Appendices

For Online Publication

A Health categories

The 21 highest level ICD-10 diagnosis categories are; *"Certain infectious and parasitic diseases"*, *"Neoplasms"*, *"Diseases of the blood and blood-forming organs and certain disorders involving the immune mechanism"*, *"Endocrine, nutritional, and metabolic diseases"*, *"Mental and behavioural disorders"*, *"Diseases of the nervous system"*, *"Diseases of the eye and adnexa"*, *"Diseases of the ear and mastoid process"*, *"Diseases of the circulatory system"*, *"Diseases of the respiratory system"*, *"Diseases of the digestive system"*, *"Diseases of the skin and subcutaneous tissue"*, *"Diseases of the musculoskeletal system and connective tissue"*, *"Diseases of the genitourinary system"*, *"Pregnancy, childbirth, and the puerperium"*, *"Certain conditions originating in the perinatal period"*, *"Congenital malformations, deformations, and chromosomal abnormalities"*, *"Symptoms, signs, and abnormal clinical and laboratory findings, not elsewhere classified"*, *"Injury, poisoning, and certain other consequences of external causes"*, *"External causes of morbidity and mortality"*, and *"Factors influencing health status and contact with health services"*.
The level 1 categories of the ATC are; *"Alimentary tract and metabolism"*, *"Blood and blood forming organs"*, *"Cardiovascular system"*, *"Dermatologicals"*, *"Genito-urinary system and sex hormones"*, *"Systemic hormonal preparations, excluding sex hormones, and insulins"*, *"Antiinfectives for systemic use"*, *"Antineoplastic and immunomodulating agents"*, *"Musculo-skeletal system"*, *"Nervous system"*, *"Antiparasitic products, insecticides, and repellents"*, *"Respiratory system"*, *"Sensory organs"*, and *"Various"*.

B Charlson's comorbidity index codes

Table 4: ICD-10 codes for Charlson's index diagnosis.

Charlson's Comorbidity Category (weight)	ICD-10
Myocardial infarction (1)	I21; I22; I23
Congestive heart failure (1)	I50; I110; I130; I132
Peripheral vascular disease (1)	I70-I74; I77
Cerebrovascular disease (1)	I60-I69
Dementia (1)	F00-F03; F051; G30
Chrononic pulmonary disease (1)	J40-J47; J60-J67; J684; J701; J703; J841; J920; J961; J982; J983
Connective tissue disease (1)	M05; M06; M08; M09; M30; M31; M32; M33; M34; M35; M36; D86
Ulcer disease (1)	K221; K25-K28
Mild liver disease (1)	B18; K700-K703; K709; K71; K73; K74; K760
Diabetes (1)	E100; E101; E109; E110; E111; E119
Hemiplegia (2)	G81; G82
Moderate to severe renal disease (2)	I12; I13; N00-N05; N07; N11; N14; N17-N19; Q61
Diabetes with end organ damage (2)	E102-E108; E112-E118
Any tumor (2)	C00-C75
Leukemia (2)	C91-C95
Lymphoma (2)	C81-C85; C88; C90; C96
Moderate to severe liver disease (3)	B150; B160; B162; B190; K704; K72; K766; I85
Metastatic solid tumor (6)	C76-C80
AIDS/HIV (6)	B21-B24

Note: Charlson weights and ICD-10 codes.

Table 5: Weight comparison of the original and the time-varying Charlson's index.

Charlson's weights	**Original**	**Female**	**Male**
Myocardial infarction	1.000	0.541	0.243
Congestive heartfailure	1.000	1.892	2.000
Peripheral vascular disease	1.000	2.000	1.811
Cerebrovascular disease	1.000	1.054	1.027
Dementia	1.000	2.189	2.108
Chronic pulmonary disease	1.000	2.216	2.081
Connective tissue disease	1.000	0.865	0.622
Ulcer disease	1.000	0.703	0.649
Mild liver disease	1.000	2.784	3.297
Diabetes	1.000	0.568	0.595
Hemiplegia	2.000	1.432	1.378
Moderate to severe renal disease	2.000	2.459	2.000
Diabetes with end organ damage	2.000	1.784	1.784
Any tumour	2.000	5.162	3.946
Leukemia	2.000	3.676	2.946
Lymphoma	2.000	3.216	2.757
Moderate to severe liver disease	3.000	2.054	2.000
Metastatic solid tumour	6.000	3.459	3.081
AIDS/HIV	6.000	2.108	2.919

Note: This table contain the weights associated with the original weights in the Charlson's comorbidity index as well as the gender separate weights produced by our modified Charlson's index. Diabetes in this table includes both type-I and type-II diabetes.

