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ABSTRACT

Ageing, Health and Predicting Future Employment Exits: A Penalised Regression Approach*

We examine the role of baseline health in predicting future employment exits, alongside established socioeconomic, job-related and demographic predictors. Using UKHLS, we track employed respondents over 10 years to assess subsequent employment exits. Baseline health is captured using an unusually rich set of measures: self-assessed health (SAH), self-reported diagnosed conditions, psychological distress, allostatic load (composite biomarker index), and epigenetic biological age. Applying a LASSO penalised regression approach, we find that epigenetic biological age and SAH, rather than self-reported conditions, psychological distress, or allostatic load, predict subsequent employment exits, independent of other predictors. A Shapley-Shorrocks decomposition highlights epigenetic biological age as a stronger predictor than SAH. Nevertheless, chronological age is the dominant predictor of future employment exits. Epigenetic biological age measures do allow us to disentangle the role of chronological age, mainly reflecting institutional structures such as retirement eligibility and societal norms, from other contributions that capture age-related health decline that are more directly reflected in epigenetic biological age measures.

JEL Classification: C5, I10, J01, J20

Keywords: epigenetics, biological age, biomarkers, LASSO, supervised machine learning, employment exit, labour market

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1. Introduction

Ageing populations are having significant impacts on public finances - including public expenditure, labour tax revenues and social security contributions - as well as creating pressure on the sustainability of the public pension system (Galasso, 2008; Government Office for Science, 2016; Kim and Dougherty, 2020). In 2022 there were around 12.7 million people (or 19% of the total population) aged 65 or over in the UK (Barton et al., 2024). Office for National Statistics (ONS) population projections suggest that by 2072 this could rise to 22.1 million people, or 27% of the population (Barton *et al.*, 2024). The 2021 Census shows the number of people aged 65 years and over in England and Wales increased from 9.2 million (or 16.4% of the population) in 2011 to over 11 million (or 18.6% of the population) in 2021 (ONS, 2023).

Increasing life expectancy, associated with advances in social and economic development as well as in health care technology, significantly contributes to demographic change (Crimmins, 2015; United Nations, 2024). Concerns may arise about whether this reflects disability-free gains in longevity as well as highlights the need of distinguishing between chronological age and more direct measures reflecting the viability of the body, such as biological measures of age (Scott, 2020). It is therefore important to understand whether people are remaining in the workforce for longer, as opposed to spending more of their adult lifetime in retirement or other forms of economic inactivity prematurely (e.g., Galasso, 2008).

Enhancing our understanding of the risk factors that predict future decisions to exit the labour force for those who are currently employed may help us better characterise the profile of those who are more likely to exit employment prematurely. For example, existing policies that provide incentives to discourage earlier employment exits may not be sufficient if individuals cease working due to health-related issues. In that case, potential policies targeted at improving workforce health or implementing preventative interventions - such as flexible working arrangements to retain those experiencing health problems in the labour force - may be more effective (e.g., Bazzoli, 1985; García Gómez and López Nicolás, 2006; García-Gómez *et al.*, 2010; Jones *et al.*, 2010).

In this study, we explore the predictive role of baseline health in future labour market exits, while accounting for the potential influence of additional baseline factors, such as demographics (including chronological age), other human capital proxies (apart from health), job-related characteristics, and socioeconomic status measures. We use data from Understanding Society, the UK Household Longitudinal Study (UKHLS), focusing on respondents who were in *employment* (self-employed, in paid employment, or on maternity leave) at baseline (2010-13) and who were followed up in subsequent waves up to 10 years from baseline (covering the period from 2010-13 to 2021–22) to track future employment exits. Capitalising on an unusually wide range of health indicators in the UKHLS, we employ several measures to proxy baseline health: conventional self-assessed health (SAH), self-reported diagnosed chronic health conditions, a measure of psychological distress as well as a composite measure of nurse-collected and blood-based biomarkers (known as allostatic load) and epigenetic biological age measures.

There are many empirical studies in the broader literature exploring health and labour market outcomes (e.g., Bazzoli, 1985; Bound, 1991; Bound *et al.*, 1999; Chatterji et al., 2017; Datta Gupta and Larsen, 2010; Disney et al., 2006; García Gómez and López Nicolás, 2006; García-Gómez *et al.*, 2010; Jones *et al.*, 2010; Lenhart, 2019; Lin *et al.*, 2025; Lindeboom *et al.*, 2016; McGarry, 2004; Riphahn, 1999; Siddiqui, 1997). Most of these studies focus on older individuals and on the effects of health shocks on retirement decisions (Bazzoli, 1985; Bound, 1991; Bound et al., 1999; Chatterji et al., 2017; Datta Gupta and Larsen, 2010; Disney et al., 2006). Fewer studies examine the impact of health shocks on labour market outcomes employing working samples that also include younger individuals (e.g., García Gómez and López Nicolás, 2006; García-Gómez *et al.*, 2010; Lenhart, 2019; Lindeboom *et al.*, 2016).

Many of the existing studies investigating the relationship between health/health shocks and labour market outcomes rely on self-reported health measures, such as the SAH, self-reported diagnosis of certain conditions, and/or self-reported disability (e.g., Bound, 1991; Bound *et al.*, 1999; Gómez and López Nicolás, 2006; García-Gómez et al., 2010; Jones *et al.*, 2010; Lindeboom *et al.*, 2016; McGarry, 2004). Some related studies, however, employ more objective measures, such as date of death (to measure longevity at a certain time period) or registry-based hospital admissions data (e.g., Bound, 1991; Datta Gupta and Larsen, 2010; Lin *et al.*, 2025; McGarry, 2004).

It has been shown that measurement error in covariates can significantly affect the prediction performance of prediction models (e.g., Khudyakov *et al.*, 2015); this is of relevance to our prediction analysis of future employment exits based on individuals' baseline characteristics. There are several reasons to expect measurement error in self-reported health measures in research on health and labour marker/retirement outcomes. Self-reported health is inherently subjective, which limits comparability across individuals (e.g., Bound, 1991; García-Gómez *et al.*, 2010; Jones *et al.*, 2010). Moreover, individuals may misreport their health for various reasons: to rationalise being out of the labour force (the so-called "justification bias" in the economics literature) and/or due to potential financial incentives that some individuals may face to report ill-health as a means of obtaining disability benefits (García-Gómez *et al.*, 2010; Jones *et al.*, 2010; McGarry, 2004).[1]

More objective health measures used in some studies, while avoiding some of the subjectivity issues, are also not without limitations for prediction analysis. Specifically, longevity measures at baseline (based on subsequent mortality data) or hospitalisation records/diagnosis data do not necessarily capture an individual's future capacity to work (Bound, 1991).[2] For example, hospitalisation events may result from accidents, unexpected emergencies, or rapidly developing conditions that may not impair future employment (e.g., McGarry, 2004). Hospitalisation records may also reflect temporary health disruptions or routine procedures with minimal long-term impact on work capacity.

Our study contributes to the existing literature by providing an unusually broad set of health indicators to proxy health status at baseline and followed up in

[1] In the UK, individuals in poor health may exit the labour market with relatively minor financial consequences—a phenomenon referred to as the "disability route" into retirement (Blundell et al., 2002; Jones et al., 2010).

[2] Along these lines, a study of heart attack and stroke survivors in Taiwan has shown that low-income individuals are more likely to remain employed after the health shocks, and that those who were non-employed at baseline are more likely to start working, which could be attributed to increased financial needs following the health shocks (Lin *et al.*, 2025).

subsequent waves – these health indicators span the conventional self-reported health measure, self-reported diagnosis of chronic conditions, psychological distress, allostatic load, and, in particular, epigenetic biological ageing measures.

Epigenetic biological ageing reflects the interaction between genes and the environment through reversible mechanisms that regulate the function of the genome in response to environmental exposures and, thus, moderate the ageing process (Bafei and Shen, 2023; Davillas and Jones, 2025; Horvath and Raj, 2018). Davillas and Jones (2025) argue that biological ageing can be considered a more direct measure of cumulative adverse health exposures, depreciation over time, and health-related investments, in line with Grossman's seminal work (Grossman, 1972). As such, changes in physical functioning and psychological performance, resulting from the biological ageing process, as well as workplace exposure to adverse factors (physical, environmental, and organizational), are captured by biological age measures and, thus, these measures may be relevant to predict limitations in work capacity (World Health Organization, 1993).

