‘Reduced’ HUNT model outperforms NLST and NELSON study criteria in predicting lung cancer in the Danish screening trial

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ABSTRACT

Hypothesis We hypothesise that the validated HUNT Lung Cancer Risk Model would perform better than the NLST (USA) and the NELSON (Dutch-Belgian) criteria in the Danish Lung Cancer Screening Trial (DLCST).

Methods The DLCST measured only five out of the seven variables included in validated HUNT Lung Cancer Model. Therefore a ‘Reduced’ model was retrained in the Norwegian HUNT2-cohort using the same statistical methodology as in the original HUNT model but based only on age, pack years, smoking intensity, quit time and body mass index (BMI), adjusted for sex. The model was applied on the DLCST-cohort and contrasted against the NLST and NELSON criteria.

Results Among the 4051 smokers in the DLCST with 10 years follow-up, median age was 57.6, BMI 24.75, pack years 33.8, cigarettes per day 20 and most were current smokers. For the same number of individuals selected for screening, the performance of the ‘Reduced’ HUNT was increased in all metrics compared with both the NLST and the NELSON criteria. In addition, to achieve the same sensitivity, one would need to screen fewer people by the ‘Reduced’ HUNT model versus using either the NLST or the NELSON criteria (709 vs 918, p=1.02e-11 and 1317 vs 1668, p=2.2e-16, respectively).

Conclusions The ‘Reduced’ HUNT model is superior in predicting lung cancer to both the NLST and NELSON criteria in a cost-effective way. This study supports the use of the HUNT Lung Cancer Model for selection based on risk ranking rather than age, pack year and quit time cut-off values. When we know how to rank personal risk, it will be up to the medical community and lawmakers to decide which risk threshold will be set for screening.

INTRODUCTION

Lung cancer is the leading cause of cancer mortality worldwide,1 and early diagnosis is paramount for increasing survival. Currently two studies have shown survival benefit of lung cancer screening: the National Lung Screening Trial (NLST) and the Dutch-Belgian randomised lung cancer screening trial NELSON study (abstract only). The NLST was the largest prospective trial showing that low-dose high-resolution computed axial tomography (CT) scanning versus X-ray of heavy smokers (>30 pack years, <15 years quit time) ages 55–74 at inclusion time and at 6 years of follow-up reduced lung cancer mortality by 20%.2 At the World Congress of Lung Cancer 2018, the NELSON results revealed that CT screening showed a 26% reduction in lung cancer deaths at 10 years of study follow-up.3 However, an estimated 26.7% of those who develop lung cancer in a general US population fulfil the NLST inclusion criteria for CT screening, and for the NELSON such an estimation is not available.4

In a current European Union position statement recently published in the Lancet Oncology, risk stratification is one of the keys to ensure the successful implementation of future low-dose CT screening programmes in Europe.6 Unfortunately, there is no international consensus on which criteria or models to use for the optimal selection for lung cancer screening.
Several multivariable risk prediction models have been proposed to improve the selection of individuals for lung cancer screening. In addition to NLST’s pack years, quit-time, and age, these models also have considered other potential risk factors, such as history of respiratory diseases, exposure to occupational dust (asbestos, coal, silica), socioeconomic status, body mass index (BMI), history of cancer, race, education, forced expiratory volume and biochemical parameters (eg, carcinoembryonic antigen, alpha-fetoprotein, and C reactive protein). However, these models and corresponding exclusion criteria were; body-weight >130kg, former lung, breast or kidney cancer or malignant melanoma, >5 years after treatment for other cancers, symptoms of lung cancer (hemoptysis, chest pain, weight loss >6kg, dyspnoea at rest), CT scan within last year or treatment for tuberculosis less than 2 years ago.

