and constant autoecology and synecology. Autoecology is the study of single organisms or a single species with its environment, whereas synecology is more complex and studies the interactions of multiple organisms or species with each other and within their environment. Assuming ecological requirements or interactions are constant through time is dangerous because phenotypic plasticity can alter ecological requirements and species interactions through time (Miner *et al*. 2005, Berg and Ellers 2011, Turcotte and Levine 2016). However, these temporal changes are not conserved when looking at short to moderate periods (one lifespan - $10^6$ years). Ecological niches are often conserved which means that ecological requirements are on average constant through time (Townsend Peterson 2011). Other assumptions stem from the use of the Prentice-Sugita algorithm, which have been discussed in detail in section 3.1.2.

The requirement of ecological continuity means that the MSA can only be applied to periods that are alike the current interglacial period in which we live (Bunting and Middleton 2009). The MSA realises and tries to negate the uncertainties associated with the use of PBR methods, unlike other methods such as the LRA. However, as stated before, the use of the Prentice-Sugita pollen dispersal method needs an update, or as Theuerkauf *et al*. state, could benefit from the adoption of new dispersal models, such as a Lagrangian stochastic models (2013, 2014, 2016). Other improvements for the MSA might be the inclusion of archaeological finds/settlements or archaeological evidence for human presence and agriculture, which can be integrated in the GIS-part of the MSA, as these factors influence precisely where plants are located, but also which plants can be found there (referring in this case to plants associated with human activity).

Continuous improvements are being made to the MSA. The way in which the software was constructed leaves room for the inclusion of different pollen dispersal and deposition models. The Prentice-Sugita pollen dispersal and deposition model assumes that the surrounding lands are flat but Bunting *et al*. have shown that it is possible to apply the MSA to hilly landscapes, by making changes to the simulation of pollen dispersal by wind (2008). Besides the application to hilly areas, attempts have also been made to model the effect of human management of woodlands (Bunting *et al*. 2016). Besides these model improvements, scaling improvements have not been made. The MSA is best applicable to areas that are relevant for archaeological reconstructions, and not at superregional scales or larger, which the LRA does. However, since both methods are based on pollen production and dispersal methods, the scale of reconstructions is technically determined by the RSAP, which in turn determines the extent to which the vegetation of a certain location can be reconstructed. In practice however, the MSA has been mostly applied to address 'landscape-scale' questions in cultural landscapes, which often means that the research is done in an archaeological context, or which means that the reconstruction tries to model the local effect of humans on the surrounding (woodland) vegetation (Bunting and Farrell 2017, Bunting *et al*.

2018). Combining several pollen records to obtain information on a larger scale is possible too, but the modelling process is time-consuming, making it difficult to be applied on a super-regional scale.

Although the MSA has gained attention in literature reviews today (Richer and Gearey 2017, Birks and Berglund 2018), the method has not yet been subjected to a critical assessment. Some of the uncertainty coming from this method is similar to that which comes from the LRA, namely the uncertainty from the use of PPEs. Mazier *et al*. (2012) used Plant functional trait estimates based on a REVEALS analysis and showed that fluctuations in PPEs have no significant effect on the result of the REVEALS analysis. Thus, the MSA too seems to be an appropriate method to address research questions coming from an archaeological context. The preparing part of this method is done in a GIS environment, and this map-based approach is continued into the final stages of the method, because it produces a vegetation map for a certain point in time as result.

### 3.2.3. Applicability of the model

The MSA has gained traction in the last years in the field of palynology, but not as much as the LRA. It is a decent method to quantitatively reconstruct vegetation for certain time slices, and subsequently to analyse changes in the vegetation by comparing time slices. It incorporates the often looked-over concept of equifinality, which addresses the uncertainties that are normally associated with palaeoecological reconstructions. Reconstructions using the MSA are available for Sweden (Karlsson 2008), Scotland (Pratt 2006, Bunting *et al*. 2007, 2018), and northern England (Bunting *et al*. 2008; Bunting *et al*. 2018). A new effort to reconstruct the Humberhead Levels (Yorkshire, northern England) has just started as well. All these reconstructions were carried out in an archaeological context. Besides these reconstructions that were carried out within the research group of Bunting, not many other groups have adopted this method, although efforts are being made to reconstruct areas in Estonia and Tasmania as well.

The MSA can be viewed as a thought experiment where one ponders over the factors that determine the structure and composition of the vegetation, and therefore, it is useful if the user has ecological knowledge so as to understand the method better. In multidisciplinary teams, this method provides an excellent way to quantitively reconstruct the vegetation surrounding archaeological sites, and furthermore how the people interacted with their surroundings. Especially in archaeological contexts, this method can provide landscape reconstructions to bring archaeological investigations into a broader perspective. The method can be used to reconstruct cultural landscapes, from open landscapes to managed woodlands, and it can even detect which management strategy was used in the past (Bunting and Farrell 2017).

The basis of the method is that a great number of vegetation maps are produced, that each produce pollen signals that can be compared statistically to actual pollen assemblages obtained from the field or previously published literature. The best-fitting maps are the most likely reconstructions of the past vegetation, or at least the best approximation of a correct reconstruction (see figure 3 for an example). These vegetation maps are then the result of the reconstruction, and can show the percentage cover for plant communities in the landscape. The communities are assigned places in the landscape based on random factors, but also topography and soil maps. However, a great freedom in the MSA is that the researcher determines which communities will be modelled. If there is historical evidence of woodland management, the researcher can include a community of managed woodland, and the same goes for cropland or pasture. The cover of all communities is given in percentages, which is very useful to HYDE. The composition of each community is known, so it is easy to work out the proportion of each taxon in the landscape for the use in a PFT reconstruction. This is not necessary if the focus of the research has been the anthropogenic changes in the landscape, because then the MSA will already have reconstructed pasture and cropland, for example. The main issue with the MSA is the scale of the results. Due to the production of >$10^4$ maps, the method is time-consuming, and duration increases exponentially the more factors are added into the simulation, and the same goes for increases in the area that will be reconstructed. A 50 km by 50 km grid (1/4 of a $1^{o}$ grid cell) is as large as the software can handle and using grids bigger than this also leads to less reliable results (Bunting, pers. comm.). The MSA has a lot of value for archaeological research questions, and that these efforts could be incorporated in HYDE, especially for areas with a high human impact. It would however be a time-consuming job to carry out MSA reconstructions at a scale that would most benefit HYDE.