Allostatic load provides a proxy for the "wear and tear" on the body caused by chronic exposure to stress (Geronimus *et al.*, 2006; McEwen and Seeman, 1999; Turner *et al.*, 2016); as such, this differs from epigenetic biological age, which shows how old the body really is at the cellular level. While both allostatic load and epigenetic biological age measures are influenced by a broad set of environmental exposures, lifestyle, and stress, they provide complementary insights into ageing and disease risk.

Given the range of potential predictors available in UKHLS, we use least absolute shrinkage and selection operator (LASSO) regression analysis to assess which health measures most accurately predict an individual's employment exits. LASSO is a supervised machine learning algorithm that performs variable selection and regularisation to enhance the accuracy and interpretability of the resulting predictive model for future employment exits (Tibshirani, 1996; Hastie *et al.*, 2015).[3]

[3] LASSO has two major advantages compared to OLS as outlined in the seminal work of Tibshirani (1996). First, LASSO sets some of the coefficient estimates exactly to zero (due to the L1 norm constraint) and, thus, removes these particular predictors completely from the model. As such, LASSO offers a model selection technique and better facilitates model

Our forward-looking analysis, that predicts future employment decisions based on individuals' baseline characteristics, could provide insights for policy-making. For example, given the demographic changes towards an older population, a higher proportion of inactive individuals relative to active workers can put further strains on public finances and social security systems (Galasso, 2008; Kim and Dougherty, 2020). Over and above these potential fiscal implications, it may be considered as a human capital loss at the country level if people leave the labour force prematurely. As such, obtaining more accurate and generalisable predictions of individuals' later-life employment decisions that are valid under real-world data is important. In this study, our adoption of supervised machine learning methods, particularly LASSO, is useful in this context as it facilitates the identification of predictors and enables accurate, generalisable predictive analytics of future employment exits of those in employment at baseline (Padula *et al.*, 2022).

Penalised regression methods predict future employment exits for those who are active in the labour market at baseline (self-employed, in paid employment, or on maternity leave), by selecting the subset of predictors from a pool of variables that minimizes out-of-sample prediction error (e.g., Tibshirani, 1996; Hastie *et al.*, 2015). Specifically, the LASSO estimator minimises the out-of-sample prediction error, balancing bias and variance to build an accurate predictive model. In other words, LASSO selects the predictors to be included in the model such that the fitted model is suitable for making out-of-sample predictions. LASSO, as a regularisation technique, aims to prevent overfitting and enhance predictive accuracy. As such, of particular interest is the fact that our analysis allows us to assess the predictive role of chronological age, after accounting for an unusually wide set of health proxies at baseline, including biological age measures, as potential predictors.

Evidence that chronological age is a strong predictor of future employment exits (over and above the role of other socioeconomic and demographic predictors

interpretation (Ahrens *et al.*, 2020; Tibshirani, 1996). Secondly, in terms of prediction accuracy, LASSO outperforms OLS. LASSO improves model generalization, i.e., an increased probability of generalisability of the findings to new data, by limiting the risk of overfitting and enhanced performance, as well as it offers a deeper insight into the underlying data generated processes (Padula *et al.*, 2022).

including respondents' baseline health proxies) may suggest a potential basis for lifespan-based employment decisions and policy structures, such as those related to retirement age. Specifically, in this context, identifying a predictive role for chronological age (net of the contribution of other factors) may reflect policy structures (like retirement eligibility) and societal norms on future employment decisions. Conversely, identifying which of our baseline health measures more accurately predict an individual's health-related work capacity and exits may provide valuable insights for policymakers on identifying which health dimensions are better reflected in individuals' subsequent employment exits, as well as on how to allocate resources towards facilitating continued work for people with health problems.

We find that biological age, rather than self-reported chronic health conditions, psychological distress, or the more objectively measured composite allostatic load measure, predicts subsequent employment exits. Moreover, in line with existing studies, the conventional SAH measure is also a consistently selected as a predictor by LASSO in our future employment exit models. Post-estimation analysis using Shapley-Shorrocks decompositions allows us to explore which of the selected predictors are more relevant in shaping individuals' subsequent labour market exits. We find that the contribution of biological age is much more pronounced compared to the role of SAH. However, chronological age exerts the dominant contribution to predicting subsequent employment exits. Additional analysis, where the epigenetic biological age measure is omitted from our set of potential predictors, shows that chronological age alone accounts for nearly all of the combined contribution of biological and chronological age. After adjusting for demographic and socio-economic predictors, epigenetic biological age measures allow us to disentangle the role of chronological age – mainly reflecting institutional structures such as retirement eligibility and societal norms - from other contributions that capture age-related health decline, reflected in epigenetic biological age measures.

2. Data

The UKHLS, also known as Understanding Society, is a nationally representative longitudinal study, with a design that involves overlapping 2-year waves. Each panel member has been interviewed annually since the initial wave (Wave 1) conducted between 2009 and 2010 (with only a few respondents interviewed up to March 2011). At UKHLS Wave 2, its predecessor, the British Household Panel Survey (BHPS), was incorporated into the UKHLS. Given the needs of our study, one relevant feature of UKHLS is the inclusion of biosocial data – such as nurse-collected physical health measures, blood-based biomarkers, as well as genetic and epigenetic markers (Benzeval *et al.*, 2023).[4]

Physical health measures and non-fasted blood samples were collected at nurse visits, conducted on average five months after the main Wave 2 interview (conducted between January 2010 and March 2012) for the UKHLS and similarly after Wave 3 (conducted between January 2011 and July 2013) for the BHPS sample. We pooled the UKHLS and BHPS nurse-visits sub-samples (Waves 2 and 3 for the UKHLS and BHPS sub-samples, respectively) to define our baseline, and we follow these participants in subsequent waves up to ten years from baseline, ending with UKHLS Wave 13 (where, more than 98% of the respondents were interviewed between 2021 and 2022). We focus on respondents who are employed at baseline (self-employed, in paid employment or on maternity leave) and who are followed up in subsequent waves. In each of the subsequent waves the current labour force status for each participant is collected.

We employ a set of different health measures (including composite biomarker and epigenetic biological age measures) to capture respondents health at baseline (Waves 2 and 3). Given the availability of the epigenetic biological age measures, our potential sample of *employed* respondents at baseline is restricted to those for whom the epigenetic biological age measures are recorded (2,080 individuals in total) — a sub-sample of the pooled Wave 2 (UKHLS sample) and Wave 3 (BHPS sample) of employed participants at baseline that is restricted (by survey design) to those for whom nurse visits were conducted, blood samples were taken and the epigenetic measure of biological ageing was available. Our working sample is

[4] Respondents were eligible for nurse visits (where physical health measures were taken by nurses) and for the collection of blood samples if they were aged 16 or over, lived in England, Wales or Scotland, were not pregnant, had no clotting or bleeding disorders, and no history of fits. Participants gave informed written consent for their blood to be taken and stored for future scientific analysis. Nurse data collection at UKHLS has been approved by the National Research Ethics Service (10/H0604/2).

restricted to follow-up respondents for whom labour market status measures are collected in at least one of the UKHLS Waves 7-13; this results in a sample of 1,655 respondents. This potential sample is further restricted to 1,089 individuals, after excluding missing data on our set of additional health measures (with the most significant reduction attributed to our composite biomarkers measure – allostatic load). Our final working sample is 1,071 *employed* respondents at baseline after excluding missing information on all additional predictors used in our analysis (demographic characteristics, human capital proxies, job-related factors, and socio-economic status). Table 1 provides the mean values for the employment exit outcome and all potential predictor variables included in our models.

To provide evidence on the potential implications of restricting our sample to valid epigenetic biological ageing and composite biomarker measures, Table A.1 (Appendix) shows comparisons of descriptive statistics between our final working sample of employed respondents (without missing data on all variables used in our analysis) and a comparison sample of employed individuals at baseline on whom we have imposed the same restrictions as our working sample without conditioning on having valid biological age data and data on our composite biomarker measure. Despite the considerable difference in the sample sizes between the two samples, mean values are similar between the two samples. This may suggest that conditioning on valid epigenetic biological ageing as well as composite biomarker measures alone (over and above restricting the data to employed participants at baseline with non-missing data on the remaining explanatory covariates as well as successive follow-ups at subsequent wave) may have limited impact on the comparability of our final working sample to the full, nationally representative UKHLS data.