C Method implementation details

All of the models are trained on the sample in the years 1995-2010 and used to predict/-forecast in the years 2011-2018 (i.e., the hold-out sample). Both the Lasso and the random forest requires tuning of hyper-parameters that are estimated using internal k-fold cross-validation. The Lasso has one hyper-parameter, the penalization parameter λ. For the random forest, we tune the minimum node size, the amount of chosen variables to grow each tree in a forest using the Gini splitting criterion for each tree. See Breiman (1996) for notes on the splitting criterion. The chosen parameters are the ones the provide the highest accuracy on a validation set. The amount of trees used for the final prediction are chosen to be 1000. The amount of trees in each forest is not, in general, a tuning parameter a critical tuning parameter for the final prediction as long as it is chosen to be reasonably high (the largest gain in accuracy is often obtained after the first 100 trees) (Probst and Boulesteix, 2017; Probst et al., 2019). We have tried to see the difference between a 100 and 2000 trees, and the improvements in MSE and cross-entropy are small. For all methods, we use 2-fold cross-fitting to speed up the training process of the models and to allow

for inference directly on the out-of-bag set. See Chernozhukov et al. (2018) for a theoretical discussion of cross-fitting procedures in general.

D Age-averaged by year evolution of health over time

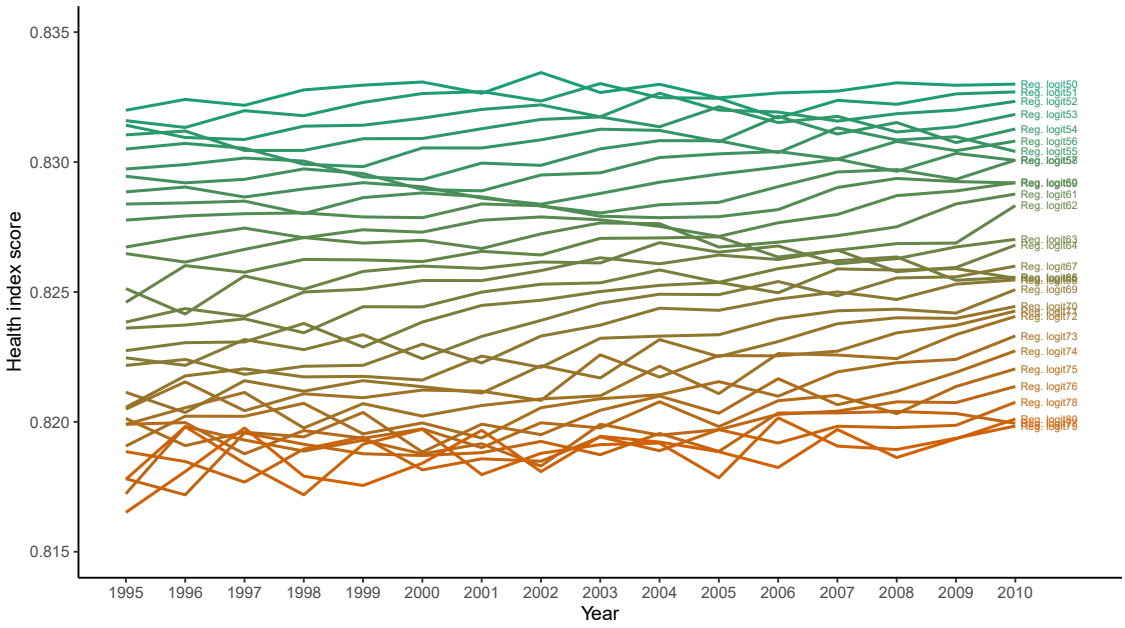


Figure 9: By age path evolution of health captured by Regularized logit.