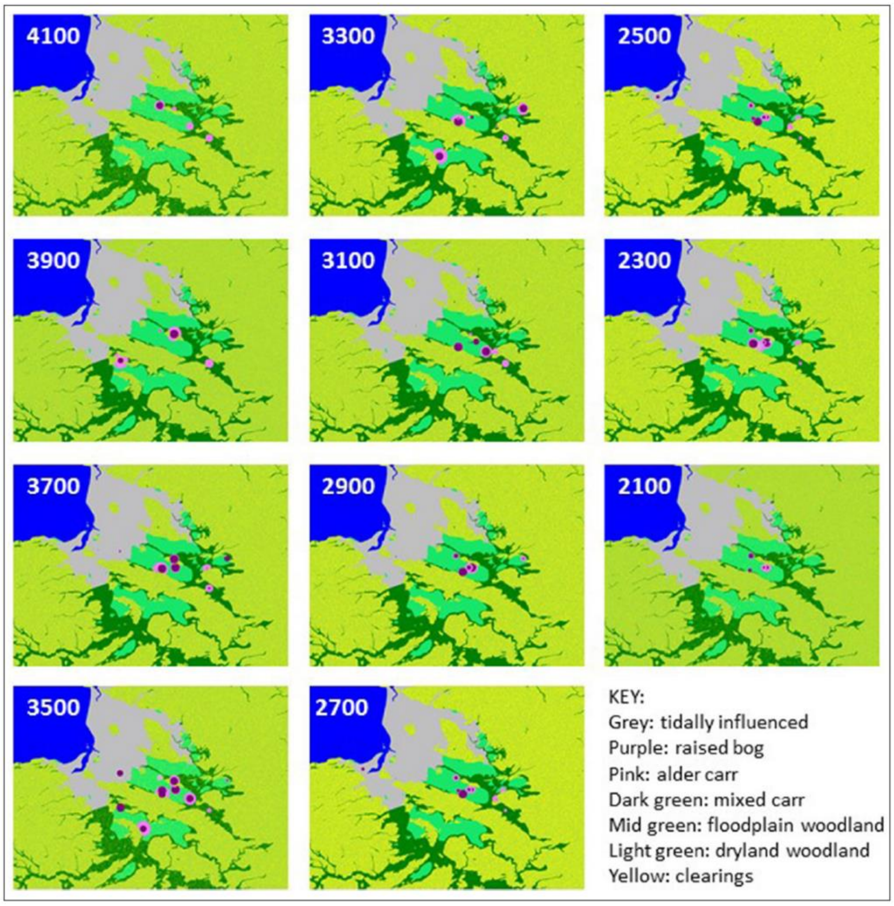


**Figure 3.** Example best-fit vegetation maps for a study area in Somerset (England). Maps were made in time slices of 200 years. From: Bunting *et al*. 2018)

## 3.3. The Extended Downscaling Approach (Theuerkauff and Couwenberg 2017)

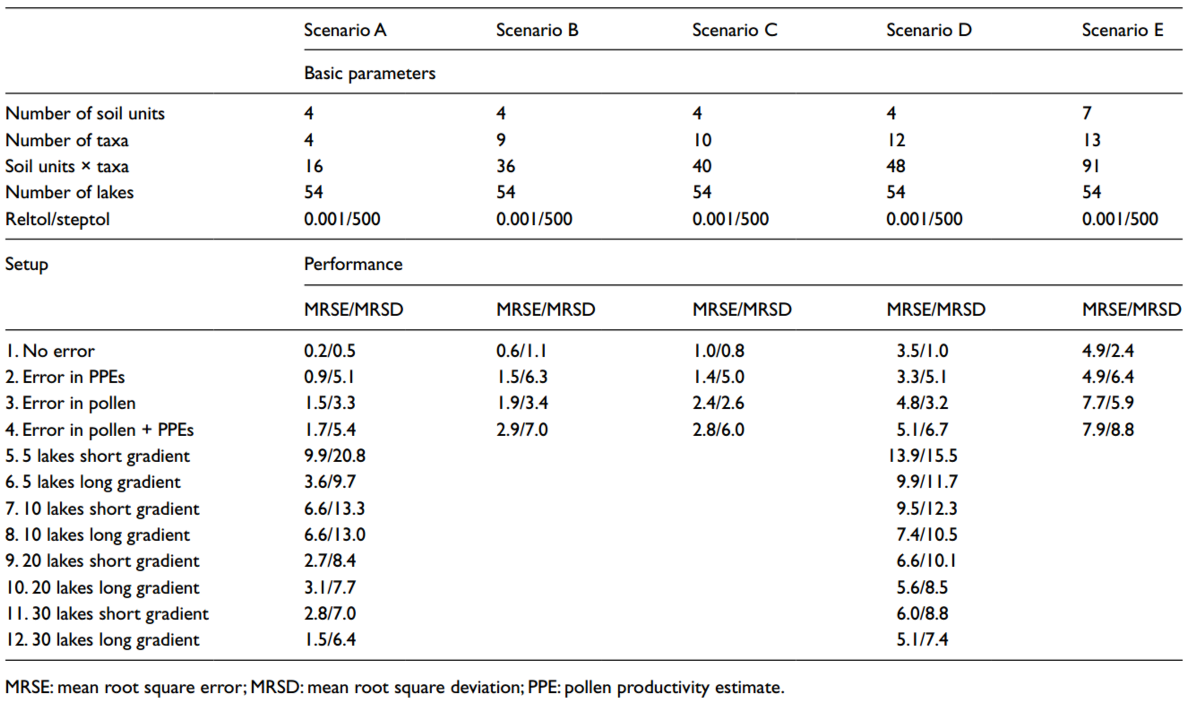
### 3.3.1. Background of the model

The extended downscaling approach (EDA) was developed by Theuerkauf and Couwenberg (2017), although there have been some instances in which the method was used, but not officially called the EDA (Theuerkauf and Joosten 2009, Theuerkauf *et al*. 2014). The most recent and formal discussion of the method will be used, which is Theuerkauf and Couwenberg (2017). The EDA uses a similar approach as the MSA: simulated pollen depositions are compared to empiric pollen assemblages, but it uses multiple sites. This allows the researcher to use forward modelling to determine the vegetation cover in the research area. The EDA uses abiotic conditions (e.g. soil type, relief) and translates these into the pollen source areas for a number of study sites. Subsequently, it translates them into plant cover by using a random key, which defines species composition in the landscape. Then, a pollen dispersal model (a Lagrangian stochastic model, developed by Kuparinen *et al*. 2007, in: Theuerkauf and Couwenberg 2017) simulates pollen depositions. The EDA then uses the DEoptim optimisation function (Ardia *et al*. 2011a, 2011b, in: Theuerkauf and Couwenberg 2017) to adjust the random key until the simulated pollen assemblage is most similar to the empirical pollen assemblage. The distance between these simulations and the empirical data (before the optimisation) is calculated as the weighted least square distance. The EDA also simulates multiple pollen assemblages, and thus takes the problem of equifinality into account.

### 3.3.2. Critical analysis of the method

The assumptions of the model are similar to those used in the MSA, which is that ecological requirements are constant through time, and soil types of today have not changed through time either. In 3.2.2 these issues have been discussed in more details. The pollen dispersal model used here is different from the Prentice-Sugita model used in the LRA or the MSA. A Lagrangrian stochastic model might be better at simulating pollen dispersal, as evidenced by simulation experiments (Theuerkauf *et al*. 2013, 2014, 2016), but the authors are unclear about the way in which the model was calibrated. The EDA was tested using different 5 scenarios, which all differ slightly in the way the substrate or soil is built up (scenarios are marked A-E). Within these scenarios, there are twelve different set-ups: a setup with no error in pollen data or PPEs, a setup with added uncertainty to the pollen data or/and PPEs, and a setup where the amount of sampled lakes (5, 10, 20, 30 lakes with a short/long gradient) is varied. Mean root square errors (MRSE) were calculated to show the uncertainty of each setup, and in their method, the MRSE represents the percentage area for which the reconstructed vegetation was wrong. Mean root square deviations were calculated to show the percentage area for which the reconstructions vary over 100 runs (see table 2 for the results of their analysis). They showed that errors in PPEs contribute less uncertainty to the approach than errors in pollen data, or errors in PPEs and pollen data, Furthermore, the more sites used, the smaller the error becomes. With error added to the pollen data and/or the PPEs, and a decrease in the amount of lakes used, the amount of variation between iterations also increases (see table 2).