Employment exits

As we are interested in prediction of subsequent employment exits, we focus on respondents who are employed (i.e., self-employed, in paid employment, or on maternity leave) at baseline (UKHLS Waves 2 and 3) and are successfully followed up in subsequent waves. We create a binary variable for employment exit that takes the value of one when individuals report being out of employment (unemployed, retired, on long-term disability/sick leave, or in family care) at any follow-up wave, and zero otherwise.[5]

We implement certain tasks to ensure that participants who leave employment at any point after the baseline remain out of employment throughout the period for which follow up data are available in our sample. Specifically, a few respondents who exit employment post-baseline and return for one or two short spells of employment at subsequent waves are treated as out of employment, as we are interested in their long-term employment outcomes at subsequent waves following baseline. In contrast, a few respondents (about 180 cases in total) who leave employment after the baseline but frequently transition in and out of employment across subsequent waves are excluded from the analysis.[6]

Health measures at baseline

We employ a large set of measures to proxy respondents physical and mental health at baseline (UKHLS Waves 2 and 3). Specifically, capitalizing on the richness of our available data, we use self-reported diagnosis of health conditions, SAH, GHQ scores to capture psychological distress, a composite biomarker measure (allostatic load) and epigenetic biological age; Table 1 provides a description of the relevant variables, along with their mean values.

Diagnosed Health Conditions

We account for pre-existing diagnosed health conditions obtained from self-reports made before the nurse visits (where biomarkers and blood samples used for

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[5] It should be noted that although the state pension age in the UK has been 66 for both men and women since 2020, there is no legal retirement age (with the abolition of compulsory retirement occurring at almost the same time as our UKHLS baseline Waves 2 and 3). Moreover, individuals can claim the UK state pension while continuing to work, as there is no earnings test (Cribb, 2023). In other words, employers can no longer force employees to retire at a particular age (although there are a few exceptions for certain jobs requiring specific physical abilities or where a mandatory retirement age is already established for a particular occupation). To further discourage premature retirement, UK policies focus on incentives for longer working lives, such as through partial and flexible retirement; this means individuals may reduce their working hours and draw down part of their pension while still employed. As such, there is no need to restrict our working sample to any specific upper age limit, as the law does not require compulsory retirement at any particular chronological age.

[6] Additionally, we exclude a few respondents who, despite being employed at baseline, report being in full-time education, on an apprenticeship, or working in an unpaid family business at any point after baseline.

estimation of the epigenetic age measures are collected) as part of Waves 2 (for the UKHLS sample) and 3 (for the BHPS sample). Specifically, we create a dichotomous variable that takes the value of one if the individual reported any diagnosis of a long-lasting health condition (asthma, chronic bronchitis, congestive heart failure, coronary heart disease, heart attack or myocardial infarction, stroke, cancer or malignancy, diabetes, high blood pressure, arthritis, and liver condition) before the baseline biomarker measurements were taken, and zero otherwise.

Self-assessed Health (SAH)

SAH measures are widely used in the economics literature (e.g., Currie *et al.*, 2015; García-Gómez *et al.*, 2010; Johnson, 2010), and known to be a strong predictor of people's future mortality risks (e.g., Jylhä, 2009). Despite concerns about reporting biases—such as justification bias due to its self-reported nature—SAH remains a common measure, either on its own or as a basis for constructing health shock variables, in studies examining the relationship between health and employment outcomes (e.g., Bound, 1991, Bound *et al.*, 1999; Dolls and Krolage, 2023; García-Gómez *et al.*, 2010; Jones *et al.*, 2010; Lenhart, 2019). In the UKHLS the SAH question collects responses on a five-point scale ranging from 1 = "excellent" to 5 = "poor" health. We group the worst two SAH categories (due to their small sample size), giving a four-point scale from 1 = "excellent" to 4 = "fair" or "poor" health.

The 12-item General Health Questionnaire (GHQ-12)

The GHQ-12 is a widely used measure of non-psychotic psychological distress (e.g., Chaudhuri and Howley, 2022; Cornaglia *et al.*, 2015; Davillas and Jones, 2021); it is characterised by excellent psychometric properties (Bowling, 1991; Goldberg *et al.*, 1997). The GHQ-12 is based on self-reports of 12 items designed to detect common psychological distress[7]; the underlining questionnaire uses a four-category scale indicating the extent to which participants have recently experienced particular symptoms or behaviours ('not at all', 'no more than usual', 'rather more than usual' and 'much more than usual'). Employing the Likert scoring method that sums all 12 dimensions, the continuous GHQ-12 index ranges

[7] Specifically, the 12 dimensions of the GHQ include: concentration, loss of sleep, feeling of playing a useful role, ability to make decisions, coping under strain, overcoming difficulties, enjoying activities, facing problems, feeling depressed or unhappy, confidence, feelings of worthlessness, and general happiness.

from 0 (least distressed) to 36 (most distressed). Following the existing literature (e.g., Davillas *et al.*, 2016; Davillas and Jones, 2021), the Likert scoring method allows GHQ-12 to be treated as a pseudo-continuous measure in our analysis.

Epigenetic Biological Age

DNA methylation-based measures (that are often called epigenetic age measures) are considered robust biomarkers of biological ageing (e.g., Horvath and Raj, 2018; Jylhävä *et al.*, 2017). Methylation is a mechanism that drives human ageing and varies across people of the same chronological age (Fransquet *et al.*, 2019). Specifically, the so-called "epigenetic clocks" estimate biological age by using algorithm-based weighted averages of DNA methylation levels across various regions of the genome (Benzeval *et al.*, 2023; Institute for Social and Economic Research, 2025).

Unlike chronological age, which increases at the same rate for everyone, some people experience a higher or lower biological age than their chronological age. Despite the correlation between chronological and biological age, biological age captures the epigenetic interaction of genes and the environment, with DNA methylation influencing the decline in viability of bodily organs over time (Cavalli and Heard, 2019). Existing literature shows that higher biological age is associated with higher mortality and morbidity risks, functional limitations, and cognitive dysfunction compared to chronological age, or after adjusting for chronological age (Chen *et al.*, 2016; Faul *et al.*, 2023; Li *et al.*, 2022). In essence, our employment exit prediction models include epigenetic age measures to capture the predictive role of a baseline measure of how old participants' bodies really are at the cellular level, as biological ageing is particularly relevant for researching healthy ageing (Horvath and Raj, 2018).

Recently released UKHLS data provide epigenetic clocks, based on DNA methylation analysis of frozen blood samples collected at nurse visits as part of UKHLS Waves 2 and 3. These epigenetic clocks are estimated for a sub-sample of participants from whom blood samples were collected and who consented to genetic analysis of their blood data (Institute for Social and Economic Research, 2025). We estimate separate employment exit prediction models using two alterative epigenetic biological age measures: the "PhenoAge" and the "Belsky" biological age measure. "PhenoAge" is an epigenetic biomarker of ageing proposed by Levine *et al.* (2018). We employ "PhenoAge" as a leading second-generation epigenetic measure, which outperforms the first-generation biological age proxies and strongly predicts a variety of ageing outcomes, such as all-cause mortality, cancer, and physical functioning (Levine *et al.*, 2018; Zavala *et al.*, 2024). Alternatively, we employ the "Belsky clock" as our measure for capture biological age years in separate employment exit prediction models estimated using LASSO. This is a more recently developed – and often considered as a third-generation – biological age measure proposed by Belsky *et al.* (2020, 2022).[8] Existing studies have shown that the Belsky epigenetic biological age measures are strong predictors of worse physical and cognitive functioning, along with other aging outcomes, after adjusting for chronological age (Belsky *et al.*, 2020, 2022).

