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The global prevalence of Huntington’s disease: a systematic review and discussion

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PRACTICE POINTS

- Calculating something as simple as the prevalence of Huntington’s disease (HD) is problematic and contentious.
- Multiple sources are available to ascertain HD cases in a given population.
- Populations that employed diagnostic testing of HD have increased their ascertained prevalence measures over the last two decades.
- The estimated prevalence of HD in North America, North Western Europe and Australia ranges from 5.96 to 13.7 cases per 100 000 population.
- The ascertained prevalence of HD in Asia is much lower than Western populations.
- Using multiple sources for ascertainment of HD cases, although time-consuming, is more likely to determine the true prevalence of the disease in a given population.
**ABSTRACT**
The ascertained prevalence of Huntington’s disease (HD) increased significantly following the provision of diagnostic testing. A systematic review was conducted to estimate the prevalence of HD in the post-diagnostic testing era. 22 studies with original data pertaining to the prevalence of HD (1993-2015) were included and analysed. A global meta-analysis was not performed due to heterogeneity in study methods and geographical variation. The prevalence of HD is significantly lower in Asian populations compared to Western Europe, North America and Australia. The global variation in HD prevalence is partly explained by the average CAG repeat lengths and frequency of different HTT gene haplotypes in the general population. Understanding the prevalence of HD has significant implications for healthcare resource planning.

**Key Words**
Huntington’s disease – Epidemiology – Diagnosis

**INTRODUCTION**
Huntington’s disease (HD) is a slowly progressive autosomal dominant neurodegenerative disorder characterised by motor abnormalities, cognitive impairment and psychiatric disturbances [1]. The disease is caused by an expanded CAG triplet repeat in the HTT gene which encodes an abnormal polyglutamine expansion in the huntingtin protein [2].

HD was classically a clinical diagnosis made in the context of a positive family history of the condition. After the identification of the underlying genetic mutation in 1993 [2], diagnostic testing became widely available. This enabled clinicians to make a confident diagnosis of individuals with typical neurological features but without a known family history of the condition; this group may represent up to 10% of new HD cases [3]. As a consequence, the ascertainment of HD in populations has increased and the measured prevalence of HD in several populations is substantially higher in the post-diagnostic testing era [4–6]. Studies performed prior to 1993 may therefore underestimate the true prevalence of HD.

The management of HD requires the co-ordination of professionals from multiple domains including
neurologists, psychiatrists, psychologists, specialist nurses, physiotherapists, occupational therapists, social services and carer services. In order to allocate the optimal and appropriate amount of scarce resources, an accurate calculation of the scope of disease burden on the population is imperative. If previous estimates of prevalence underestimate the true prevalence, the current provision of health and social care services allocated to individuals with HD may be underequipped.

The second issue that arises from uncertain prevalence measures is that healthcare services are unable to identify the number of individuals at-risk of developing HD. The ratio of symptomatic individuals (prevalence) to individuals at 50% risk of developing HD has been described, on theoretical grounds, as being 1:5 [7] and approximately 1:4.2 in empirical studies [8,9]. At present, identifying these individuals is important to be able to offer predictive testing, genetic counselling, emotional support and recruitment for clinical research. In the future, characterising and quantifying this population is significant as future disease-modifying therapies may be targeted at gene positive individuals in the pre-symptomatic period of HD.

**AIMS**

The present study will attempt to:

1. Identify the published measurements of HD prevalence made in the era of diagnostic testing.
2. Reconcile the geographical variation in HD prevalence explaining the factors that determine variation in the true and ascertained (measured) prevalence of HD.

**METHODS**

**Search Strategy**

A systematic literature search was conducted using a predetermined protocol. Two computer-stored databases, MEDLINE (1993-2015) and EMBASE (Excerpta Medical Database; 1993-2015), were searched for studies investigating the prevalence of Huntington’s disease in a defined population. The search strategy was developed after consultation with a research librarian and is detailed in Appendix 1.

