Measuring the impact of chronic pain in the UK Biobank: the Chronic High Impact Pain Project (CHIPP)

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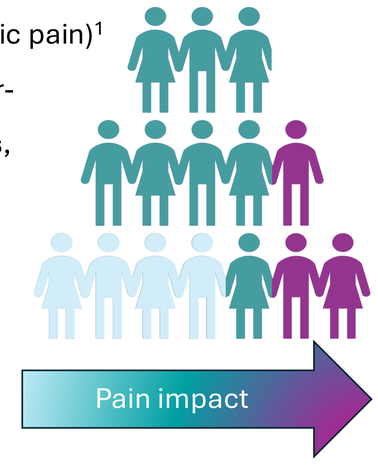
Come and find me if you have any questions!

Lay summary

- The **Chronic High Impact Pain Project (CHIPP)** aims to identify patterns of chronic pain impact that can be used to understand its causes and how it changes over time
- This analysis demonstrates that **some people with chronic pain experience impact in similar ways** to others, and there may be up to four groups of "chronic pain impact"
- This project will enable high impact chronic pain to be recognised earlier, leading to new treatment targets and **better outcomes for patients**

Introduction

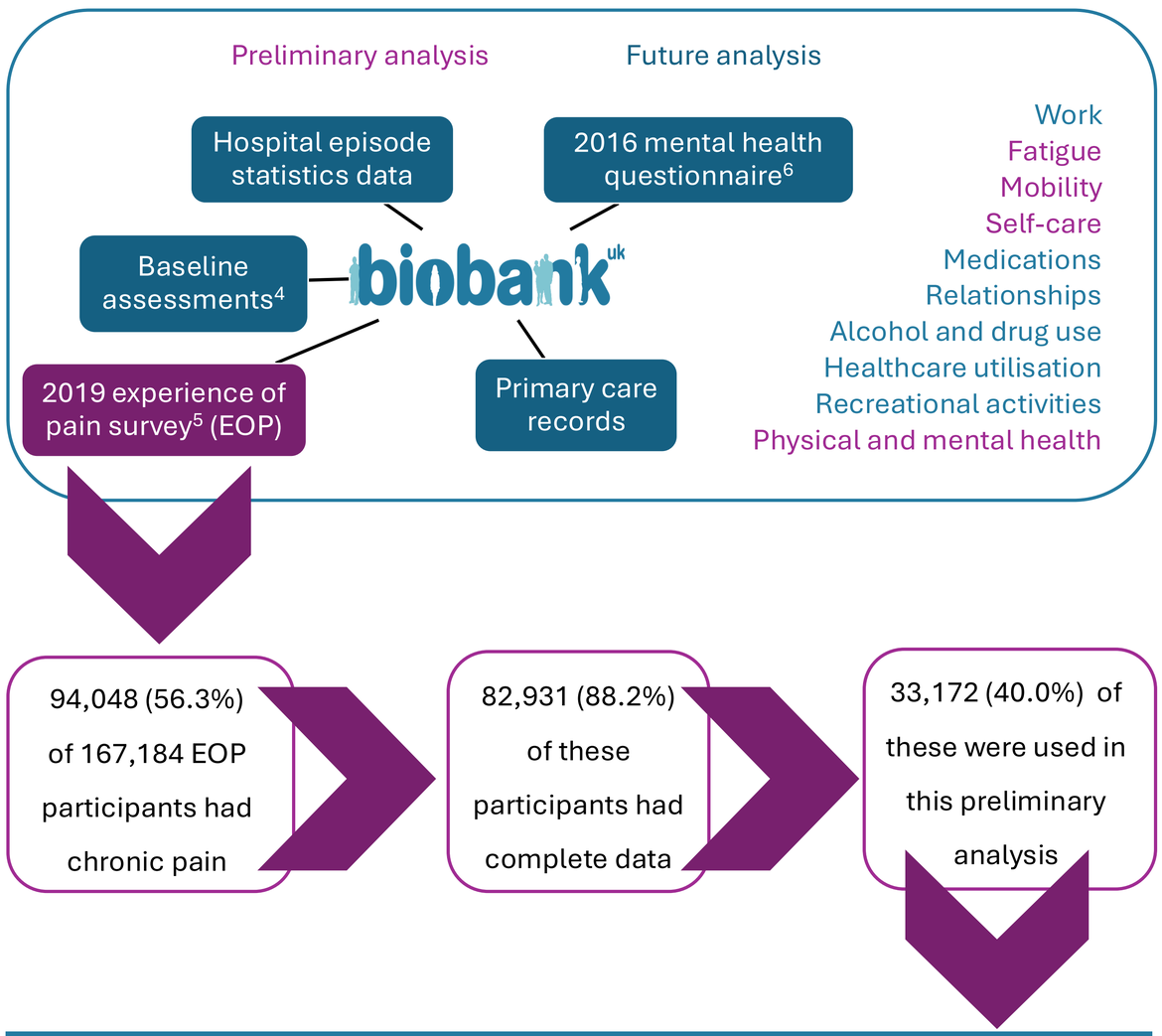
- ~ 50% of UK adults have pain for > 3 months (i.e., chronic pain)[1]
- ~ ¼ of these report high-impact chronic pain (HICP); far-reaching, negative impact, leading to disability, distress, social isolation, and high healthcare needs[2]
- Assessments of HICP include:
  - Graded Chronic Pain Scale-Revised (GCPS-R)[2]
  - The Brief Pain Inventory (BPI)[3]
- Aspects of impact not captured in these scales