Allostatic Load

Allostatic load is a composite index of nurse-collected blood-based biomarkers, which gives an assessment respondents "wear and tear" on the body caused by chronic exposure to stress (Davillas and Pudney, 2017; Howard and Sparks, 2016; Seeman *et al.*, 2004). Higher allostatic load values are associated with increased morbidity and all-cause mortality risks (Parker *et al.*, 2022). Allostatic load is used as predictor in our employment exit prediction models to proxy chronic physiological dysregulation at baseline (Waves 2 and 3 for the UKHLS and BHPS data, respectively). It should be noted here that biological age and allostatic load assess different dimensions of health — physiological (allostatic load) vs. molecular (biological age) — and, thus, provide complementary insights into ageing and illness risks that the respondents experience at baseline (UKHLS Waves 2 and 3), but from different angles (McCrory et al.,2020).

In line with existing studies (e.g., Davillas and Pudney, 2020; Davillas and Jones, 2025), we create the allostatic load index by combining markers for adiposity (waist-to-height ratio), systolic blood pressure, resting heart rate, lung function (forced vital capacity, FVC – the total amount of air forcibly blown out after a full

[8] For the purposes of our prediction models on subsequent employment exits estimated using LASSO, we use the "Belsky clock" to capture biological age (in years), rather than any Belsky measures that are themselves adjusted for respondents' chronological age. Chronological age is included as a separate predictor in our prediction models (described in detail below).

inspiration), inflammation (C-reactive protein), blood sugar levels (HbA1c – a sugar in the blood biomarker which is a validated diagnostic test for diabetes), cholesterol levels (high-density lipoprotein cholesterol, HDL), liver function (albumin) and a steroid hormone (dihydroepiandrosterone sulphate, DHEAS).[9] These nurse-collected and blood-based biomarkers are collected at nurse visits as part of our baseline waves (Waves 2 and 3 for the UKHLS and BHPS samples, respectively). Following existing studies, we convert HDL, FVC, Albumin and DHEAS to negative values to reflect ill-health rather than good health, then transform each of the biomarkers into a z-score; these nine z-scores are summed to produce the composite allostatic load measure at baseline.

Other predictors

We include a set of additional predictors which have been shown to be associated with respondents' labour market decisions (e.g., García-Gómez *et al.*, 2010; Jones *et al.*, 2010; Riphahn *et al.*, 1999). These variables (presented in Table 1) are collected at baseline, as part of the ULHLS waves 2 (for the UKHLS sample) and Wave 3 (for the BHPS sample).

First and foremost, we account for chronological age. Chronological age is a derived variable in our dataset capturing completed years from date of birth up to the nurse visit date (when the biological data used in our study are collected). We include chronological age to capture the age-related predictive power on future employment exit decisions. Given that we account for a wide and detailed set of baseline health measures, the predictive role of chronological age may reflect policy structures (e.g., retirement eligibility) and societal norms.[10] Moreover, we also account for sex, acknowledging differences in labour market behaviours and trajectories between males and females.

Household income captures the total incomes of all household members; it is adjusted for inflation (given the within-wave interview dates variations and the pooling of Waves 2 and 3 to define our baseline), using monthly Retail Price

[9] DHEAS is associated with cardiovascular risk and all-cause mortality through psycho-social mechanisms (Ohlsson *et al.*, 2010).

[10] Although we include a comprehensive set of baseline health measures as potential predictors in our LASSO model, we cannot rule out that chronological age may also still capture age-related health differences not reflected in these measures.

Indexes, to facilitate comparisons over time. It is then equivalised (using the modified OECD equivalence scale) to account for household composition, and log-transformed. Educational attainment is captured using a dichotomous variable of whether respondents have completed secondary or below education as opposed to tertiary education. We also account for housing tenure (non-rented versus a rented home) as an additional proxy for respondents' socio-economic position at baseline.

Job-related physical demands may also be important predictors of individuals' decisions to exit employment, as well as potential confounding factors in the association between health and subsequent labour market outcomes (Datta Gupta and Larsen, 2010; Gustman *et al.*, 1995; Sauré *et al.*, 2025). General physical activity scores —covering both the level and importance of physical activities for each occupation— are available for each Occupational Information Network (O*NET) occupational code.[11] Specifically, O*NET descriptors provide scores for general physical activities required on the job, defined as activities involving considerable use of the arms and legs and movement of the whole body (e.g., climbing, lifting, balancing, walking, stooping, and handling materials). Using the scores for both the level and importance of physical activity for each O*NET occupational code, we calculate average physical demand scores (for both "importance" and "level") at the 2-digit O*NET level. These average scores are then linked to 3-digit SOC occupational codes in the UKHLS.[12] The resulting variables ("Job physical activities: importance score", and "Job physical activities: level score") capture job-related physical activity in respondents' current job at baseline (UKHLS Waves 2 and 3).

Following the existing literature on the potential determinants of individual's labour supply and retirement decisions (e.g., García-Gómez *et al.*, 2010; Jones *et al.*, 2010), we also account for marital status (married/cohabitating vs non-married/non-cohabiting) and for the number of children in the household at

[11] Both the level and importance physical activity scores for each occupational code are, by design, standardized to a scale ranging from 0 to 100. These scores are available via the O*NET OnLine website (https://www.onetonline.org/find/descriptor/result/4.A.3.a.1). Standardized scores facilitate comparisons of physical activity scores—regarding both level and importance—across and within different occupations.

[12] The crosswalk from the 3-digit SOC 2000 to the 2-digit O*NET classification is available elsewhere (Burdett *et al.*, 2024, Appendix).

baseline.[13] A dichotomous variable for living in an urban area and a set of regional dummies (capturing the nine Government Office Regions in England, as well as Scotland and Wales) are also included in our set of predictors. Finally, we account for wave dummies to capture time effects as pooled data from Waves 2 and 3 are used.

[13] It should be noted that the aim of our study is not to examine how labour supply is jointly determined within couples as a result of health shocks experienced by either spouse (e.g., García-Gómez *et al.*, 2013; Fadlon and Nielsen, 2021). Empirical models that assess joint labour market decisions within couples are beyond the scope of this study. Instead, we focus not on a sub-sample of married or cohabiting individuals, but on a full sample of employed individuals at baseline who are followed in subsequent waves to determine their employment exits.

Table 1: Summary statistics for the outcome and predictors.

	Mean
Employment exit outcome	
Employment exit†	0.331
Predictors	
PhenoAge	40.537
Belsky clock	46.630
Chronological age	46.713
Initial diagnosed health condition: none†	0.715
Initial diagnosed health condition: present†	0.285
Allostatic load	-0.175
SAH	
Excellent†	0.214
Very good†	0.426
Good†	0.289
Fair/poor†	0.071
GHQ	10.444
Job physical activities: importance score	44.592
Job physical activities: level score	40.281
Female†	0.504
Male†	0.496
Log household income	7.554
Secondary/below education†	0.577
Tertiary education†	0.423
Non rented home†	0.857
Rent home†	0.143
Non-married/non-cohabiting†	0.198
Married/cohabitating†	0.802
Number of children in HH	0.660
North East†	0.058
North West†	0.097
Yorkshire and the Humber†	0.077
East Midlands†	0.097
West Midlands†	0.091
East of England†	0.100
London†	0.048
South East†	0.128
South West†	0.104
Wales†	0.092
Scotland†	0.108
Rural†	0.289
Urban†	0.711
Wave 2†	0.602
Wave 3†	0.398
Sample size	1,071

† Dichotomous variable.

3. Methods

Our objective is to assess which of our detailed set of baseline health measures play a predictive role in individuals' future employment decisions (up to a maximum of 10 years from baseline), along with people's chronological age and our baseline predictors (demographic characteristics, human capital proxies, job-related factors, and socio-economic status). We adopt a model selection approach based on penalised regressions. As the emphasis is on selecting a sparse set of predictors, we adopt the standard LASSO (least absolute shrinkage and selection operator) estimator. LASSO performs variable selection and regularisation, enhancing the prediction accuracy of the selected model (Tibshirani, 1996; Hastie *et al.*, 2015). Our interest is to explore which of the baseline health measures are included as predictors at the selected prediction models of subsequent employment decisions (of those employed at baseline) over and above the role of chronological age and other predictors.