E Driving factors extended

We first consider the CCI. The importance ranking, based on the weights derived from the method we described in Section 3.1, is shown in Figure 10. Compared to the other methods, the CCI is entirely focused on a few specific diagnoses. One potential caveat of this index is that Charlson's weights may poorly reflect the health state, or associated mortality risk, see Chandra et al. (2010). Figure 10 illustrates the difference between the weights of the original health index and our time-varying Charlson's index. The time-varying index allows the current weights to reflect current mortality risk of the diagnosis. This difference is especially highlighted in the weights for *AIDS/HIV* where the original index has the highest possible weight for the *AIDS/HIV* diagnosis. In comparison, the time-varying Charlson's index only gives the weight 2-3 to this diagnosis. The difference is likely explained by the mortality risk of *AIDS/HIV* being historically much higher than it currently is (Deeks et al., 2013). We see the same for the *Metastatic tumour* while *Any tumour*, *Lymphoma* or *Leukaemia* have a higher weight taking into account time variation.

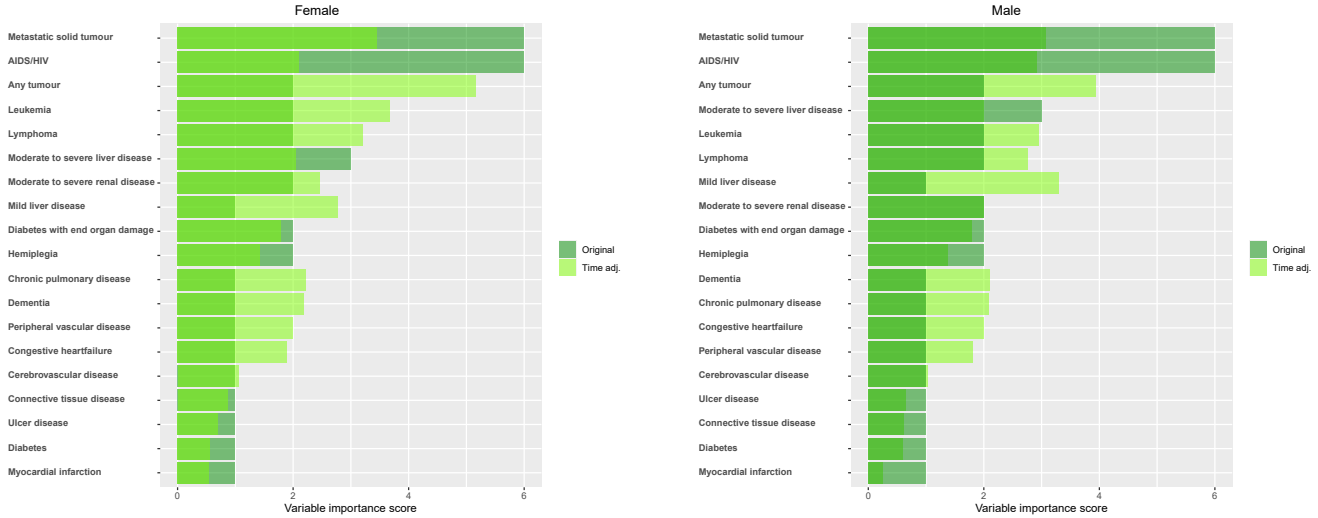
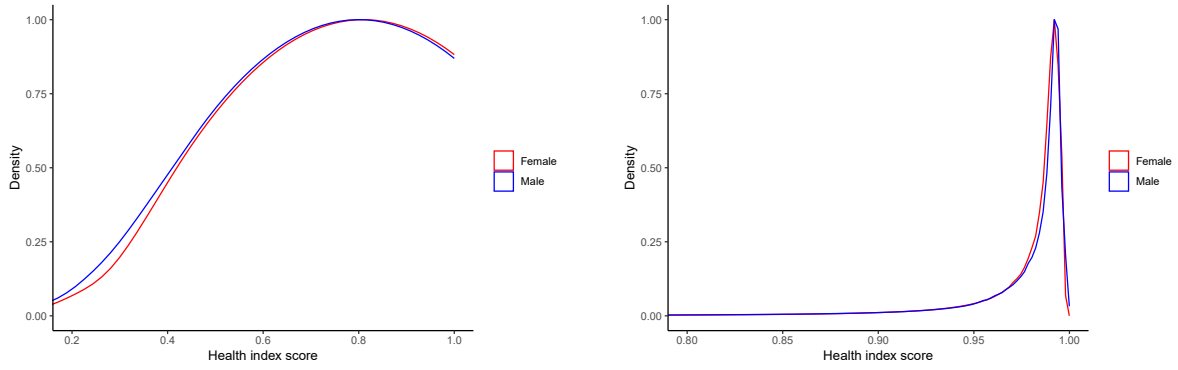