METHODS

DLCST cohort

The DLCST was conducted in Denmark, a prospective lung cancer screening trial randomising participants to a baseline and four annual CT scans versus no follow-up. Between the 1 November 2004 and 31 March 2006, a total of 4104 participants (mean age 58 years; 45% women) were enrolled, starting with an initial (baseline) screening and followed by four annual screening rounds and follow-up until 2015. All cancers diagnosed were histologically or cytologically verified. Participants had to be smokers or former smokers with at least 20 pack years, less than 10 years quit time and age 50–70. The participants also had to be able to walk 36 stair-steps up without stopping, and have lung function (forced expiratory volume in one second) >50% of predicted. The exclusion criteria were; body-weight >130kg, former lung, breast or kidney cancer or malignant melanoma, >5 years after treatment for other cancers, symptoms of lung cancer (haemoptysis, chest pain, weight loss >6kg, dyspnoea at rest), CT scan within last year or treatment for tuberculosis less than 2 years ago.

Developing the ‘Reduced’ HUNT model based on the HUNT Lung Cancer Model methodology

The original HUNT Lung Cancer Model was developed based on the Nord-Trøndelag Health Study 2 (HUNT2), which is a collaboration between HUNT Research Centre (Faculty of Medicine and Health Sciences, Norwegian University of Science and Technology), Nord-Trøndelag County Council, Central Norway Health Authority, and the Norwegian Institute of Public Health. In short, from 1995 to 1997, HUNT2 invited 93 898 residents of Nord-Trøndelag County in Norway, aged 20 years more or less, to participate in a health survey, and ≈70% (n=65 237) responded. The data were collected through questionnaires on demographic characteristics, medical history and lifestyle (199 variables). In 2012, our group was granted access to analyse the HUNT2 data to identify lung cancer cases and establish the HUNT2 discovery dataset. This dataset was linked with the national 11-digit personal identification number of each participant to the Norwegian Cancer and Death Cause Registry. The resulting risk prediction model, called HUNT Lung Cancer Model included seven variables: age, pack years, smoking intensity, years since smoking cessation, BMI, cancer history, forced expiratory volume, and body mass index.
The ideal scenario would be to test the HUNT Lung Cancer Model with all seven variables in the Danish cohort. However, two variables were not recorded in the DLCST, namely ‘daily cough in periods of the year’ and ‘hours of indoor smoke exposure’. The original variables were measured in DLCST were by default included in the model; sex, age, pack years, BMI (height and weight were given and used for BMI estimation), quit years, cigarettes per day, adjusted for sex. This ‘Reduced’ HUNT model (named HUNT model hereafter) was trained in the HUNT2 subcohort of 12 091 ever-smokers aged 50–70 (online supplementary table S1), which is the DLCST inclusion age, to ensure applicability to the Danish cohort.1 In this HUNT subcohort, 227 lung cancers were diagnosed within 10 years follow-up. The same statistical methodology as described in Markaki et al14 was applied, excluding the feature selection step; the five variables measured in DLCST were by default included in the model. In more detail, the original variables were non-linearly transformed whenever necessary, as in the original paper; hence pack years, quit time and BMI were logarithmically transformed. Missing values were imputed using multiple imputation with predictive mean matching (R package mice), resulting in 30 complete datasets. For each of them, 200 bootstrap datasets were generated for the internal validation of the model using R package rms.14 Discrimination power measured by the C-index and calibration were assessed as performance metrics. In calibration plots, the Hosmer-Lemeshow test was used to denote goodness of fit between the predicted and observed individual risks. To analyse the model with the clinical criteria on equal grounds, we set a risk threshold that defines equal number of screenings to the ones suggested by NLST or NELSON and compare the numbers of false positives and false negatives with the χ² test (p<0.05 deemed significant). The χ² test was also used for comparing percentage of screenings according to the HUNT model to achieve the same sensitivity as the NLST and NELSON (p<0.05 deemed significant).