Table 2. Graph and description obtained from Theuerkauf and Couwenberg 2017. Basic parameters of scenarios A-E performance of the EDA when applied with these scenarios and different model setups. MRSE denotes the percentage area for which reconstructed vegetation cover was wrong, and MRSD the percentage area for which reconstructions vary over 100 runs.



| | Scenario A | Scenario B | Scenario C | Scenario D | Scenario E |
|---|---|---|---|---|---|
| | Basic parameters | | | | |
| Number of soil units | 4 | 4 | 4 | 4 | 7 |
| Number of taxa | 4 | 9 | 10 | 12 | 13 |
| Soil units × taxa | 16 | 36 | 40 | 48 | 91 |
| Number of lakes | 54 | 54 | 54 | 54 | 54 |
| Reltol/steptol | 0.001/500 | 0.001/500 | 0.001/500 | 0.001/500 | 0.001/500 |
| Setup | Performance | | | | |
| | MRSE/MRSD | MRSE/MRSD | MRSE/MRSD | MRSE/MRSD | MRSE/MRSD |
| 1. No error | 0.2/0.5 | 0.6/1.1 | 1.0/0.8 | 3.5/1.0 | 4.9/2.4 |
| 2. Error in PPEs | 0.9/5.1 | 1.5/6.3 | 1.4/5.0 | 3.3/5.1 | 4.9/6.4 |
| 3. Error in pollen | 1.5/3.3 | 1.9/3.4 | 2.4/2.6 | 4.8/3.2 | 7.7/5.9 |
| 4. Error in pollen + PPEs | 1.7/5.4 | 2.9/7.0 | 2.8/6.0 | 5.1/6.7 | 7.9/8.8 |
| 5. 5 lakes short gradient | 9.9/20.8 | | | 13.9/15.5 | |
| 6. 5 lakes long gradient | 3.6/9.7 | | | 9.9/11.7 | |
| 7. 10 lakes short gradient | 6.6/13.3 | | | 9.5/12.3 | |
| 8. 10 lakes long gradient | 6.6/13.0 | | | 7.4/10.5 | |
| 9. 20 lakes short gradient | 2.7/8.4 | | | 6.6/10.1 | |
| 10. 20 lakes long gradient | 3.1/7.7 | | | 5.6/8.5 | |
| 11. 30 lakes short gradient | 2.8/7.0 | | | 6.0/8.8 | |
| 12. 30 lakes long gradient | 1.5/6.4 | | | 5.1/7.4 | |

MRSE: mean root square error; MRSD: mean root square deviation; PPE: pollen productivity estimate.

These simulations suggest that with a low number of taxa, the reconstructions using EDA are possible, and with limited uncertainty. False positives are obtained when the most extensive scenario was tested, suggesting that this method needs to be improved if it needs to be applied in empirical studies. Even though uncertainty is added by introducing errors to the data, the vegetation reconstructions are still correct for >90% of the time (when 2000 pollen grains are counted, which is double the amount necessary for the LRA). Other uncertainties are associated with the use of the pollen dispersal model, even though it performs better than the Prentice-Sugita model. The Lagrangian stochastic model does not take into account differences between night and day, changing wind conditions, or changes in landcover. Furthermore, ecological requirements are not considered either, and vegetation is purely assigned on the basis of the soil type, which represents an oversimplification in the least.

In its current form, the model produces percentages of cover for every pollen type/taxa, so no vegetation maps are produced using this method. Spatial distribution of all taxa within the research area is not available, although it would increase the usefulness of the method for people who do not work in the field of palaeoecology, but depend on the landscape reconstruction data. The scale of the reconstruction for these simulations was a ring with a 50km radius around each lake that was used (all lakes were brought back to a size of 600 ha). The scale of these reconstructions is around 50km per basin, and this was determined by modelling with a Lagrangian stochastic model. They found that pollen in a 1000m basin have a source area of ~60km around the basin, whereas modelling with Gaussian plume models leads to areas twice as big, around ~115km (Theuerkauf *et al*. 2016). Source area in this study was defined as the distance from which the total pollen deposition at a site arrives. The differences in the source areas between these models are due to the way in which the pollen trajectories are calculated. These model simulations still need to be validated with empirical data, but the current results are promising. However, it is unclear how the Lagrangian stochastic model has been verified or calibrated. The Lagrangian stochastic model is a climatic pollen dispersal and deposition model, and it is therefore necessary to calibrate the model for every geographic region, since climatological conditions can be different in every region.

### 3.3.3. Applicability of the model

The EDA, in its present form, is very abstract and theoretical, and its output is similar too. The method needs the application of empirical data, to verify the method in the field. Palaeoecologists have the first hand in picking up the method and to get to work with it, because the method seems promising. The software available for this method is easily accessible in R, with the DISQOVER package, making it easy for the scientific community to propose improvements to the model. For archaeologists, there are other methods more suitable for the reconstruction of the vegetation: this method did not incorporate taxa indicative of human presence or activity. One scenario uses Cerealia (cereals) and *Secale* (rye), and then only in low amounts. The EDA can be used to reconstruct the natural vegetation surrounding lakes or mires but is less capable of modelling the effect of humans (that is, in the model's current form).

The model produces simulated pollen assemblages which can be compared to real pollen assemblages from the field. The simulations are based on randomly assigning plant species in the relevant source area of pollen around multiple sites in a study area (a ring with a radius of 50km, which is around ¼ of a 1° grid cell). The random key can be found in the appendix to Theuerkauff and Couwenberg 2017. The method shows the cover in these areas for all taxa included in the simulation (see figure 4). This includes 90% quantiles of the cover reconstructed for 100 iterations of the model. The model has not been tested using real data, or real field sites yet, but the preliminary investigations have shown that the method is quite consistent if no errors are introduced in the method. The data could thus easily be translated into land cover proportions of different taxa into land cover in 1° grids, although individual sites can only cover up to a quarter of a 1° grid cell. The method still needs field testing, or the use of a real dataset, and after that it could possibly be used to make improvements to HYDE.