Further studies were identified from the following sources

1. Searching within references of relevant articles.
2. Searching for articles that cited the studies identified using the search strategy.
3. Information from articles on the uptake of predictive testing
4. Specialist textbooks on Huntington’s disease
5. Web searches.
6. Online databases [10,11]

Selection of Studies
All studies identified by the search strategy were screened by one reviewer (S.S.B.) who excluded those that were irrelevant. The abstracts of the remaining studies were screened by one reviewer (S.S.B.) who excluded studies which were not observational or did not investigate the epidemiology of Huntington’s disease. Full texts of all the remaining studies and assessed by two independent reviewers (S.S.B. and O.W.J.Q).

Inclusion/Exclusion Criteria
Articles were included based on the criteria established in Table 1. Studies performed prior to 1993 were excluded for two major reasons. Firstly, as diagnostic genetic testing became available in 1993, studies before this relied solely on a clinical diagnosis of HD and, as such, had the possibility of incomplete ascertainment of HD cases. Secondly, as discussed in greater detail in the discussion, there is a suggestion that the true prevalence of HD may be increasing as the life expectancy in the general population rises [4], the most current studies were felt to be of most relevance. In several cases, HD prevalence measures on populations made before 1993 had been repeated and updated; it is these recent studies with higher ascertainment that were included in the present analysis.

The measurement of the prevalence of HD in a population is typically performed through a cross-sectional, observational study. In some cases, where a registry for HD was established, the prevalence is established by means of a cohort study. Our qualification of observational studies is important as there are several studies published in the literature which estimate the prevalence of HD in different populations by using computational models based on the mean CAG repeat length in the general population and the common HTT
gene haplotypes rather than on observed data on the number of individuals with a diagnosis of HD.

**Data Extraction**

For each study, data extracted included the region studied, population size, prevalence date, sources of case ascertainment, diagnostic criteria, number of cases of Huntington’s disease, prevalence per 100 000 population and methodological limitations of the study. 95% confidence intervals were calculated for each prevalence estimate using the Agresti Coull method [12].

**Data Analysis**

Due to the heterogeneity between studies with respect to their methods of identifying, diagnosing and recording Huntington’s disease cases, it was felt to be inappropriate to combine all the studies and perform a meta-analysis to provide pooling statistics. Where pooled estimates were reported, a DerSimonian and Laird random effects model for the logit transformed prevalences was assumed. [13]. All calculation was performed using the meta package in R 3.2.3.

**RESULTS**

Figure 1 shows the selection of cases for the systematic review. 3397 studies were identified through MEDLINE, EMBASE, web searches, citation searches, searches within references from previous review articles and selected studies, textbooks and from prior knowledge. Titles were screened for 2030 non-duplicate studies and 217 abstracts were screened. 175 abstracts were excluded as they were either duplicates or did not meet the inclusion criteria. 41 full text articles and 8 conference abstracts were assessed in detail for eligibility with 19 excluded. In addition, twelve review articles on HD epidemiology were identified but searches through the references did not yield any additional studies [14–25].

Of the excluded studies: five estimated the HD prevalence before 1993 [26–30], four studied specific subgroups that were not representative of the whole population [31–34], four were not population-based observational studies and estimated the prevalence indirectly [35–38], two studied small geographical clusters of high prevalence [39,40], two had insufficient information regarding case ascertainment [41,42], one did not differentiate between symptomatic individuals and asymptomatic mutation positive individuals [43] and one
was not written in English [44].

Twenty-two studies examining HD prevalence (eighteen original articles and four conference abstracts) were included in the qualitative analysis. Fifteen studies were conducted in European populations, one in North America, two in Australia and four in Asia. The hypothetical global mean prevalence based on pooling all the data from the studies included in the present systematic review in a meta-analysis would be 5.5 per 100,000; however, the interpretation and application of this figure as an average global prevalence of HD would be inappropriate due to the heterogeneity between the included studies.

Table 2 details the results of the systematic review. It contains the ascertained prevalence of HD in different populations from four continents. Figure 2 shows a funnel plot of prevalence (per 100,000 population) against population size. The hypothetical global mean prevalence is shown as a dashed vertical line, as are 95% control limits. Significant overdispersion is evident, suggesting that variation in prevalence estimates is due to causes other than simple sampling variability. There is no evidence of a relationship between prevalence and population size, though regional differences are clearly seen.

Figure 3 shows Forest Plots representing studies of HD prevalence from four continents. Figure 4 illustrates the ascertained prevalence of HD in different studies geographically.