To identify a high-risk group, we consider as a high-risk individual anybody with a risk score in the top 16 quantile, as proposed by Royston and Altman and used in the original HUNT model study.15

**NLST and NELSON study criteria**
The criteria for inclusion in the NLST are the following: age 55–74, >30 pack years and <15 years quit time. For the NELSON study, the respective criteria are: age 50–75, >15 cigarettes a day >25 years, or >10 cigarettes a day >30 years, 10 or less years quit time. The two sets of criteria were enforced on the DLCST to characterise individuals as high-risk and predict that they would develop lung cancer.

**RESULTS**

**DLCST cohort descriptive statistics**
The DLCST included 4104 individuals (2052 screened, 2052 non-screened) where 4051 (98.7%) individuals had registered all the five variables required for the HUNT model and 149 of 153 (97.3%) lung cancers developed in this group. The univariate distributions of each of the five measured variables, as well as sex do not significantly differ between the screened and non-screened groups (table 1).

**Performance of the HUNT model on the DLCST cohort**
Internal validation in the HUNT2 subset produced a C-index=0.783. The C-index metric equals the probability that the model assigns a higher risk to the person that experiences the event first (lung cancer diagnosis) between a pair of randomly chosen individuals. External validation on the Danish cohort produced a lower C-index (total group 0.663, non-screened 0.709, screened 0.638). The calibration was reliable for the HUNT2 subset (p=0.452) and marginal for the Danish cohort (p=0.0681) (online supplementary figure 1). This finding is explained by the fact that the HUNT2 and DLCST have significantly different distributions of risk factors (table 2) due to the fact that the DLCST is a selected, heavy-smoker population.

Setting as threshold the top 16 quantile risk score of the HUNT in the DLCST would have selected for

<table>
<thead>
<tr>
<th>Variables</th>
<th>All</th>
<th>Screened</th>
<th>Non-screened</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex, males (%)</td>
<td>54.70</td>
<td>56.03</td>
<td>54.63</td>
<td>0.3737</td>
</tr>
<tr>
<td>Age median (iqd)</td>
<td>57.61 (53.72–61.21)</td>
<td>57.73 (53.66–61.23)</td>
<td>57.45 (53.79–61.20)</td>
<td>0.7836</td>
</tr>
<tr>
<td>Pack years median (iqd)</td>
<td>33.75 (27.00–42.00)</td>
<td>34.00 (27.00–42.22)</td>
<td>33.00 (26.25–42.00)</td>
<td>0.2402</td>
</tr>
<tr>
<td>BMI median (iqd)</td>
<td>24.75 (22.65–27.27)</td>
<td>24.74 (22.64–27.38)</td>
<td>24.76 (22.66–27.17)</td>
<td>0.7336</td>
</tr>
<tr>
<td>Quit time, years median (iqd)</td>
<td>0 (0–0)</td>
<td>0 (0–0)</td>
<td>0 (0–0)</td>
<td>0.1855</td>
</tr>
<tr>
<td>Cigarettes per day median (iqd)</td>
<td>20 (15–20)</td>
<td>20 (15–20)</td>
<td>20 (15–20)</td>
<td>0.4665</td>
</tr>
</tbody>
</table>

BMI, body mass index; DLCST, Danish Lung Cancer Screening Trial.
Table 2  Modified Cox-regression model (‘Reduced’ HUNT model) of cancer risk for ever smokers in HUNT2, restricted to age 50–70 as in the Danish cohort, with no previous cancer, no cancer at inclusion and 10 years follow-up (n=12 091). Body mass index, pack years and smoking quit time had a non-linear association with lung cancer, and these variables were logarithmically transformed.