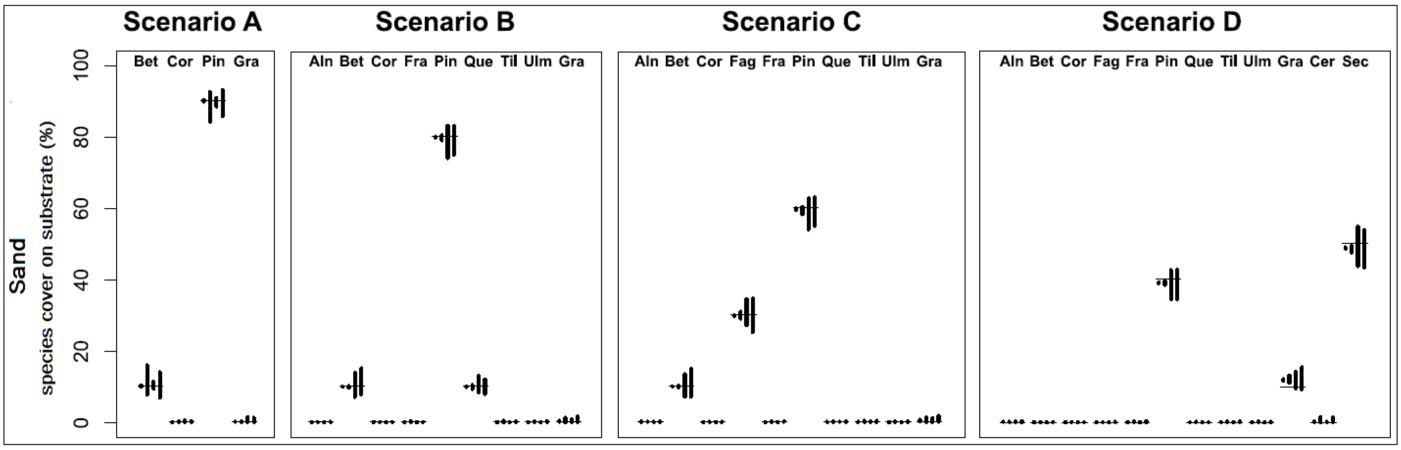


**Figure 4**. Results from an EDA analysis showing the cover of different taxa on sand. The scenarios are the same as in table 2. For each taxon, 4 lines are shown, from left to right: no error, error in pollen data, error in PPEs, and error in both.

### 3.4. Indicator species approaches: Plant Functional Types (e.g. Davis *et al*. 2015) and the Pseudobiomisation method (Fyfe *et al*. 2010).

### 3.4.1. Background of the models

Pollen data can also be divided into globally consistent ecological categories, using a method that is relatively easy and repeatable. Two models exist that deserve attention: first, the plant functional type approach, and second, a method that is a variation on the previous one, the pseudobiomisation approach. The major advantage of these methods is the coarse-grained scale in which the method is applied: superregional and global questions about vegetation changes can be answered. The main difference between the two methods is how the pollen data is translated into ecological categories: the PFT approach uses only natural vegetation (e.g. cold grass shrubs, boreal evergreen conifers), whereas the pseudobiomisation approach takes cultural categories into account as well (e.g. coniferous woodland, arable lands). In the pseudobiomisation approach, PFTs are called Land cover categories (LCCs). The steps to take are as follows. Firstly, the original pollen data needs to be converted into percentages. Secondly, ecological categories need to be defined, and the pollen taxa need to be assigned in one of these categories. This is done by an algorithm which groups pollen taxa into PFTs based on certain vegetation criteria, and then calculates the PFT scores as a sum of the total pollen count (Davis *et al*. 2015). Thirdly, weighted values are given to each pollen sample, which determines in which PFT/LCC category the sample falls (open landscape, semi-open, or wooded). The criteria of these weighted values can differ per paper, but here the example of Fyfe *et al*. 2010 is used: The sum of LCC scores are normalised to 100, after which the LCC scores are recalculated for all samples again. They now range from -100 to +100. Experimental modelling with a set of representative pollen assemblages and comparison with the interpretations of the original analysts determined where the line between semi-open and wooded, and semi-open and open landscapes was (Fyfe *et al*. 2010). These scores were not interpolated on maps, instead, the LCC values were compared between sites and different times. For the plant functional type approach, the values for the PFT assemblages were interpolated on a map and the changes in time were tracked too at a scale of 1° (Davis *et al*. 2015). Climate change has a different effect on vegetation along a vertical line than at the horizontal line and the method keeps this into account as well (Davis *et al*. 2015). Although the pseudobiomisation approach just presents affinity scores of the different LCC categories (Fyfe *et al*. 2010), and the PFT approach can divide pollen assemblages into biomes, landscape openness, and mean-scored distance from modern conditions, both are not real quantitative reconstruction of the landscape.

### 3.4.2. Critical analysis of the methods

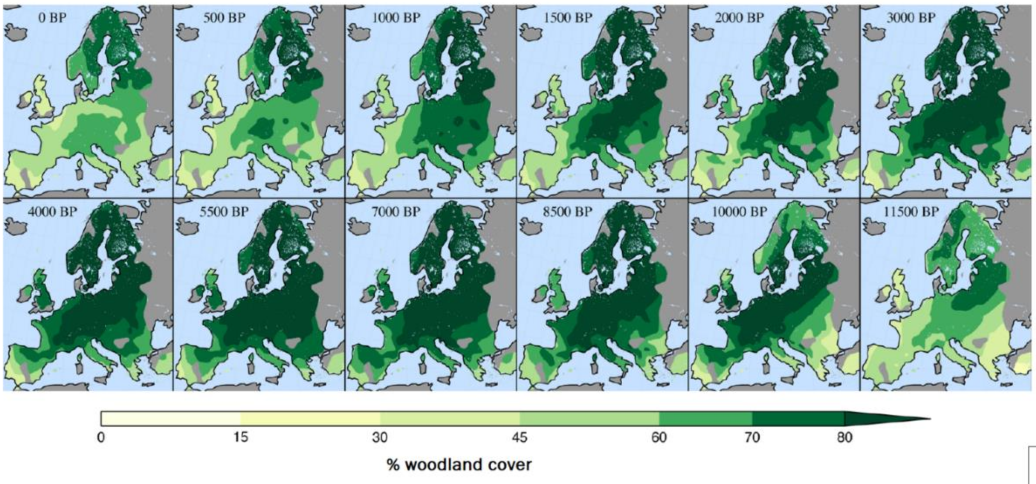
These methods are not fully quantitative because they divide pollen assemblages in categories, and a specific pollen taxon can only fit into one PFT/LCC category. For some taxa, this is not problematic, however, for other taxa (e.g. Poaceae, grasses) this is. Furthermore, once those PFT/LCC categories are made, it becomes unclear what the exact vegetation composition of each category is. The LCC affinity scores tell something about the openness of the landscape, and on average what kind of vegetation one might expect in a certain category, but it does not take into account the differences within and between the same category. The pseudobiomisation approach is not based on a thorough understanding of pollen-vegetation relationships, but it does a better job at making large scale land cover changes insightful than just the use of AP/NAP ratios (Fyfe *et al.* 2010). They do a decent job at this, although one could argue that with the application of REVEALS to superregional scale, the viability of these methods is in question, because of the possibility of REVEALS to give more detailed information about the past vegetation cover and the changes in the vegetation cover. Improvements to these methods might come from the amount of ecological categories used, or the differentiation between these ecological categories. One of the main advantages of the pseudobiomisation approach is the scale of reconstructions, besides the quick application of the method (Fyfe *et al*. 2015).

The PFT approach produces superregional vegetation maps, useful to make changes in the vegetation insightful. The pseudobiomisation approach only plots the LCC affinity scores, which is a measure of openness. Plotting the LCC together with time shows the relative change through time, but as stated before, both methods give no insight into the actual composition of the vegetation, just in the cover of biomes and the changes of cover through time. There is low uncertainty using this method, because of its lack of much detail, which is an advantage. Some uncertainty can come from the use of the PFT assigning algorithm. The PFT approach uses an algorithm developed in the 1990s (Peyron *et al*., 1998, in: Davis *et al*. 2015), which may need review or revision. Furthermore, this algorithm is specifically developed for Europe, which means that for each geographical region, an optimised version of a standard algorithm needs to be developed, if this method is to be implemented on the global scale.