For a sample of respondents who are active in the labour market at baseline, we define a linear model to predict subsequent employment exits (y_i), for each individual i ($i = 1, 2 \ldots, N$), using the set of potential predictors ($x_1, x_2, \ldots x_p; j = 1, 2, \ldots p$). Assuming sparsity, LASSO minimises the mean squared prediction error subject to the L1 norm constraint on the absolute parameter values – this penalises the complexity of the model. Specifically, the LASSO estimator $\widetilde{\beta_\lambda}$ of $\boldsymbol{\beta}$ minimises:

$$Q_\lambda(\boldsymbol{\beta}) = \frac{1}{N}\sum_{i=1}^{N}(y_i - \boldsymbol{X}_i'\boldsymbol{\beta})^2 + \lambda\sum_{j=1}^{p}|\beta_j| \qquad (1)$$

where, $\lambda \geq 0$ is a penalty or tuning parameter. The potential predictors are captured by the vector $\boldsymbol{X}$ in eq. (1); for estimation purposes, these predictors are standardised so that the selection of predictors does not depend on their measurement scales. The penalty has the effect of forcing some of the coefficient estimates to be exactly equal to zero when the λ parameter is sufficiently large LASSO minimises the objective function (eq. 1) f*or a grid* of values of λ. The algorithm chooses the solution that minimises the out-of-sample prediction error based on 10-fold cross validation (CV).[14]

In the employment exit models, we include a set of potential predictors for the algorithm to select from: a detailed set of baseline health measures (self-reported long-standing health conditions, SAH, GHQ-12, allostatic load and epigenetic biological age) along with chronological age and a set of other predictors at baseline (as described in the Data section); we also include polynomials of biological and chronological age to capture non-linearities in the association between these variables and subsequent employment exit decisions. As we experiment with two alternative (second- and third-generation) epigenetic biological age measures—"PhenoAge" and the "Belsky clock"—that are frequently used in the medical literature and show significant advantages over their predecessors (Belsky *et al.*, 2020, 2022; Levine *et al.*, 2018; Zavala *et al.*, 2024), we estimate separate employment exit prediction models using either "PhenoAge" or the "Belsky clock" as our epigenetic biological age measure. For estimation purposes, we transform all our continuous predictors into z-scores, each with a mean of zero and a standard deviation of one.

Focusing on the selected employment exit models, we further implement post-estimation analysis. Specifically, Shapley-Shorrocks decompositions (Shorrocks, 2013) of the R-squared are computed to explore the relative contribution of the selected predictors (as selected by the LASSO) to the explained variance of the subsequent employment exit outcome. This analysis may help us to identify which of the selected predictors are more relevant to predicting individuals' subsequent labour market exits. It identifies the relative contribution of the LASSO-selected baseline health measures (from the rich set of health measures included in our predictor pool), as well as the role of chronological age in predicting future employment exit decisions.

[14] k-fold cross-validation randomly divides the data into k folds. For each fold of the data a penalized regression is fit on the other nine folds and the mean squared error (MSE) is computed for that fold. These MSEs are averaged to give the CV mean prediction error. CV stops when the minimum of the CV function is found, and it sets the selected λ_{cv} to the λ that gives the minimum.

4. Results

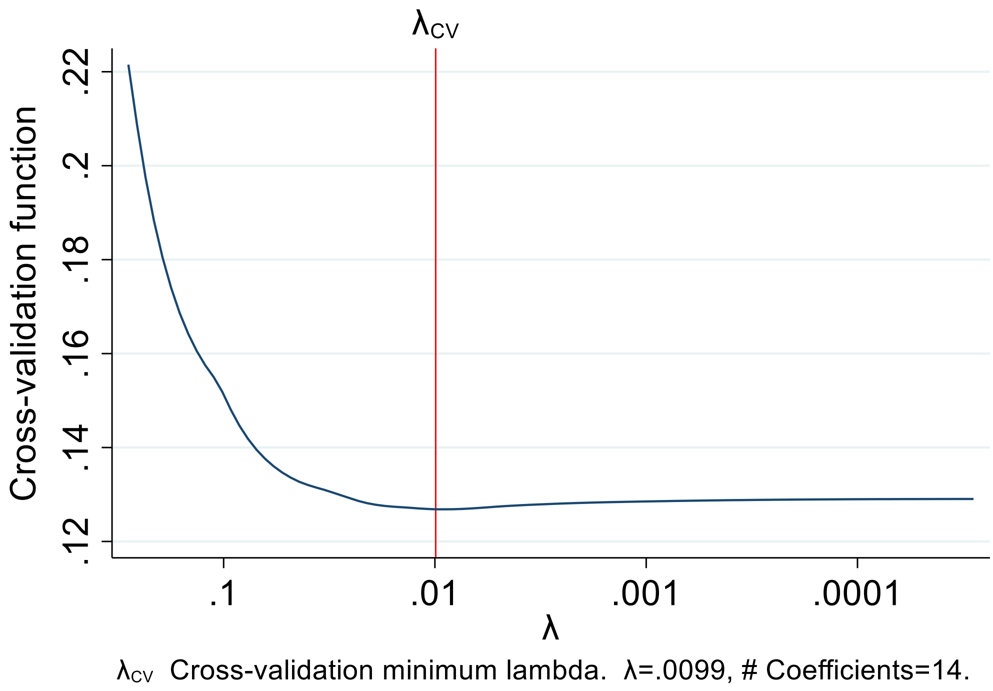
4.1 Main results

In this sub-section, we present the main results of our prediction models. As we experimented with alternative measures of biological ageing, we present our results separately where "PhenoAge" or the "Belsky clock" are used as our biological age measures.

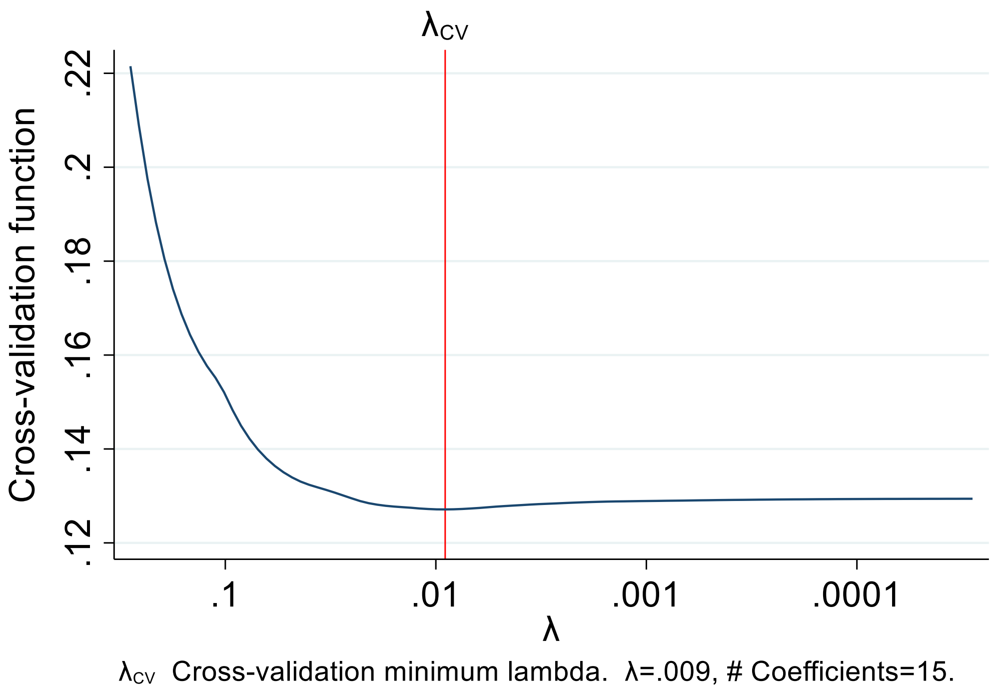
Figure 1 presents the cross-validation plots for our LASSO estimates. These graphs illustrate that cross-validation chooses the model that minimizes the CV mean prediction error over the search grid for λ (the penalty parameter). For the case when "PhenoAge" is used to proxy biological age, the selected λ (λ_{cv}) that gives the minimum is λ_{cv}=0.0099 (corresponding to a model with 14 selected predictors). Specifically, Figure 1 (Panel a) shows that the CV mean prediction error decreases as the penalty λ decreases until λ_{cv}=0.0099, after which it increases again reflecting the trade-off between bias and precision. As expected, a similar pattern is observed when the "Belsky clock" is used instead as a predictor to proxy biological ageing (Figure 1, Panel b). The relevant plot (Figure 1, Panel b) shows that the λ that minimises the CV mean prediction error is practically identical to the model that employs "PhenoAge" as a biological age predictor (λ_{cv}=0.009), corresponding to 15 selected predictors.