Figure 10: Variable of importance: Charlson's comorbidity index (CCI)

We also aim to accommodate the heterogeneity in mortality risk across genders by estimating our modified CCI for each gender. We find that the Charlson's category *Any tumour* has a much higher association with 1-year mortality in females compared to males over time. Our gender-specific weights set contrast to the original, fixed, weights. Otherwise, due to the weight estimation strategy, the importance ranking by the CCI based on our time-varying weights is not much different from that based on the original weights. A full table of exact Charlson's weights is included in the appendix in Table 5.

F Counts and Distributions of Health Scores.



(a) Regularized logit

(b) Random forest

Figure 11: Kernel density estimates of latent health based as either health index for regularized logistic regression or random forest. All densities are estimated using Epanechnikov kernels (Epanechnikov, 1969) and a rule-of-thumb bandwidth estimator (Silverman, 1986).

Table 6: Health Quintile Group Distribution by Age and Gender (1995-2010)

	Females			**Males**		
Age groups	**50-59**	**60-69**	**70-80**	**50-59**	**60-69**	**70-80**
Years 1995-1999						
Health quintile group 1 (poor health)	330714	233875	217067	334093	216991	163231
Health quintile group 2	330689	232068	217100	335047	215179	163260
Health quintile group 3	330637	235991	217190	332712	219236	162942
Health quintile group 4	330663	233621	217069	334631	216612	163312
Health quintile group 5 (excellent)	330666	233918	217009	334111	217067	163515
Years 2000-2004						
Health quintile group 1 (poor health)	354576	253774	206045	357872	241878	161770
Health quintile group 2	354599	253641	206080	362320	243284	161801
Health quintile group 3	354481	253966	205942	352641	240624	162335
Health quintile group 4	354728	253878	206238	358782	241833	161277
Health quintile group 5 (excellent)	354581	253707	206038	357836	241877	161774
Years 2005-2010						
Health quintile group 1 (poor health)	402183	372654	246937	403567	361458	206233
Health quintile group 2	402242	372585	246976	405433	360309	206318
Health quintile group 3	402290	372839	247268	401881	362643	206343
Health quintile group 4	402122	372651	246681	403487	361380	206162
Health quintile group 5 (excellent)	402193	372665	246949	403580	361615	206258

Table 7: Descriptive Table by Health Quintile

	Female		Male	
	Mean	SD	Mean	SD
Age				
Very Poor Health	52.2819	17.1616	50.1560	15.8210
Poor Health	52.2782	17.1631	50.0099	15.8011
Around Median Health	52.2882	17.1607	50.0725	15.8326
Good Health	52.2823	17.1630	50.0675	15.8189
Excellent Health	52.2795	17.1601	50.0755	15.8166
No. of GP-visits (Yearly)				
Very Poor Health	6.3324	7.0263	5.4841	7.0324
Poor Health	4.1600	4.6773	2.8033	4.2646
Around Median Health	3.4014	3.9037	1.9914	3.1819
Good Health	3.5730	3.9288	1.9393	2.6283
Excellent Health	4.4500	3.9811	2.6907	2.6019
No. of outpatient treatments (Yearly)				
Very Poor Health	2.9140	10.6202	2.9661	12.4392
Poor Health	0.8599	3.8280	0.7048	3.7356

Table 7: continued ...