The use of PFT in the mapping of contemporary land use is a more successful approach, but even there, producing PFT data from satellite data shows that there is disagreement between these methods too (Poulter *et al*. 2011). The disagreement often stems from the definition of land cover categories, which were too broadly defined. Each pollen taxon is furthermore only ascribed to one ecological category it complicates the use of this method even more. This shows that generalisations of vegetation categories, although useful to map land cover on a global scale, still shows a lot of uncertainty. The pseudobiomisation approach was also compared to remote sensing data and showed a good correspondence between proportions of LCCs for both methods, but at small scales, there were large difference between the methods at a site-specific level (Woodbridge *et al*. 2014).

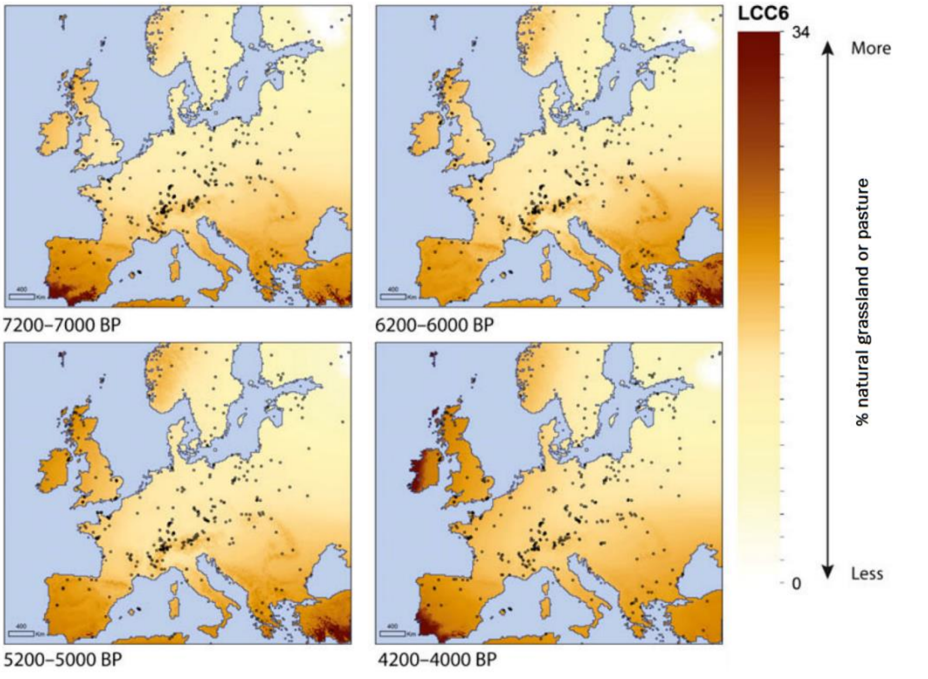
### 3.4.3. Applicability of the models

The pseudobiomisation approach has gained some attention in recent years, although it has been exclusively applied to reconstruct the forests of Europe (Woodbridge *et al*. 2014, Fyfe *et al.* 2015, Roberts *et al*. 2018) and the same goes for the PFT approach (Davis *et al*. 2015, Roberts *et al*. 2018). The use of the pseudobiomisation and the PFT approach shows large uncertainties at the site-level, which means that a lot of sites need to be used to come to a certain reconstruction. For Europe and perhaps North America, this is not an issue, because plenty of pollen records are available (for example, see the Neotoma Palaeoecology Database for availability of pollen records across the world). For other continents, however, this might prove more challenging, which poses a major problem to the application of the methods on a global scale.



5a

5b



7200–7000 BP

6200–6000 BP

5200–5000 BP

4200–4000 BP

**Figure 5a**. Woodland cover map for Europe, showing changes over time in 500 years. Detail from a figure from Davis *et al*. 2015.
**Figure 5b**. Pasture/natural grassland cover in Europe per 1000 years for periods of 200 years. Detail from a figure taken from Fyfe *et al*. 2015.

The PFT approach interpolates PFT-abundances from the pollen sites used in the study onto a 1° grid using a 4D thin plate spline (latitude, longitude, altitude, time) (Davis *et al*. 2015), see figure 5a for an example. This approach is useful for HYDE, because it makes cover (open/closed, anthropogenic land) insightful on the scale already used in HYDE. The pseudobiomisation approach groups pollen taxa in similar groups like the PFT approach and then interpolates the results on a vegetation map using a thin plate spline (Fyfe *et al*. 2015). The method can only place 'pure' LCCs on a map, and placing semi-open LCCs occurs by using thresholds between open and closed landscapes. Figure 5b shows an example of a pseudobiomisation vegetation map for meadows. The spatial resolution of the cells is around 20km. This may seem small, but the scale of the reconstructions ultimately becomes superregional due to the use of many sites (where available). This makes the approach useful for the global carbon cycle models, including HYDE. The method is inaccurate at the small scale, meaning that archaeological or local vegetation investigations are not appropriate for this method. The scale of the reconstructions, combined with the fact that the reconstructions are highly uncertain at the local scale makes the pseudobiomisation and the PFT approach less suitable than the LRA, MSA, or EDA approaches for regional studies. To conclude, the two indicator species approaches have shown to work well on superregional scale, but lack this power on a smaller scale. For HYDE, they could be used to improve the method, although as said before, the PFT and pseudobiomisation approach both come with more uncertainties than the LRA, although it is a quick method to reconstruct the past land cover.

### 3.5. Bayesian modelling: the Paciorek and McLachlan Bayesian model (Paciorek and McLachlan 2009), and STEPPS (Spatio-Temporal Empirical Prediction from Pollen in Sediments, Dawson *et al*. 2016)

#### 3.5.1. Background of the models

The application of Bayesian modelling in biology has gained a lot of attention in recent years, and an approach has been developed to model past forest composition using pollen data, and historical data on the abundance of trees (Paciorek and McLachlan 2009, Dawson *et al*. 2016). This method is now formally known as STEPPS (Spatio-Temporal Empirical Prediction from Pollen in Sediments), although the approach is similar to the more informally named Paciorek and McLachlan Bayesian modelling approach. These models have been applied to reconstruct American forests. First, the model uses historical and contemporary data on tree abundance and pollen data from sediment cores that match the period for which tree abundance was scored, to model the relationship between pollen assemblages and vegetation abundance (Dawson *et al*. 2016). Subsequently, this relationship is used to predictively model plant abundance for periods for which no tree abundance data is available, using pollen data as a proxy, and assuming the relationship pollen-plant abundance does not change over time (Paciorek and McLachlan 2009). The predicting model can plot the results on a vegetation map and place it in the correct time. STEPPS can function without the need for parameters that the other PBR methods use (e.g. PPEs, fall speed of pollen), and instead uses historical data for the calibration of a predictive model (Paciorek and McLachlan 2009, Dawson *et al*. 2016).