**DISCUSSION**

The present study is the most comprehensive systematic review of Huntington’s disease (HD) epidemiology conducted in the post-diagnostic testing era. It identifies prevalence estimates from populations in four continents and indicates marked variation in the prevalence of HD. It indicates that the ascertained prevalence of HD has increased significantly following the advent of diagnostic testing and details the higher prevalence of HD in European, North American and Australian populations relative to Asian populations.

The recorded prevalence of HD in several individual populations has increased after the introduction of genetic testing [4–6,9,45,46]. The study performed in Finland showed a four-fold increase in the prevalence of HD following the introduction of genetic testing [6]. This may partly be explained by the ability to diagnose...
individuals with a negative family history (new mutations, historical misdiagnosis in family members, non-penetrance, non-paternity) through genetic testing [1]. Additionally, as the life expectancy in the general population increases, individuals may present with HD in later life; this may be particularly relevant individuals with reduced penetrance alleles who develop symptoms in later life [4,47]. Other factors that may contribute towards the increase in recorded prevalence of HD over time include the use of diagnostic testing earlier in the course of the illness e.g. with early cognitive or behavioural symptoms with subtle motor symptoms in the context of a positive family history. In populations where the prevalence of HD has previously been low, increased clinician familiarity with the disease entity may contribute to the increase in recorded prevalence.

In the UK, two recent studies used primary care research databases to determine the current prevalence of HD which resulted in two strikingly different estimates of 5.96 [48] and 12.3 [5] per 100,000 of the population. The larger estimate, however, describes the prevalence in the over 20 population where HD is far more common. When the findings of Evans et al were combined with an additional publication by their group describing the prevalence of HD in the under-21 population [49], the HD prevalence in the UK in 2010 was estimated to be 9.28 per 100 000 population. The residual difference between the two primary care research databases remains unaccounted for.

There is significant global variation in the prevalence of HD. A substantial proportion of the measured differences in HD prevalence is secondary to variation in the true prevalence of HD i.e. geographical differences that would persist even if there was complete ascertainment of every case of HD. Nevertheless, this variation may, in part, be explained by factors that affect the complete ascertainment of individuals with HD. The possible reasons for differences in true and ascertained prevalence of HD are summarised in Table 3.

A major biological determinant of differences in the true prevalence of HD between populations is the mean CAG repeat length in the general population. Populations with a higher prevalence of HD e.g. European populations have been shown to have a higher mean CAG repeat length in the HTT gene in the non-affected population when compared to populations with a lower prevalence of HD e.g. Japan and China [50,51]. There is thought to be a causal relationship between the two factors as populations with a greater proportion of individuals with CAG repeat lengths in the high-normal range serve as a pool of potential new mutations with
expansion of the CAG repeat length in subsequent generations, first into the intermediate allele range (27-35 repeats) and then into the affected range (≥ 36 repeats) [47]. Another significant biological determinant of variation in the true prevalence of HD is the haplotype of the \textit{HTT} gene. Warby \textit{et al} (2009) determined that, in a European population, CAG expansion in the \textit{HTT} gene occurs with significantly increased frequency on two haplotypes, A1 and A2, compared to haplogroups B and C [52]. In East Asian individuals, however CAG expansions are associated most with haplotype C [53]. Warby \textit{et al} (2011) further demonstrated that these high risk haplotypes, A1 and A2, are present in 20% of the individuals from the general European population (with < 27 CAG repeats) but were absent in a sample of the general population of East Asia [53]. The proposed explanation of these findings is that the mutation rate of the CAG expansion in the \textit{HTT} gene is more likely to occur on haplotypes A1 and A2 because other \textit{cis} elements make these CAG repeat length on these chromosomes more unstable. As these haplotypes are more common in European populations compared to East Asian populations, this may explain the markedly higher prevalence of HD in the former. Thirdly, in geographically isolated populations such as Iceland and Malta, the founder effect may explain some of the variation seen. [54,55].

As mentioned, variation in HD prevalence may be explained by factors that affect the ascertainment of individual cases of HD when healthcare researchers attempt to determine prevalence measures. There are several data sources utilised by healthcare workers in order to identify individuals with HD; each of these has its own advantages, disadvantages, sensitivity, specificity and error rate. For instance, a study which takes data from a centralised testing centre which runs a regional HD service led by a small number of clinicians who are intimately involved in the local HD community and who actively characterise HD pedigrees in order to determine accurately the prevalence [4,56] is more likely to have a higher prevalence figure than a data source which relies on coding such as hospital discharge summaries.