Aims

- To estimate the prevalence of HICP in the general population
- To use 'clustering' methods to separate people into groups with similar traits
- To identify novel patterns of impact that can be used in future analyses in CHIPP
- Ultimately, to examine the causes of HICP and to identify treatment targets

Data selection



Data processing

- Participants with missing data were removed from analysis
- Binary variables or Likert scales converted to numeric and scaled to normalise:
  - PHQ-9 (Anxiety and depression scale)
  - FSS (Fatigue severity scale)
  - EQ-5D-5L (Quality of life metric), weighted to recommendations for England
- Variables were included individually, not combined into single scores
- Future work will include numeric and categorical data

Data analysis

- Uniform Manifold Approximation and Projection (UMAP) and Principal Components Analysis (PCA) for visualisation
- K-Means, an unsupervised clustering algorithm, to group similar participants away from dissimilar participants
- Optimal number of clusters identified using a scree plot
- Analysis carried out using R version 4.1.1 (2021-08-10), using packages 'uwot', 'tidyverse' and 'factoextra'

Preliminary results

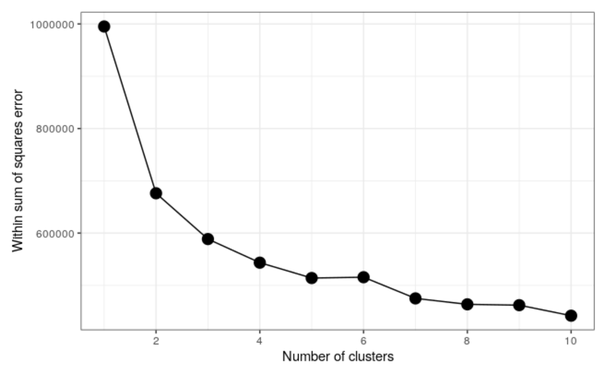


Figure 1: Scree plot of K-means clustering algorithm

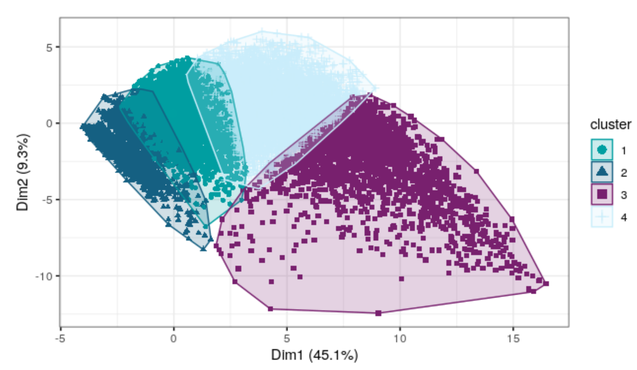


Figure 2: PCA of clusters identified by K-means clustering algorithm

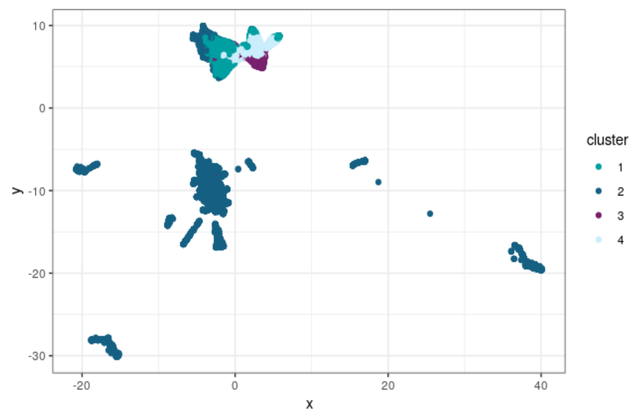


Figure 3: UMAP showing clusters identified by K-means clustering algorithm

- Clusters evident within the data
- Scree plot suggests K-means identifies 4 clusters
- K-means does not discriminate well between clusters
- Total Within Sum of Squares (WSS) in K-means = 45.2%
- UMAP suggests 2-4 clusters

Discussion

- K-means clustering is computationally efficient but requires complex data to be in a single simple format, which can lead to less meaningful results
- Clustering algorithms suitable for complex data likely to improve performance
- Future research will investigate how clusters of HICP change over time and whether these clusters exist in other datasets, so that definitions can be agreed
- This will enable future research to facilitate early identification and recognition of HICP, empowering patients and healthcare professionals to make informed decisions

Acknowledgements and disclosures

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