#### 3.5.2. Critical analysis of the methods

The estimation and prediction model rely heavily on statistical knowledge borrowed from statistical ecology and other related disciplines (Paciorek and Mclachlan 2009). It is a method to describe changes in the composition of woodland areas, but is not applicable to other landscape types, because it relies on surveys of past vegetation abundance, which are likely only available for wooded areas. The approach itself is based on three major assumptions. Firstly, it assumes that the estimation model can accurately describe the relation between pollen assemblages and past tree abundance. It uses a self-learning algorithm that learns the relation of pollen data with tree surveys of early colonisers of North America, and uses this to predict the abundance of trees for areas that only have a pollen record. Secondly, it assumes that this relation does not change through time. And lastly, the method assumes that the predictive model can accurately translate pollen abundance into tree abundance and forest composition. The use of historical data for untouched wooded areas, however, is limited to only a few areas. It works in north America, because it was a relatively untouched landscape. Other areas in the world are less untouched, especially Europe, so the method is not applicable in these areas. This means too that these Bayesian models using historical data are unsuitable to be used in a global land use model are, and therefore, the applicability of the Bayesian models will not be discussed in a separate chapter.

The model produces coverage data for all taxa included in the form of heatmaps, thus different categories of abundance get assigned different colours (see figure 6. However, because only arboreal taxa are included in the analysis, the vegetation maps coming from this analysis or not useful for HYDE at the moment. They only focus on woodland, which is only a small part of the total possible landscape. In itself, this does not mean that the method is unsuitable to supplement HYDE, it just needs to include other land cover categories in the future.

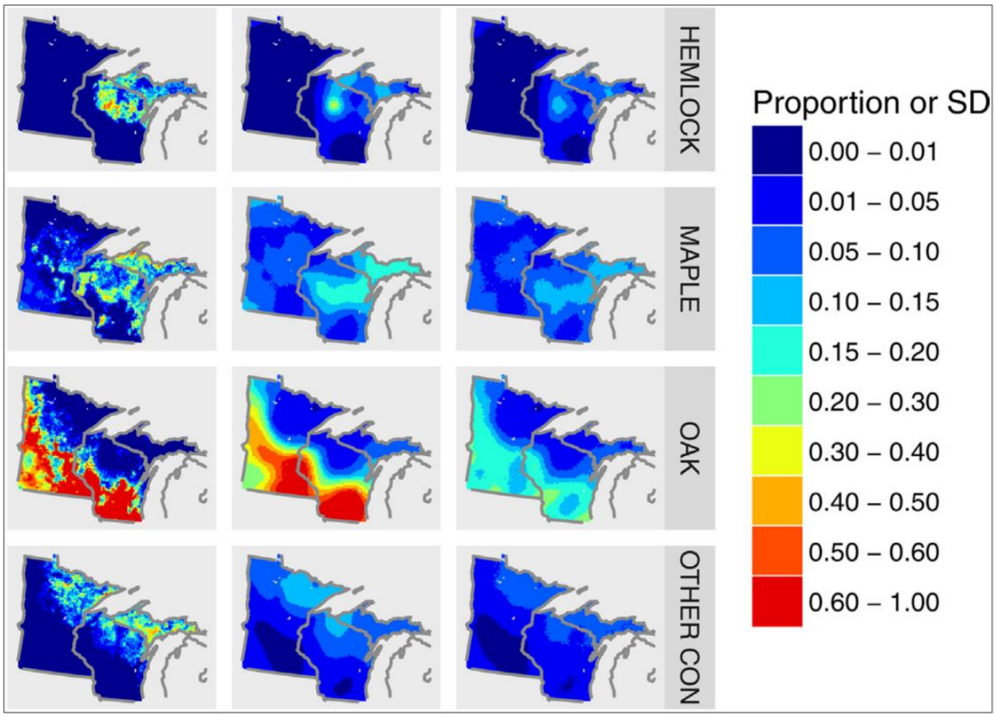


**Figure 6**. Heatmaps for 4 different taxa of reconstructed woodland in the north-eastern USA. Detail from a figure from Dawson *et al*. 2016)

## 4. Discussion

> *"Essentially, all models are wrong, but some are useful."*
>
> --- George Box, 1987 p. 424

This quote from statistician George Box points out one of the most important things to keep in mind when using or analysing models, which is that models are simplifications of the truth and do not reflect reality. It is important to state, however obvious it may seem, that the PBR models reviewed in this paper are not true representations of the past landscape (McCoy and Ladefoged 2009, Richer and Gearey 2017, Caseldine *et al*. 2008, Edwards *et al*. 2015)). They are useful in some ways, but have limitations too. All PBR methods offer an improvement for the traditional uses of pollen analysis: they are a better representation of the past vegetation composition because they account for differences in pollen production, or other ecological constraints and sometimes topographical constraints. Each model offers an improvement, but all have their flaws too. I will first shortly discuss the ways in which HYDE can be improved, then general problems associated with all PBRs, and lastly discuss what each method can improve to HYDE. Table 3 (next page) shows an overview of all the PBR methods discussed in this paper.

### 4.1 General problems associated with Pollen-based Reconstructions

Hyde is a global land use model, and therefore highly dependent on methods that can possibly reconstruct the land cover on a national/continental/global scale. The model relies on estimations of past populations and historical land use. As discussed in section 2.1, PBR methods can improve HYDE in a number of ways and increase the certainty of the land use reconstructions. The hindcasting method for obtaining past population numbers and per capita land use. However, there are several pitfalls associated with the use of pollen in reconstructions. Some basic improvements to the use of pollen in reconstructions is the dating of the sediments from which the pollen is obtained. Dating of cores has to be done precisely and with a good strategy (i.e. attempting to obtain 2 dates per millennium, which constitutes a doubling of dates per core in most cases, Blaauw *et al*. 2018). Furthermore, age-depth models need to be constructed using Bayesian-modelling, because these models produce more reliable reconstructions and confidence intervals, than do the traditional methods, such as the linear interpolation method (Blaauw *et al*. 2018).

**Table 3**. Overview of pros and cons for each PBR method discussed in this paper.

| Model | Ease of use | Coverage | Output | Pros |
|---|---|---|---|---|
| REVEALS | Quick and dirty | Supra-regional: Europe, North America, China, Australia | % cover of pollen taxa | Most used PBR method |
| MSA | Time-consuming | Regional: UK | Vegetation maps | Detailed, smaller scale reconstructions; equifinality |
| EDA | Time-consuming | - | - | Equifinality |
| PFT | Fast | Supra-regional: Europe | Cover of land use categories | Quick method; produces cover in land use categories |
| PBM | Fast | Supra-regional: Europe | Cover of land use categories | Quick method; produces cover in land use categories |
| BayMod | Time-consuming | Regional: North America | Heatmaps, cover of individual taxa | Cover of pollen taxa |

| Model | Cons | Useful for HYDE? | Theoretical or empirically tested? | Rank of usefulness (1=most useful) | Source |
|---|---|---|---|---|---|
| REVEALS | Method improvements needed | Y | E | 1 | Sugita 2007a, 2007b |
| MSA | Coding and methodological improvements | Y | E | 3 | Bunting and Middleton 2009 |
| EDA | Not empirically tested | N | T | 4 | Theuerkauff and Couwenberg 2017 |
| PFT | Low detail, therefore more uncertain | Y | E | 2 | Davis *et al*. 2015 |
| PBM | Low detail, therefore more uncertain | Y | E | 2 | Fyfe *et al*. 2010 |
| BayMod | Model assumptions unrealistic | N | E | 5 | Paciorek and McLachlan 2009, Dawson *et al*. 2016 |

The uncertainties increase with decreasing amounts of dated samples, but this is the case with all age-depth models.