Figure 1: Cross-validation function over the search grid for the penalty parameter lambda — separate models accounting for: a) the "PhenoAge", and b) the "Belsky clock".

Predictor: "PhenoAge" (a)



Predictor: "Belsky clock" (b)



Tables 2 and 3 show the values of lambda (λ) at which predictors are selected (knots), along with the corresponding CV mean prediction errors for our models predicting future employment exit. The value of λ that minimizes the CV mean prediction error (λ_{CV}) is indicated in the tables with a star. For comparison, and to confirm that the CV mean prediction error increases lambdas lower than the λ_{CV}, two subsequent knots that come after the λ_{CV} are also presented in Tables 2 and 3. It should be explicitly noted that the predictors corresponding to each of the knots up to λ_{CV} (the value of lambda indicated with a star in Tables 2 and 3) constitute the final set of predictors selected by LASSO in the resulted prediction models.

For the case of the model that uses "PhenoAge" to proxy biological age (Table 2), chronological age and chronological age squared are among the predictors that are selected in the first knots. Moreover, the number of children in the household at baseline and being a female contribute to the prediction of future employment exit, selected as early as in the second and fifth knot, respectively. Turning to our set of baseline health measures included in our set of predictors, only SAH (and particularly the "Fair/poor" and the "Excellent" category) and biological age (proxied by "PhenoAge") are selected as predictors by LASSO. Household income and educational attainment (Secondary/below education) are the selected SES predictors. Finally, some regional dummies, an urbanisation indicator and a wave dummy are selected as predictors; in line with existing literature, these capture regional variations in the labour market and employment exits decisions (García-Gómez *et al.*, 2010; Jones *et al.*, 2010) as well as wave dummies, given that pooled Wave 2 and 3 data are used for the baseline.

These results suggest that the predictive power of chronological age on future employment exits may be independent of health-related influences as baseline health measures are also selected as predictors by the LASSO. Moreover, the fact that, among our set of potential predictors capturing different health aspects at baseline, biological age is selected over and above the predictive role of SAH. This suggests that biological age and SAH rather than baseline mental health and pre-existing health conditions (which are also included in the pool of potential predictors) are the key predictors of subsequent labour market exits.

Turning to the model that employs the “Belsky clock” as a proxy for biological age, a similar set of predictors is selected (Table 3). Specifically, chronological age (and its square), baseline biological age (as measured by the “Belsky clock”), and self-assessed health (SAH) at baseline contribute to predicting future employment exits, over and above a set of demographic and socioeconomic characteristics, which include gender, number of children in the household, marital status, household income, education, and regional, urbanisation, and wave dummies.

Table 2: CV mean prediction error and selected predictors across knots – when “PhenoAge” is used for biological age.

Lambda	No. of nonzero coef.	CV mean prediction error	Selected predictors
0.2572	1	0.208837	Chronological age
0.1014	3	0.151862	Number of children in HH; Chronological age squared
0.0365	4	0.131479	SAH: Fair/poor
0.0332	5	0.130960	Log household income
0.0276	7	0.129780	SAH: Excellent; Female
0.0229	8	0.128598	PhenoAge
0.0190	9	0.127810	South East
0.0173	10	0.127567	North West
0.0158	12	0.127404	Rural; Secondary/below education
0.0131	13	0.127171	Yorkshire and the Humber
0.0119	14	0.127032	Wave 2
***0.0099**	**14**	**0.126849**	
0.0090	15	0.126850	Non-married/non-cohabitating
0.0062	16	0.127126	South West

Note: The parameters in bold (*) correspond to the lambda selected by cross-validation. Estimation sample size: 1,071.

Table 3: CV mean prediction error and selected predictors across knots – when "Belsky clock" is used for biological age.

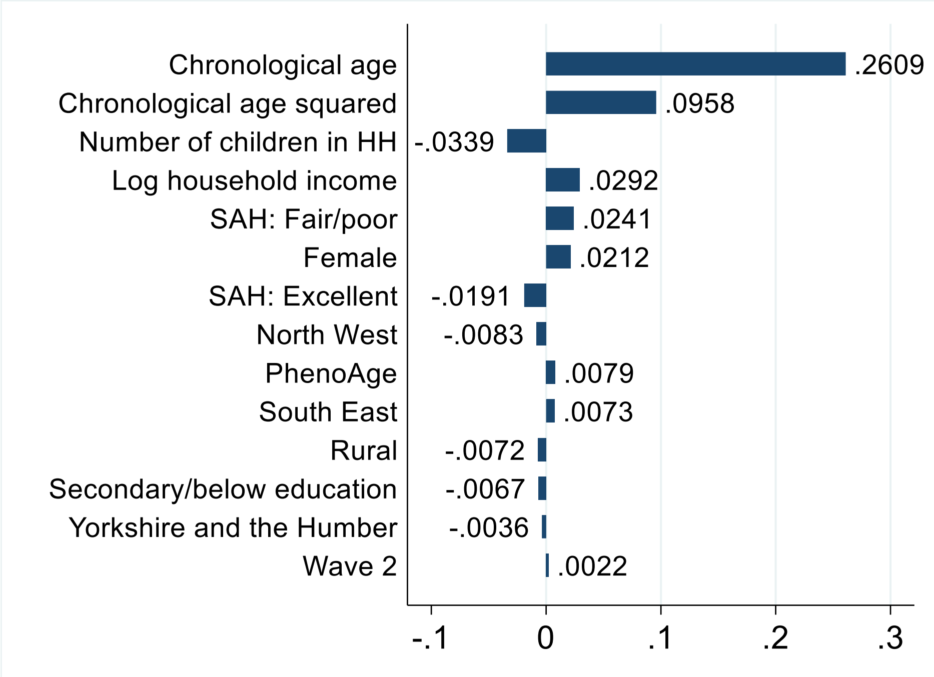
Lambda	No. of nonzero coef.	CV mean prediction error	Selected predictors
0.2572	1	0.2088	Chronological age
0.1113	2	0.1552	Belsky clock
0.1014	4	0.1521	Number of children in HH; Chronological age squared
0.0365	5	0.1318	Log household income
0.0332	6	0.1313	SAH: Fair/poor
0.0276	8	0.1301	SAH: Excellent; Female
0.0209	9	0.1285	South East
0.0173	11	0.1279	Secondary/below education; North West
0.0158	12	0.1277	Rural
0.0131	13	0.1275	Wave 2
0.0119	14	0.1273	Yorkshire and the Humber
***0.0090**	**15**	**0.1271**	**Non-married/non-cohabitating**
0.0062	17	0.1274	South West; Initial diagnosed health conditions: none
0.0057	18	0.1276	East Midlands

Note: The parameters in bold (*) correspond to the lambda selected by cross-validation. Estimation sample size: 1,071.