Table 7: Descriptive Table by Health Quintile

	Female		Male	
	Mean	SD	Mean	SD
Around Median Health	0.4807	2.5079	0.3458	2.1351
Good Health	0.7491	2.7399	0.2890	1.5255
Excellent Health	1.9094	3.2693	1.2338	1.9569
No. of days admitted (Yearly)				
Very Poor Health	4.1949	13.6704	3.9733	12.9881
Poor Health	0.6077	3.8246	0.4304	2.8330
Around Median Health	0.2269	2.0599	0.1294	1.2081
Good Health	0.2100	1.6271	0.0672	0.6224
Excellent Health	0.6722	1.9938	0.1002	0.5303
No. of diagnoses (Yearly)				
Very Poor Health	2.6745	4.9535	2.6897	5.0258
Poor Health	0.7113	1.8822	0.5622	1.5898
Around Median Health	0.3926	1.3116	0.2691	0.9851
Good Health	0.6298	1.5562	0.2297	0.8220
Excellent Health	2.0894	2.9494	1.0672	1.1687
Gets prescription drugs				
Very Poor Health	0.9435	0.2308	0.8953	0.3061
Poor Health	0.8784	0.3268	0.6008	0.4897
Around Median Health	0.8148	0.3885	0.4928	0.4999
Good Health	0.7526	0.4315	0.6086	0.4881
Excellent Health	0.8488	0.3583	0.7775	0.4159
1-year Mortality				
Very Poor Health	0.0488	0.2154	0.0500	0.2179
Poor Health	0.0127	0.1121	0.0122	0.1097
Around Median Health	0.0078	0.0879	0.0077	0.0875
Good Health	0.0052	0.0719	0.0051	0.0711
Excellent Health	0.0027	0.0521	0.0031	0.0559
3-year Mortality				
Very Poor Health	0.1089	0.3115	0.1123	0.3158
Poor Health	0.0460	0.2096	0.0447	0.2067
Around Median Health	0.0324	0.1772	0.0324	0.1770
Good Health	0.0246	0.1550	0.0237	0.1522
Excellent Health	0.0173	0.1303	0.0182	0.1338

Table 7: continued . . .

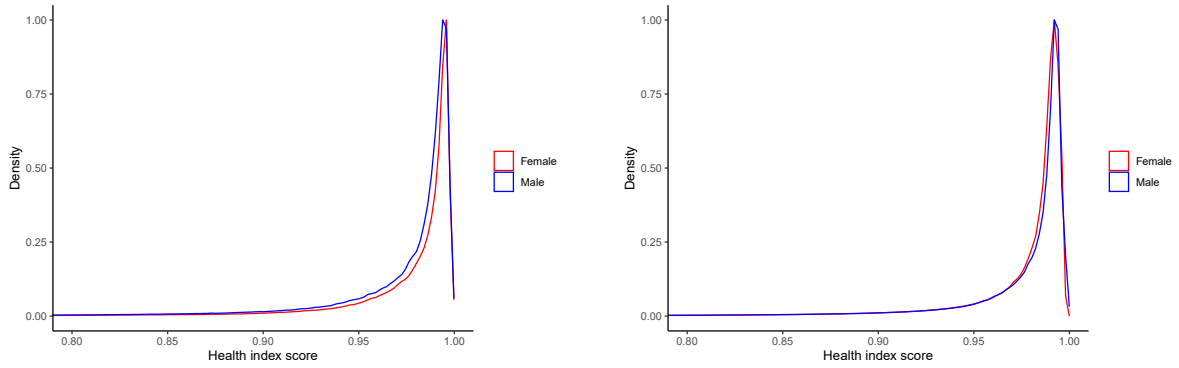
Table 7: Descriptive Table by Health Quintile

	Female		Male	
	Mean	SD	Mean	SD
5-year Mortality				
Very Poor Health	0.1568	0.3636	0.1623	0.3688
Poor Health	0.0791	0.2698	0.0773	0.2671
Around Median Health	0.0592	0.2361	0.0595	0.2366
Good Health	0.0474	0.2125	0.0455	0.2084
Excellent Health	0.0360	0.1862	0.0372	0.1892

Note: Very poor, poor, Around median, good, and very good health groupings are created based on the quintiles of the health index score distribution, i.e., very poor health individuals has a health index in the 0-20% percentile of the total health index distribution, poor health in the 21-40% and so on. The amount of person-year observations for men and women used to calculate the means and standard deviations are $14,419,741$ and $13,839,459$ respectively over the period 1995-2010 for individual at the ages from age 25+.