Errors in the measured prevalence of HD prevalence can arise through multiple routes. For instance, if individual cases are not cross-referenced with death notifications, deceased individuals may incorrectly be included in point prevalence measures; in essence, the reported prevalence may in fact be the cumulative incidence over the study period. In addition, the onset of HD is insidious; therefore, ideally, a prevalence date needs to be a little earlier than the study date to allow for the fact that some individuals in the study
population will be symptomatic but undiagnosed at the time of the study but were affected at the time of the earlier prevalence date. Individuals who have been identified as having an abnormal CAG expansion through a predictive testing but who are currently presymptomatic should not be included within prevalence measures of HD. However, in studies where data on individuals with HD is extracted from the relevant administrative code on a large databases e.g. primary care records and national insurance databases, there is a possibility that some presymptomatic individuals may have been incorrectly coded as having a diagnosis of HD. This can be overcome by healthcare researchers accessing the clinical records of all cases of HD identified in large datasets to confirm the diagnosis, however, this requires additional ethical approval and a greater number of resources. There are a number of conditions which may be incorrectly diagnosed as HD but are not caused by an abnormal CAG expansion in the HTT gene. These conditions, termed ‘HD phenocopy syndromes’ can clearly be ruled out by the use of diagnostic genetic testing, however, in individuals with a purely clinical diagnosis of HD, upto 1% of cases actually represent HD phenocopy syndromes [57]. Further, poor response rates and incomplete information from clinician surveys, family surveys and family pedigrees can lead to an underascertainment of cases.

The use of multiple sources to identify individuals with HD has been instrumental in improving the ascertainment of HD prevalence. In British Columbia, the use of several sources for identifying individuals with HD yielded the highest prevalence estimate of HD in a Western population [4]. The issues that arise with multiple source ascertainment include its time-consuming and costly nature, the possibility of including the same individual twice or more in prevalence measures (‘double-counting’) and the practical difficulties in carrying this out in a large population.

A key limitation of the current study is the absence of studies that were not conducted in the English language. The authors are aware of one such study in the San-in area of Japan [44]; however, the estimated prevalence in the abstract of this study does not appear dissimilar to quoted figures from Japan in 1996 [58] and 2015 [59].

Conclusions
The present study demonstrates an increase in the ascertained prevalence of Huntington’s disease (HD) in several populations and indicates marked global geographical variation in the prevalence of the disease which is likely explained by the mean CAG repeat length in the unaffected population, HTT haplotypes and the variable use of multiple sources of ascertainment to determine the prevalence of HD. Optimising the ascertainment of HD cases in a given population requires the recording of cases from multiple sources with safeguards to prevent double-counting of individuals in the reported estimates.

FUTURE PERSPECTIVE

Five studies on HD prevalence were published in 2015 suggesting there is continued interest in the epidemiology of HD [6,39,46,59,60]. Accurately characterising the prevalence of the condition is necessary to allocate the optimal amount of resources for health and social care resource provision, research funding and psychological counselling.

The aim of the future treatment for HD is to alter the natural history of the disease. Ideally, treatment should start in the pre-symptomatic phase. The ratio of 50% at-risk individuals to symptomatic individuals is either 4.2:1 or 5:1 [7,8]. There are currently several active clinical trials for drug therapy in HD; if even a single study shows a neuroprotective effect, it is likely that the demand for predictive testing services will markedly increase. Therefore, accurately determining the prevalence of HD, and thereby the at-risk population size, may become increasingly important in the future.

REFERENCES

   **This is an important up to date and authoritative review of Huntington’s disease.

   **This paper describes the identification as an unstable expansion of the CAG repeat length as the cause of Huntington’s disease.


This paper is the most recent estimate of the prevalence of Huntington’s disease using multiple methods of ascertainment.


*This paper describes the latest estimate of the prevalence of Huntington’s disease in the UK. It gives the prevalence for the population ≥21 years and needs to be read in conjunction with the paper from Douglas et al 2012 (Ref 49) if a comparison is to be made with other prevalence studies.