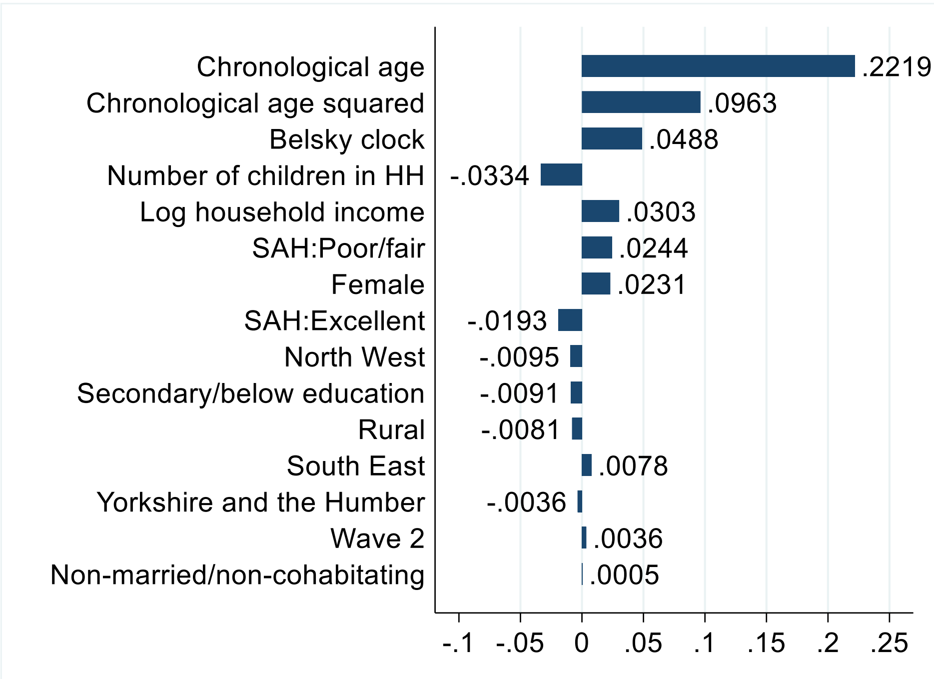
Figure 2 presents the penalised LASSO coefficient estimates for the selected predictors (as outlined in Tables 2 and 3). Overall, across both prediction models, using "PhenoAge" or "Belsky clock" to proxy biological age (Figure 2, Panels a and b), the coefficient signs are as expected. For example, baseline chronological age (and age squared) has a positive sign for employment exits, suggesting that higher chronological age positively predicts employment exits, with non-linearities suggesting a more pronounced predictive role for chronologically older respondents (Figure 2, Panel a and b). Turning to the baseline SAH measure, the "Fair/poor" SAH category has a positive sign, while the "Excellent" SAH category has a negative sign with subsequent employment exits (Figure 2, Panels a and b). Moreover, our biological age measures (either "PhenoAge" or "Belsky clock") at baseline, with higher values suggesting a lower viability of the body, have a positive sign across the models (Figure 2, Panels a and b). Higher household income, indicative of higher socioeconomic status at baseline, has a positive sign in the models predicting subsequent employment exits, while lower educational attainment ("Secondary/below education" versus "Tertiary education") is negatively associated with future employment exits. Regarding family-related predictors, the number of children in the household has a negative sign, while being non-married/non-cohabitating has a coefficient with a positive sign (as marital status is a selected predictor only in the model that includes the "Belsky clock" as biological age measure; Figure 2, Panel b).

Figure 2. Penalised coefficients for the (standardized) predictors — separate models accounting for: a) the “PhenoAge”, and b) the “Belsky clock”.

Predictor: “PhenoAge” (a)



Predictor: “Belsky clock” (b)



Typically, the use of LASSO for prediction analysis does not focus on the magnitude of the penalised coefficients. Thus, we employ post-estimation analysis using Shapley-Shorrocks decompositions (Shorrocks, 2013) of the R-squared for models that use the set of predictors selected by LASSO. This analysis allows us to explore which of the selected predictors are more relevant in predicting individuals' subsequent labour market exits.

The results from the Shapley-Shorrocks decomposition analysis of the resulting models are presented in Table 4, separately for the two alternative measures of biological age used in our analysis: "PhenoAge" (Panel a), and "Belsky clock" (Panel b). Chronological age exerts the dominant contribution to the predicting subsequent employment exits – this suggests that chronological age plays a major predictive role in future employment exits, which is of particular importance as it is over and above baseline measures of health (along with all other socio-economic and demographic predictors accounted for in our prediction models). Turning to baseline health measures, biological age proxies (either using the "PhenoAge" or the "Belsky clock") make the most pronounced contribution of all the predictor included apart from chronological age. Of particular interest, the contribution of biological age is much more pronounced compared to the role of SAH (with the role of SAH being around 2%). Among the remaining predictors, the number of children in the household makes the most pronounced contribution (approximately 11%), while the others each contribute significantly less (below 2%).

Overall, Table 4 (Panels a and b) shows that the combined contribution of chronological age and biological age is around 83% (either when the PhenoAge or the Belsky clock is used). An important caveat to this finding is shown in Table 4, Panel c, which repeats the post-estimation decomposition analysis based on the selected models by LASSO without biological age included in the set of potential regressors; the overall R-squared is unaffected, at 0.453, and the percentage contribution attributable to chronological age increases to 79.28%. So, including biological age, which is highly collinear with chronological age, does not add to the overall goodness of fit of the regressions. Nevertheless, these results suggest that the decomposition into epigenetic age and other aspects of age may offer useful insights that would have been masked in the absence of epigenetic measures of biological age. However, collecting information on biological age comes at considerable cost, including a reduced sample size compared to an analysis that could be done using the remaining health measures and chronological age in UKHLS.

Table 4. Shapley decomposition of R^2 for post-selection linear regressions – accounting for: a) "PhenoAge", b) the "Belsky clock", c) without biological age.

	(a)	(b)	(c)
Chronological age	55.37%	47.97%	79.28%
PhenoAge	27.24%	-	-
Belsky clock	-	35.00%	-
SAH	2.31%	2.29%	2.55%
Log Household Income	1.63%	1.61%	1.56%
Educational attainment	0.23%	0.31%	0.18%
Gender	0.57%	0.69%	0.55%
Marital Status	-	0.24%	0.27%
Number of children in the HH	11.41%	10.59%	14.48%
Region of residency	0.85%	0.84%	0.84%
Urbanisation level	0.24%	0.26%	0.21%
Wave dummies	0.15%	0.20%	0.08%
Total	**100.00%**	**100.00%**	**100.00%**
R^2	**0.453**	**0.454**	**0.453**

4.2 Robustness checks

Our employment exit outcome, measured up to ten years from baseline (i.e., up to UKHLS Wave 13), includes part of the COVID-19 period (2020-2022). We conduct a sensitivity analysis defining employment exits based on data up to UKHLS Wave 10 (with 98% of the respondents' interviews conducted between 2018 and 2019) – a period that excludes the COVID-19 outbreak in the UK. The results of this sensitivity analysis (Table A2, Appendix) do not differ substantially from our base-case results presented in Tables 2 and 3 (in terms of the selected predictors).

Moreover, we also perform sensitivity analysis for the number of folds used for the k-fold cross-validation. It has been argued that the most commonly used in empirical research, 10-fold (as in our base-case analysis), provides a good balance between bias and variance (Cameron and Trivedi, 2022).[15] Robustness checks using 5 or 20 CV folds suggest no changes to selected predictors, at least as far as the key demographic and socioeconomic predictors as well as chronological age and the baseline health measures.

As additional sensitivity analyses, we re-ran our prediction models using probit LASSO, rather than the linear models in our base-case analysis, as well as adaptive LASSO, rather than the CV used in the base-case analysis, to select the tuning parameter (Tables A3 and A4, Appendix). These sensitivity analyses do not affect the key selected predictors as compared to the base-case models presented in the study (Tables 2 and 3); specifically, chronological age (and chronological age squared), baseline SAH and biological age measures, along with baseline socioeconomic position and regional/urban dummies. We note however that our main results remain based on prediction models estimated using CV LASSO, rather than adaptive LASSO, because CV LASSO is a widely employed estimation method when the goal is prediction, which is the main scope of this study.

5 Conclusion

In this study, we use supervised machine learning techniques, in particular the LASSO, to examine the predictive role of individuals' baseline health in future employment exits, while also accounting for the potential influence of additional baseline factors affecting labour force decisions. Using longitudinal data from a nationally representative UK dataset - *Understanding Society: the UK Household Longitudinal Study (UKHLS)* - we focus on individuals who were employed at baseline (specifically, self-employed, those in paid employment, or on maternity leave) and were followed for up to 10 years to track subsequent employment exits. Drawing on an unusually wide range of health indicators, we employ several measures to proxy respondents' baseline health: conventional self-assessed health (SAH), self-reported diagnosed chronic conditions, a measure of psychological

[15] A larger number of folds implies that the training set size increases and, thus, bias decreases; at the same time however, the fitted models are more likely to overlap and, thus, the test set predictions are more correlated leading to greater variance in the estimate of the expected prediction error.

distress, and a composite indicator of nurse-collected and blood-based biomarkers (allostatic load), as well as epigenetic biological age measures.