G The Combined CCI and Simple Index Against the Complex Input Index.

The benefit of using individual-level data is more pronounced when quantifying latent health. Figure 12 shows that the high-dimensionality of data leads to a smoother distribution with more variation.



(a) Small data input.

(b) Large data input.

Figure 12: Distribution comparison of latent health (random forest). These figures contain kernel density estimates of latent health based as either health index. All densities are estimated using Epanechnikov kernels (Epanechnikov, 1969) and a bandwidth estimator (Silverman, 1986).

A higher variation in the distribution of latent health is key to allow for the existence of more heterogeneity in health states. This is clearly better captured using the individual-level index in Figure 12b than the small-scale index in Figure 12a. The small-scale index is, however, still able to produce a reasonable approximation. Therefore, even a small amount of available objective health variables may produce a viable health index. This feature becomes extremely useful in the study of populations for which detailed health registers do not exist.

H Data-Augmented Duration Model Forecasting Setup Extended.

To give details about the data structure, let $y_{i,t}$ denote the binary mortality outcome variable, and $X_{i,t}$ a set of covariates, see Table 1, used in the forecast model that also includes period-specific time dummies $D_{i,t}$. We define $X_{i,t}$ exactly in the forecast models below. Moreover, let $\Delta_i = j, j \in \{0, 1\}$ denote whether an individual dies one year after the last in-sample period for the 1-year mortality outcome variable. Then the data augmentation is implemented such that a data block for individual i, $\mathcal{M}_{\mathcal{L},i}$ is structured, for each individual i, as

$$\mathcal{M}_{\mathcal{L},i} := \begin{array}{c} \begin{array}{cccccc} y_{it} & D_{i,1} & D_{i,2} & \cdots & D_{i,T} & X_{i,t} \end{array} \\ \begin{pmatrix} 0 & 1 & 0 & \cdots & 0 & X_{i,1} \\ 0 & 0 & 1 & \cdots & 0 & X_{i,2} \\ 0 & 0 & 0 & \cdots & 0 & X_{i,3} \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ j & 0 & 0 & \cdots & 1 & X_{i,T} \end{pmatrix} \end{array} \text{ if } \Delta_i = j$$

If an individual has $\Delta_{i,T} = 1$ (i.e. the individual dies in the last period) then that individual is dropped and not used to form the forecast model for the following periods. As a result, N is the total number of individuals used to produce the reported model estimates and statistics in the period they enter the in-sample model. Finally, let $\mathcal{L}$ denote the likelihood for the logit type binary response duration model used in e.g. Schmid et al. (2015), then the log-likelihood can be written as

$$\ln \mathcal{L} = \sum_{i=1}^{N} \sum_{t=1}^{T} \left\{ y_{it} \log \left(\frac{\exp\left(D_{i,t} + X_{i,t}^{'}\beta\right)}{1 + \exp\left(D_{i,t} + X_{i,t}^{'}\beta\right)} \right) + (1 - y_{i,t}) \log \left(\frac{\exp\left(D_{i,t} + X_{i,t}^{'}\beta\right)}{1 + \exp\left(D_{i,t} + X_{i,t}^{'}\beta\right)} \right) \right\}. \tag{6}$$

We use the linear logistic regression model due to its relative simplicity and well-explored statistical properties. Clearly, there is a possibility of better predictive algorithms. However, in pure prediction tasks, logit specifications are often found to perform at least as well as more complex methods for mortality prediction; see e.g. Austin (2007) and Austin et al. (2010). Furthermore, this task is devised to test how well the health indices capture latent health and not which forecasting technique is best equipped to capture the most appropriate trends for out-of-sample forecasting compared to competing models.