* This paper needs to be read in conjunction with Evans et al 2013 (Ref 5). It focuses on the UK
prevalence of patients with Huntington’s disease who are ≤20 years.

   * This paper and the the one below are important for understanding the difference in CAG repeat lengths in different populations

   *This paper and the one above are important for understanding the difference in CAG repeat lengths in different populations.

   ** This paper and the one below describes HD mutations occurring on different haplotype backgrounds and provides evidence for true differences in the prevalence of HD in different populations.

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**FINANCIAL AND COMPETING INTERESTS DISCLOSURE**

The authors have no relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript. This includes employment, consultancies, honoraria, stock ownership or options, expert testimony, grants or patents received or pending, or royalties.

No writing assistance was utilized in the production of this manuscript.
APPENDIX 1

Search strategy of electronic databases (EMBASE and MEDLINE).

Search History
1. EMBASE; (Huntington* AND prevalence).ti,ab [Limit to: Publication Year 1993-2015]; 292 results.
2. EMBASE; (Huntington* AND population).ti,ab [Limit to: Publication Year 1993-2015]; 718 results.
3. EMBASE; (Huntington* AND incidence).ti,ab [Limit to: Publication Year 1993-2015]; 151 results.
4. EMBASE; (Huntington* AND epidemiology).ti,ab [Limit to: Publication Year 1993-2015]; 54 results.
5. EMBASE; 1 OR 2 OR 3 OR 4 [Limit to: Publication Year 1993-2015]; 1022 results.
14. EMBASE; exp HUNTINGTON CHOREA/; 19324 results.
15. EMBASE; (prevalence OR population OR epidemiology OR incidence).ti,ab; 2278710 results.
16. EMBASE; 14 AND 15; 1194 results.
17. EMBASE; 5 OR 16 [Limit to: Publication Year 1993-2015]; 1199 results.

Date of search: 19/10/2015.
**FIGURES**

*Figure 1:* Flow chart of systematic review procedure for identifying and selecting studies for reporting the prevalence of Huntington’s disease in discrete populations.

- **Identification**
  - Records identified through database searching \((n = 3397)\)
  - Additional records identified through other sources \((n = 11)\)

- **Screening**
  - Records after duplicates removed \((n = 2030)\)

- **Eligibility**
  - Records screened \((n = 2030)\)
  - Records excluded \((n = 1989)\)

  - Full-text articles excluded (insufficient information, not an observational study, date of prevalence measured before 1993, studied subgroup of the population or a small geographical cluster) \((n = 19)\)

- **Included**
  - Full-text articles assessed for eligibility \((n = 41)\)
  - Studies included in qualitative synthesis \((n = 22)\)
Figure 2 - Funnel plot of population size against HD prevalence using data from studies meeting the inclusion criteria.
### Figure 3

Forest plots of studies of Huntington’s disease prevalence by continent.  
A – Europe, B – North America, C – Australia, D – Asia.
Figure 4 - Ascertained Prevalence of Huntington’s Disease in Different Populations (1993-2015). Bubble diameter proportional to prevalence per 100 000 population. (Figure created using http://cartodb.com)
**Table 1 - Study Design and Selection Criteria**