Unlike self-reported diagnosed chronic conditions or the more objectively measured composite allostatic load measure, we find that the combination of epigenetic biological age, and - as expected - chronological age, predict subsequent employment exits over and above other predictors. SAH is selected by LASSO in our models predicting future employment exits. This result is broadly in line with existing studies suggesting that subjective health measures retain predictive power in labour force participation models, even after accounting for more objective measures of health (McGarry, 2004). We argue that the inherently subjective and contextual nature of self-rated health may capture health-related predispositions or bodily sensations that influence subsequent employment decisions (Jylhä, 2009).

Post-estimation analysis using Shapley-Shorrocks decompositions allows us to explore which of the selected predictors are most relevant in shaping individuals' subsequent labour market exits. Our results highlight that although both epigenetic biological age and SAH are selected predictors by LASSO, the contribution of biological age is much more pronounced compared to SAH. This suggests that biological age provides strong additional predictive power over and above SAH (along with other demographic, socioeconomic, and human capital predictors included in the model). In this context, epigenetic biological age may capture the underlying physiological decline that influences a person's capacity to work or their health-related decision to exit the labour force. On the other hand, the dominant contribution of chronological age suggests that chronological age plays a major predictive role over and above baseline health measures. Additional analysis when epigenetic biological age measure is omitted from our set of potential predictors, shows that chronological age accounts for nearly all of the combined contribution of biological and chronological age. However, the availability of epigenetic biological age measures allows us to disentangle between the role of chronological age that reflects institutional structures, such as retirement eligibility, and societal norms from other contributions reflecting age-related decline in health status that are relevant to epigenetic biological age measures. Technical improvements, such as using dried blood spots collected on filter paper instead of the conventional venipuncture procedure, may reduce the (administrative) cost of obtaining epigenetic ageing measures (Ryan, 2021). As such, epigenetic biological ageing may inform more precise tailored interventions - such as job redesign, medical support, or flexible schedules - to slow functional decline and delay premature employment exit.

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Appendix: additional tables

Table A1: Summary statistics for the predictors

	Estimation sample‡		Comparison sample (without conditioning on allostatic load and biological age)‡‡	
	Mean	Obs.	Mean	Obs.
PhenoAge	40.537	1,071	-	-
Belsky clock	46.630	1,071	-	-
Chronological age###	46.713	1,071	44.961	8,323
Initial diagnosed health condition: none†	0.715	1,071	0.689	15,245
Initial diagnosed health condition: present†	0.285	1,071	0.311	15,245
Allostatic load	-0.175	1,071	-	-
SAH		1,071		
Excellent	0.214	1,071	0.180	15,245
Very good	0.426	1,071	0.414	15,245
Good	0.289	1,071	0.312	15,245
Fair/poor	0.071	1,071	0.094	15,245
GHQ score	10.444	1,071	10.535	15,245
Job physical activities: importance score	44.592	1,071	45.787	15,245
Job physical activities: level score	40.281	1,071	41.095	15,245
Female†	0.504	1,071	0.522	15,245
Male†	0.496	1,071	0.478	15,245
Log household income	7.554	1,071	7.521	15,245
Secondary/below education†	0.577	1,071	0.572	15,245
Tertiary education†	0.423	1,071	0.428	15,245
Non rented home†	0.857	1,071	0.790	15,245
Rent home†	0.143	1,071	0.210	15,245
Non-married/non-cohabiting†	0.198	1,071	0.246	15,245
Married/cohabitating†	0.802	1,071	0.754	15,245
Number of children in HH	0.660	1,071	0.666	15,245
North East†	0.058	1,071	0.041	15,245
North West†	0.097	1,071	0.115	15,245
Yorkshire and the Humber†	0.077	1,071	0.079	15,245
East Midlands†	0.097	1,071	0.085	15,245
West Midlands†	0.091	1,071	0.079	15,245
East of England†	0.100	1,071	0.099	15,245
London†	0.048	1,071	0.067	15,245
South East†	0.128	1,071	0.147	15,245
South West†	0.104	1,071	0.097	15,245
Wales†	0.092	1,071	0.082	15,245
Scotland†	0.108	1,071	0.109	15,245
Rural†	0.289	1,071	0.255	15,245
Urban†	0.711	1,071	0.745	15,245
Wave 2†	0.602	1,071	0.772	15,245
Wave 3†	0.398	1,071	0.228	15,245

† Dichotomous variable.
‡ Estimation sample as in Table 1; represents the pooled sample of Wave 2 (UKHLS)/ Wave 3 (BHPS) respondents who are currently in employment (self-employed, in paid employment or on maternity leave) and are followed up at subsequent waves to track future employment exits, and are constrained to having non-missing information on all the utilised predictors (including allostatic load and biological age measures).
‡‡ Pooled sample of Wave 2 (UKHLS)/ Wave 3 (BHPS) respondents who are currently in employment (self-employed, in paid employment or on maternity leave) and are followed up at subsequent waves to track future employment exits, and are constrained to having non-missing information on all utilised predictors except allostatic load and biological age

measures. As opposed to the estimation sample, this sample does not condition on the availability of biological age data or allostatic load.

The mean chronological age for the comparison sample is available only for respondents who participated in the nurse visits, which were conducted an average of five months after the corresponding main Waves 2/3; this allows for direct comparison of chronological age with biological age measures as biological age measures are based on blood samples collected during those nurse visits.

Table A2. Selected predictors in order of selection: excluding the COVID-19 UKHLS waves in defining employment exits.

Predictor: "PhenoAge"	Predictor: "Belsky clock"
Chronological age	Chronological age
Number of children in HH; Chronological age squared	Belsky clock; Number of children in HH; Chronological age squared
Log household income	Log household income
SAH: Fair/poor	SAH: Fair/poor
SAH: Excellent	SAH: Excellent
Female; South East	Female; South East
PhenoAge	Wave 2
Wave 2	Yorkshire and the Humber
Yorkshire and the Humber	North West
North West	Secondary/below education
Rural	Rural
Secondary/below education	

Table A3: Selected predictors in order of selection by LASSO: when "PhenoAge" is used.

5 CV folds	20 CV folds	Probit LASSO	Adaptive LASSO
Chronological age	Chronological age	Chronological age	Chronological age
Number of children in HH; Chronological age squared	Number of children in HH; Chronological age squared	Number of children in HH	Chronological age squared
SAH: Fair/poor	SAH: Fair/poor	Chronological age squared	Number of children in HH
Log household income	Log household income	SAH: Fair/poor	SAH: Fair/poor
SAH: Excellent; Female	SAH: Excellent; Female	Log household income; PhenoAge	Log household income
PhenoAge	PhenoAge	SAH: Excellent; Female	SAH: Excellent
South East	South East	South East	PhenoAge
North West	North West	North West; Yorkshire and the Humber	Female
Rural; Secondary/below education	Rural; Secondary/below education	Secondary/below education	North West; South East
Yorkshire and the Humber	Yorkshire and the Humber	Rural	Yorkshire and the Humber
	Wave 2	Non-married/non-cohabitating	
	Non-married/non-cohabitating	London	

Table A4: Selected predictors in order of selection by LASSO: when "Belsky clock" is used.

5 CV folds	20 CV folds	Probit LASSO	Adaptive LASSO
Chronological age	Chronological age	Chronological age	Chronological age
Belsky clock	Belsky clock	Belsky clock	Chronological age squared
Number of children in HH; Chronological age squared	Number of children in HH; Chronological age squared	Number of children in HH	Number of children in HH
Log household income	Log household income	Chronological age squared	Belsky clock
SAH: Fair/poor	SAH: Fair/poor	SAH: Fair/poor	SAH: Fair/poor
SAH: Excellent; Female	SAH: Excellent; Female	Log household income	Log household income
South East	South East	Female	SAH: Excellent
Secondary/below education; North West	Secondary/below education; North West	SAH: Excellent	Female
Rural	Rural	South East	South East
Wave 2	Wave 2	Secondary/below education; South West; Yorkshire and the Humber	North West
	Yorkshire and the Humber	Rural	Yorkshire and the Humber
	Non-married/non-cohabitating	Non-married/non-cohabitating	Secondary/below education
		London	London