I Additional forecast results

Table 8: Out-of-sample forecast accuracy

	avg. RMSE(female)			avg. MCS p-value(female)			avg. RMSE(male)			avg. MCS p-value(male)		
Index type \Mortality	**1-year**	**3-year**	**5-year**	**1-year**	**3-year**	**5-year**	**1-year**	**3-year**	**5-year**	**1-year**	**3-year**	**5-year**
Base model (abs. value)	0.004	0.002	0.001	0.070	0.070	0.062	0.006	0.003	0.002	0.058	0.063	0.051
CCI	1.011	1.020	0.978	0.072	0.073	0.068	1.029	1.039	1.033	0.060	0.067	0.054
CCI (w. lag)	1.011	1.031	1.001	0.074	0.074	0.070	1.042	1.058	1.060	0.062	0.068	0.055
CCI time varying	1.026	1.021	0.963	0.072	0.072	0.066	1.048	1.061	1.058	0.059	0.065	0.054
CCI time varying (w. lag)	1.038	1.038	0.983	0.073	0.074	0.069	1.069	1.087	1.085	0.061	0.065	0.055
Regularized logit	0.986	0.988	1.004	0.078	0.082	0.076	0.802	0.789	0.755	0.087	0.107	0.091
Regularized logit (w. lag)	0.973	0.992	1.017	0.085	0.089	0.084	0.726	0.712	0.686	0.221	0.284	0.386
RF (100 trees) index	0.767	0.826	1.070	0.206	0.166	0.128	0.730	0.840	1.118	0.070	0.082	0.057
RF (100 trees) index (w. lag)	0.743	0.826	1.028	0.732	0.595	0.185	0.678	0.750	0.948	**0.725**	0.590	0.174
RF (2000 trees) index	0.714	0.771	0.922	0.110	0.120	0.127	0.625	0.597	0.608	0.092	0.113	0.072
RF (2000 trees) index (w. lag)	**0.665**	**0.712**	**0.891**	**0.807**	**0.907**	**1.000**	**0.554**	**0.514**	**0.532**	0.538	**0.775**	**1.000**

Note: This table contains the average forecast accuracy results reported as ratios relative to the base model and model confidence set p-values. Only the base model is reported in absolute values to provide a scale of reference. The MCS procedure use the squared error loss function. In this table the p-values presented stem from the procedure using the $T_{\mathcal{R}}$-statistic. The MCS statistics are based on 5000 bootstrap samples. The MCS is implemented using cluster-bootstrap that draws samples by clusters rather than consecutive time periods to accommodate the dependence structure of our augmented-data duration model setup. Entries in **bold** indicate the best performing model.

Table 9: Out-of-sample forecast accuracy

	avg. Cross-entropy(female)			avg. Cross-entropy(male)		
Index type \Mortality	**1-year**	**3-year**	**5-year**	**1-year**	**3-year**	**5-year**
Base model	0.1095	0.1028	0.0977	0.1431	0.1028	0.1278
CCI	0.1090	0.1021	0.0965	0.1422	0.1021	0.1260
CCI (w. lag)	0.1088	0.1018	0.0961	0.1419	0.1018	0.1256
CCI time varying	0.1087	0.1017	0.0961	0.1419	0.1017	0.1254
CCI time varying (w. lag)	0.1084	0.1013	0.0955	0.1415	0.1013	0.1248
Regularized logit	0.1061	0.0989	0.0929	0.1387	0.0989	0.1215
Regularized logit (w. lag)	0.1053	0.0980	0.0919	0.1377	0.0980	0.1204
RF (100 trees) index	0.1049	0.0979	0.0922	0.1379	0.0979	0.1215
RF (100 trees) index (w. lag)	0.1046	0.0976	0.0920	**0.1373**	0.0976	0.1209
RF (2000 trees) index	0.1050	0.0978	0.0918	0.1383	0.0978	0.1211
RF (2000 trees) index (w. lag)	**0.1043**	**0.0970**	**0.0909**	0.1374	**0.0970**	**0.1201**

Note: This table contains the average forecast accuracy results using the cross-entropy loss function for 1, 3 and 5 year mortality. **Bold** indicates the best performing model. This table report the absolute values of the cross-entropy loss.