To gain actual insight in the past vegetation communities, several factors that affect the production, distribution, preservation, and subsequent interpretation of pollen for palaeoecological questions need to be remembered. With regard to PPEs, used in most PBRs, there are problems with availability of this data, but also with the methodologies in which they are obtained. Pollen production depends on various factors, such as geographic location and the climatological conditions associated with the location, seasonality, pollen dispersal method (airborne, insects), and woodland management. A review of the methodology used in PPE estimation studies reported that PPEs for single taxa can differ greatly in nine study areas in Europe (Broström *et al*. 2008). Possible explanations for this are methodological issues or climate circumstances (Broström *et al*. 2008). Since it is impossible to control or negate climatic factors in field studies, it is essential that methodologies used are standardised and repeated. Farrell *et al*. (2016) showed that in woodlands and heathlands, PPEs are generally similar "to a reasonable degree" throughout the field season, showing that climate and seasonality variations are a small part of the large variety in PPEs recorded, and that a standardised method leads to smaller differences between single taxa at different sites. However, the reason for why such important work is often not carries out is simple: obtaining resources for these sampling studies is difficult (Farrell *et al.* 2016).

The number of pollen grains counted is important too, as it partly determines if a confident interference about vegetation communities in the past is made (Keen *et al*. 2014). A trade-off between time spent analysing pollen and the representability of the results needs to be made (Hill 1996). Another important factor, taphonomy, or pollen preservation, has been long established as a factor of importance in the analysis of pollen, and the representability of the analysis (e.g. Sangster and Dale 1961). Jackson (2012, p.13) points out: "[t]aphonomy is an unglamorous pursuit, yet it buttresses the inferential structure of palaeoecology … Neglect of taphonomy … [p]oses risks of ignorance creep [a process by which assumptions become taken for granted and ultimately hidden or forgotten], overconfidence, underestimation of uncertainty, and inferential errors". Although often forgotten, taphonomy is an important process that lies at the basis of interpreting fossil pollen records. Combined with the need for a representative pollen count, these are often the most likely to be overlooked. Pollen counts for the LRA need to be over 500, and for the MSA over 300, which means careful selection of previously published work is necessary. All PBR methods, however, ignore taphonomic effects on the pollen assemblages, but this is a direct result of these methods using previously published pollen diagrams, which often do not take taphonomy in account either.

Two final factors that are important in the creation of pollen assemblages and factors that influence the interpretation of the results following from pollen analysis are: pollen dispersal and deposition models and equifinality. Correctly modelling the trajectory of pollen is one of the main challenges in the application of PBR methods. The Prentice-Sugita model, currently used by the LRA and the MSA approach, is heavily built on mathematical assumptions of the relationship between pollen production, pollen source area, and landscape characteristics (Sugita 2007a,b). Other pollen deposition models, such as the Lagrangian stochastic model, is supposed to be a more accurate representation of pollen dispersal and deposition. However, from reading the publications that use the Lagrangian stochastic model, it remains unclear how the model is calibrated, and furthermore, how the superior performance of this model was determined (Theuerkauff *et al.* 2013, 2014, 2016). New modelling approaches need to be developed, perhaps using empirical data of pollen dispersal and deposition around individual trees, instead of assuming relationships that may not exist and using mathematics to explain these relations.

Similarly, another challenge is equifinality, which many PBR methods choose to ignore, or simply forget to incorporate. The MSA and the EDA both apply this principle by producing many (>$10^4$) vegetation maps of the reconstructed area, on the basis of ecological characteristics of plants, soil, and topography. They then simulate pollen assemblages from these maps, which are then compared to empirical pollen assemblages. Then statistical testing determines which of the simulated assemblages most resembles an actual pollen assemblage obtained in the field, and thus, which vegetation maps most likely resemble a representation of the past vegetation. Ignoring the problems of all the PBR methods outlined in the previous five paragraphs may lead to overconfidence in the models that exist today, which may lead "to failure to investigate ad exploit new generations of physical and biological models for pollen, release, dispersal and deposition" (Jackson 2012, p 13), and thus for PBR methods as a whole.

## 4.2 Pollen-based reconstructions reviewed

The following question was posed in the introduction of this paper: which PBRs can improve global land use models (i.e. HYDE), and in what way do they make this improvement? Although there are still some methodological problems associated with the use of PBR methods, these methods can still improve existing global land use models. Some methods are unsuitable for the improvement of HYDE: MARCO POLO (Mrotzek *et al*. 2017) and LOVE (Sugita 2007b), methods to reconstruct vegetation locally, because of their small scale reconstructions. In the case of LOVE, it means that for global reconstructions, the full approach of the LRA is not employed, instead, researchers rely solely on REVEALS. The Bayesian approach, although successful on larger scales, depends on historical data about untouched woodlands as input for its self-learning algorithm, to determine the relationship between past woodland abundance and past pollen abundance. This is a criterion that is perhaps only available in northern America, but not in Eurasia or Africa. And even in North America, there is evidence that the landscape has been greatly altered even before the arrival of European settlers, either by farming or woodland management by Native Americans (Coughlan and Nelson 2018, Ekdahl *et al*. 2004, Springer *et al*. 2010, Stinchcomb *et al*. 2011). These uncertainties make the two Bayesian models reviewed in this paper unsuitable. The other methods can each contribute to the improvement of HYDE, and they will be discussed below, in the same order used in the results section.

REVEALS can make an excellent contribution to the improvement of HYDE. It reconstructs the landscape for large areas ($10^5$-$10^7$ ha, per lake included in the reconstruction) and it produces results similar to normal pollen diagrams, namely the ratio of cover for each taxon included in the reconstruction. These land cover diagrams can be converted relatively easy in the proportion of each taxon for different time periods. They have been used in the reconstruction of Europe's land cover at a resolution of 1° grid cells (Kaplan *et al*. 2017). Although there are still some methodological issues, associated with the use of PPEs and the Prentice-Sugita model, HYDE can benefit greatly from the use of REVEALS in its reconstruction of past land use. The combination of past population estimates and assumptions of per capita land use within HYDE are unreliable because they are only partly based on actual evidence. Multiplying the two increases further uncertainty. HYDE reconstructions become more unreliable the further back in time the modelling goes, especially before 1700 CE, because data is sparse (Klein Goldewijk *et al*. 2017). Another major shortcoming is the assumption of constant land use patterns over time, which can be relieved by using REVEALS, because REVEALS can track changes in the proportion of open and wooded land cover time. For periods prior to 1700 CE, REVEALS also shows the total amount of land in use as grazing, or cropland, especially when the taxa are converted to PFT categories (Peyron *et al.* 1998, in: Davis *et al*. 2015). The output data is easily convertible to 1° grid cells, and with the introduction of global pollen databases (see a list in the reference section) it is easy to obtain data for most areas in the world, although most of the work is concentrated in Europe and North America. Some of the problems associated with REVEALS need still to be resolved. Some of the assumptions of the model are hard to be met in real landscapes, although model improvements might minimise the differences between modelled landscapes and actual landscapes.