<table>
<thead>
<tr>
<th>Study Design</th>
<th>Population-based observational studies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Criteria for Studies</td>
<td>Defined population</td>
</tr>
<tr>
<td></td>
<td>Ascertainment of symptomatic cases of Huntington’s disease</td>
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<tr>
<td></td>
<td>Study conducted from 1993 onwards</td>
</tr>
<tr>
<td>Population</td>
<td>Individuals with a diagnosis of Huntington’s disease.</td>
</tr>
<tr>
<td>Outcomes</td>
<td>Prevalence of Huntington’s disease in defined geographical populations.</td>
</tr>
<tr>
<td>Region</td>
<td>Prevalence Date</td>
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<tr>
<td>------------------------</td>
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</tr>
<tr>
<td>EUROPE</td>
<td></td>
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<tr>
<td>Finland</td>
<td>2010</td>
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<tr>
<td>Iceland</td>
<td>2007</td>
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<tr>
<td>Northern Ireland</td>
<td>2001</td>
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<tr>
<td>United Kingdom</td>
<td>2008</td>
</tr>
<tr>
<td>Wales (South Wales)</td>
<td>1994</td>
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<tr>
<td>Italy (Modena and Reggio Emilia)</td>
<td>2013</td>
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<tr>
<td>Italy (Molise)</td>
<td>2013</td>
</tr>
<tr>
<td>Greece</td>
<td>2008</td>
</tr>
<tr>
<td>Country (Region)</td>
<td>Year</td>
</tr>
<tr>
<td>-----------------</td>
<td>------</td>
</tr>
<tr>
<td>Spain (Navarra)</td>
<td>2014</td>
</tr>
<tr>
<td>Slovenia</td>
<td>2006</td>
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<tr>
<td>Russia (Bashkortostan)</td>
<td>2012</td>
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<tr>
<td>Canada (British Columbia)</td>
<td>2012</td>
</tr>
<tr>
<td>Australia (New South Wales)</td>
<td>1996</td>
</tr>
<tr>
<td>Australia (Victoria)</td>
<td>1999</td>
</tr>
<tr>
<td>Japan (San-in area)</td>
<td>1993</td>
</tr>
<tr>
<td>Japan</td>
<td>Unspecified</td>
</tr>
<tr>
<td>South Korea</td>
<td>2013</td>
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<tr>
<td>Taiwan</td>
<td>2007</td>
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**Legend for Table 2**

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>HR</td>
<td>Hospital Records and Hospital Discharge Registers</td>
</tr>
<tr>
<td>CR</td>
<td>Clinic Records</td>
</tr>
<tr>
<td>CS</td>
<td>Clinician Surveys</td>
</tr>
<tr>
<td>Lab</td>
<td>Genetic Testing Laboratories</td>
</tr>
<tr>
<td>CTC</td>
<td>Centralised Testing Centre</td>
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<tr>
<td>HDR</td>
<td>Huntington’s Disease Registry</td>
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<tr>
<td>RDR</td>
<td>Rare Disease Registry</td>
</tr>
<tr>
<td>PCD</td>
<td>Primary Care Database</td>
</tr>
<tr>
<td>NHI</td>
<td>National Health Insurance Database</td>
</tr>
<tr>
<td>HDA</td>
<td>Huntington’s Disease Association</td>
</tr>
<tr>
<td>FS</td>
<td>Family Surveys and Family Pedigrees</td>
</tr>
<tr>
<td>NH</td>
<td>Nursing Homes</td>
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<tr>
<td>VA</td>
<td>Veteran Affairs</td>
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<tr>
<td>SS</td>
<td>Social Services</td>
</tr>
<tr>
<td>DC</td>
<td>Death Certificates</td>
</tr>
<tr>
<td>THIN</td>
<td>The Health Improvement Network</td>
</tr>
<tr>
<td>GPRD</td>
<td>General Practice Research Database</td>
</tr>
</tbody>
</table>
### Table 3 - Factors that may explain the geographical variation in HD prevalence.

<table>
<thead>
<tr>
<th>Differences in the true prevalence</th>
<th>Average length of CAG repeat in the unaffected population which correlates to the new mutation rate [50,51]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Frequency of A1 and A2 HTT haplotypes in the unaffected population. [53]</td>
</tr>
<tr>
<td></td>
<td>The founder effect in small, geographically isolated populations. [54,55]</td>
</tr>
<tr>
<td></td>
<td>Life expectancy in the general population. [47]</td>
</tr>
<tr>
<td>Differences in the ascertainment of HD cases.</td>
<td>Sensitivity and specificity of the data sources used for case ascertainment.</td>
</tr>
<tr>
<td></td>
<td>The use of single or multiple sources for case ascertainment.</td>
</tr>
<tr>
<td></td>
<td>Ease of accessing healthcare services in order to diagnose HD.</td>
</tr>
<tr>
<td></td>
<td>Clinician familiarity with HD as a disease entity.</td>
</tr>
<tr>
<td></td>
<td>The presence of large private or informal healthcare sector leads to an underascertainment of HD cases in national registers.</td>
</tr>
<tr>
<td></td>
<td>Different incentives to hide a diagnosis of HD depending on local social stigma, real or perceived employment discrimination or insurance-based healthcare provision.</td>
</tr>
</tbody>
</table>