Table 10: Out-of-sample forecast accuracy

	Rel. avg. Cross-entropy(female)			**Rel. avg. Cross-entropy(male)**		
Index type \Mortality	**1-year**	**3-year**	**5-year**	**1-year**	**3-year**	**5-year**
Base model	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
CCI	0.9953	0.9928	0.9882	0.9934	0.9928	0.9861
CCI (w. lag)	0.9941	0.9908	0.9842	0.9913	0.9908	0.9826
CCI time varying	0.9927	0.9893	0.9836	0.9913	0.9893	0.9814
CCI time varying (w. lag)	0.9901	0.9859	0.9783	0.9885	0.9859	0.9766
Regularized logit	0.9694	0.9617	0.9516	0.9689	0.9617	0.9504
Regularized logit (w. lag)	0.9615	0.9532	0.9416	0.9620	0.9532	0.9422
RF (100 trees) index	0.9579	0.9519	0.9443	0.9632	0.9519	0.9508
RF (100 trees) index (w. lag)	0.9557	0.9498	0.9426	**0.9592**	0.9498	0.9460
RF (2000 trees) index	0.9596	0.9512	0.9397	0.9661	0.9512	0.9472
RF (2000 trees) index (w. lag)	**0.9524**	**0.9437**	**0.9310**	0.9596	**0.9437**	**0.9395**

Note: This table contains the average forecast accuracy results using the cross-entropy loss function for 1, 3 and 5 year mortality. **Bold** indicates the best performing model. This table report the values of the cross-entropy loss relative to those of the base model.

Table 11: Out-of-sample forecast accuracy: small-scale vs. large-scale indices.

	Index type \Mortality	**1-year**	**3-year**	**5-year**
Female	Reg. logit (ratio)	1.0687	1.0632	1.0394
	Random forest (ratio)	0.8340	0.8537	0.8983
Male	Reg. logit (ratio)	1.0000	1.0061	0.9872
	Random forest (ratio)	0.8872	0.8734	0.8810

Note: This table contains the relative average forecast between our large-scale and small-scale index. A value below 1 indicates that the large-scale index model provides a better forecast accuracy.

References

Austin, P. C. (2007). A comparison of regression trees, logistic regression, generalized additive models, and multivariate adaptive regression splines for predicting AMI mortality. *Statistics in Medicine*, *26*(15), 2937–2957. doi: 10.1002/sim.2770

Austin, P. C., Tu, J. V., & Lee, D. S. (2010, oct). Logistic regression had superior performance compared with regression trees for predicting in-hospital mortality in patients hospitalized with heart failure. *Journal of Clinical Epidemiology*, *63*(10), 1145–1155. doi: 10.1016/j.jclinepi.2009.12.004

Breiman, L. (1996). *Machine Learning*, *24*(1), 41–47. doi: 10.1023/a:1018094028462

Chandra, A., Gruber, J., & McKnight, R. (2010, mar). Patient cost-sharing and hospitalization offsets in the elderly. *American Economic Review*, *100*(1), 193–213. doi: 10.1257/aer.100.1.193

Chernozhukov, V., Chetverikov, D., Demirer, M., Duflo, E., Hansen, C., Newey, W., & Robins, J. (2018, jan). Double/debiased machine learning for treatment and structural parameters. *The Econometrics Journal*, *21*(1), C1–C68. doi: 10.1111/ectj.12097

Deeks, S. G., Lewin, S. R., & Havlir, D. V. (2013, nov). The end of AIDS: HIV infection as a chronic disease. *The Lancet*, *382*(9903), 1525–1533. doi: 10.1016/s0140-6736(13)61809-7

Epanechnikov, V. A. (1969, jan). Non-parametric estimation of a multivariate probability density. *Theory of Probability & Its Applications*, *14*(1), 153–158. doi: 10.1137/1114019

Probst, P., & Boulesteix, A.-L. (2017). To tune or not to tune the number of trees in random forest. *Journal of Machine Learning Research*, *18*(1), 6673–6690.

Probst, P., Wright, M. N., & Boulesteix, A.-L. (2019, jan). Hyperparameters and tuning strategies for random forest. *WIREs Data Mining and Knowledge Discovery*, *9*(3). doi: 10.1002/widm.1301

Schmid, M., Küchenhoff, H., Hoerauf, A., & Tutz, G. (2015, sep). A survival tree method for the analysis of discrete event times in clinical and epidemiological studies. *Statistics in Medicine*, *35*(5), 734–751. doi: 10.1002/sim.6729

Silverman, B. W. (1986). *Density estimation for statistics and data analysis* (Vol. 26). CRC press.