The MSA can improve HYDE in areas where there are multiple distinct biomes in a small area, which REVEALS cannot reconstruct as REVEALS assumes the regional vegetation is homogenous. The MSA currently reconstructs areas up to 50x50 km ($2.5 \times 10^5$ ha, or ¼ of a 1° grid cell) and produces simulated vegetation maps that produce a pollen signal that can be compared to actual pollen assemblages. Statistical comparison of "real" versus "simulated" pollen assemblages, shows which of the corresponding vegetation maps are most probable as actual reconstructions of the past landscape. The method can distinguish between forest with pure strands of lime and oak or mixed oak-lime woodland, whereas REVEALS tells you only about the proportional cover of taxa. Another main advantage is the fact that the results can be quantitatively measured. Disadvantages of the method are the large amount of computing power required, and the time it takes to do the analysis. The MSA has been mostly applied in research within an archaeological framework, and can supplement HYDE in areas where there has been urbanisation since earlier times (medieval times and before) because it can more precisely point out which kinds of human influence are present in the landscape, and also point out where these places are in the landscape. The MSA is useful in regional reconstructions, although it is not calibrated to work on national or supranational scale, and it is mostly employable for answering archaeological questions, because it leaves room for the incorporation of "hypothetical scenarios". For example, after using the MSA, a most likely, or multiple most likely scenarios of the past landscape are found, and this then allows the researcher to use these hypothetical maps to simulate what would happen if villages/clearances/crop fields would appear in the landscape, and if this has an effect has on the pollen record. The MSA is useful and beneficial for archaeologists and palaeoecologists in reconstructing anthropogenic land use around towns and cities, which can greatly benefit HYDE, although the application of the MSA is restricted by the time it takes, and the smaller scale it uses.

The EDA is a largely untested method that also uses the principle of equifinality. It has not yet been used to reconstruct actual landscapes of the past and it is therefore an unlikely improvement to HYDE as of now. It is the only mechanistic model to uses a different pollen dispersal and deposition model than the Prentice-Sugita model, namely a Lagrangian stochastic model. It is claimed that the Lagrangian stochastic model is better at modelling the trajectory of pollen than the Prentice-Sugita model, but this is not evidenced by a comparison of the two methods. It uses similar assumptions as the MSA, and produces proportion values for all taxa included in the reconstructed area. It is therefore not very different to the MSA with the exception of the pollen dispersal and deposition model, but the MSA has the built-in possibility to use different pollen dispersal and deposition models. The MSA chooses to use the Prentice-Sugita model because it is the most used and most researched model and has therefore the presumed superiority over other models.

The two indicator species approaches (the PFT approach and the pseudobiomisation approach) reconstruct biomes based on the categorisation of pollen taxa into land cover categories (LCCs) or plant functional types (PFTs). These methods are the easiest to use, because they do not rely on the transformation of pollen percentages into land cover proportions, or the use of pollen dispersal and deposition models. This is also their largest disadvantage because it is therefore the least accurate method, which does not take differences in pollen production or dispersal into account. I would argue that a combination of the PFT or pseudobiomisation approach with REVEALS yields the best results for HYDE. REVEALS on its own gives produces cover of the area for certain taxa, and by using a PFT assigning algorithm it becomes more directly clear which land use classes the landscape was built up off. Using just a PFT or pseudobiomisation approach without correction for ecological differences between taxa is dangerous, because although it may look like a correct representation of a past landscape, the reconstructed landscapes then stack multiple mistakes on top of each other, which can lead to large calculation and representation errors. The method provides a quick method to convert pollen percentages or percentages of cover into a spatial representation with biomes, and is therefore very useful for the improvement of HYDE, but only if it is preceded by a REVEALS reconstruction. This approach would not be useful for the MSA, because the MSA already uses communities with known composition, and therefore, it makes the use of a PFT or pseudobiomisation approach obsolete.

## 5. Conclusion

Most of PBR methods discussed in this paper can provide an improvement to the land allocation method used in HYDE. There are still methodological issues associated with the use of the various PBR methods, but even with these issues, they still provide an improvement to HYDE. They are better at calculating total land use than using the hindcasting methods HYDE currently employs. PBRs can also improve the land use allocation process HYDE uses. PBRs do not resolve issues such as land use intensity or agricultural yields, but it does resolve the issue of determining the total amount of land used by humans. Furthermore, the MSA can show precisely where crop land and grazing fields are situated in the landscape, and which extent they reach. REVEALS is most suitable for use in large scale reconstructions at a resolution of 1° grid cells, and the MSA can fill in the details in areas where there is doubt to the accuracy of REVEALS. Although the EDA is a promising tool for the future, its lack of in the field application is currently keeping it from being fully usable in the improvement of HYDE.

Much research into past landscapes nowadays uses PBR methods. The LandCover6k working group within the PAGES (Past Global Changes) research initiative focuses on providing new insights into past land cover and land use, and mostly uses REVEALS as a PBR method. The newest edition of the Past Global Changes Magazine illustrates this focus on REVEALS perfectly (Gaillard-Lehmdal *et al*. 2018). Five articles use PBR methods, out of which 4 times REVEALS is used, and only once the MSA. Furthermore, there is one review article for the use of PBRs for the woodland cover in Europe, which reviews REVEALS, the PFT approach and the pseudobiomisation approach, but ignores the MSA. The current interest in PBR methods is still mostly focussed on REVEALS, and is used by a large variety of researchers, whereas the MSA has spread to other research groups, but is still used mainly in cooperation with Bunting. Although REVELAS, the PFT approach, and the pseudobiomisation approach are more useful at reconstructing larger areas, the MSA deserves a chance of resolving issues of uncertainty at a smaller scale within these bigger resolutions.

To conclude, the use of PBR methods can greatly improve the land allocation function in HYDE. REVEALS seems like the most logical option, because of the large scale of its reconstructions (relying on multiple pollen records), the overall global availability of pollen records, and the ease of use. If the results from REVEALS are then being categorised in land use classes using a PFT or pseudobiomisation approach, the results, i.e. proportions of land use categories, become very useful for HYDE. On smaller scales, where there is less uncertainty on the accuracy of the REVEALS reconstruction, i.e. in areas where the assumptions of REVEALS do not agree with the actual landscape, the MSA can be used to resolve the uncertainties. However, it must be said that the use of PBR methods is not without risk. The methods are not without risk or problems, although most papers present the results as being true representations of the past landscape. PBR methods can still benefit greatly from model improvements, or better pollen dispersal and deposition models. Overconfidence in current PBR methods is still one of the major issues to be solved.

# 6. Literature

## Pollen databases

African pollen database, available at: https://www.ncdc.noaa.gov/data-access/paleoclimatology-data.

Canadian pollen database, available at: http://www.lpc.uottawa.ca/data/cpd/.

European pollen database, available at: http://www.europeanpollendatabase.net/index.php.

Indo-Pacific pollen database, available at: http://palaeoworks.anu.edu.au/databases.html.

Neotoma, global pollen database, available at: https://www.neotomadb.org/.

North American pollen database, available at: https://www.ncdc.noaa.gov/data-access/paleoclimatology-data.

Pangaea, global pollen database, available at: https://www.pangaea.de/.

## Literature

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