<table>
<thead>
<tr>
<th>Variable</th>
<th>P value</th>
<th>Beta coefficient (95% CI)</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>&lt;0.0001</td>
<td>0.0682 (0.0458 to 0.0905)</td>
<td>0.0114</td>
</tr>
<tr>
<td>Sex</td>
<td>0.7514</td>
<td>0.0479 (−0.2304 to 0.3262)</td>
<td>0.1420</td>
</tr>
<tr>
<td>Body mass index (log)</td>
<td>0.0017</td>
<td>−1.4879 (−2.4409 to 0.5350)</td>
<td>0.4862</td>
</tr>
<tr>
<td>Smoking intensity</td>
<td>0.0469</td>
<td>−0.0331 (−0.0623 to 0.0039)</td>
<td>0.0149</td>
</tr>
<tr>
<td>Pack years (log)</td>
<td>&lt;0.0001</td>
<td>1.2066 (0.8150 to 1.5982)</td>
<td>0.1998</td>
</tr>
<tr>
<td>Smoking quit time (log)</td>
<td>0.0011</td>
<td>−0.2667 (−0.4235 to 0.1099)</td>
<td>0.0800</td>
</tr>
</tbody>
</table>

screening 148 out of the 149 individuals that developed lung cancer (sensitivity 99.3%, specificity 3.31%, positive predictive value (PPV) 3.77%, negative predictive value (NPV) 99.23%, figure 1, table 3).

**Comparison of the HUNT model against the NLST criteria**

According to the NLST criteria less than half of the Danish cohort 1870/4051 (46.2%) would be considered eligible for screening. Among those selected, 104/149 cases would have been identified for screening (sensitivity 69.80%, p=1.54e-14, in favour of HUNT, figure 1, table 3).

As mentioned, the NLST criteria provide binary decisions (screen, not screen), while the HUNT model ranks individuals according to predicted risk. To compare the model with the clinical criteria on equal grounds, we set a risk threshold that defines equal number of screenings to the ones suggested by NLST. Hence, for the same number of individuals screened (n=918) suggested by NLST in the non-screened DLCST cohort (n=1 999), the HUNT model showed increased predictive performance in all metrics: sensitivity, specificity, PPV and NPV (table 4). In addition, for a risk threshold of the HUNT model so that the sensitivity achieved (percentage of detected cases out of all cases) equals the sensitivity of the NLST criteria, the number of suggested screenings by the HUNT model is significantly lower: 709 screenings for the HUNT model versus 918 screenings for the NLST (p=1.02e-11, figure 2).

**Comparison of the HUNT model against the NELSON criteria**

The NELSON study age criterion was 50–75 but had two sets of smoking criteria; >15 cigarettes a day >25 years, ≤10 years quit time (here called NELSON1), or >10 cigarettes a day >30 years, ≤10 years quit time (here called NELSON2). By using the NELSON1 in the whole DLCST 2360/4051 (58.25%) people were selected for screening resulting in 109/149 (sensitivity 73.15%) cancers being...
Table 3  Performance of the ‘Reduced’ HUNT model versus NLST and NELSON criteria based on the whole cohort (n=4051).

<table>
<thead>
<tr>
<th></th>
<th>LC (n)</th>
<th>Without LC (n)</th>
<th>Total (n)</th>
<th>Predictive value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Population</strong></td>
<td>149</td>
<td>3902</td>
<td>4051</td>
<td></td>
</tr>
<tr>
<td>‘Reduced’ HUNT*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>148 TP (3.77%)</td>
<td>3773 FP (96.23%)</td>
<td>3921</td>
<td>PPV 3.77%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>1 FN (0.77%)</td>
<td>129 TN (99.23%)</td>
<td>130</td>
<td>NPV 99.23%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>99.33%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>3.31%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>NLST†</strong></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Criteria positive</td>
<td>104 TP (5.56%)</td>
<td>1766 FP (94.44%)</td>
<td>1870‡</td>
<td>PPV 5.56%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>45 FN (2.06%)</td>
<td>2136 TN (97.94%)</td>
<td>2181</td>
<td>NPV 97.94%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>69.80%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>54.74%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>NELSON§</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>141 TP (4.08%)</td>
<td>3449 FP (96.07%)</td>
<td>3590</td>
<td>PPV 4.08 %</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>8 FN (1.71%)</td>
<td>461 TN (98.29%)</td>
<td>469</td>
<td>NPV 98.29%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>94.63%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>11.79%</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td><strong>NELSON2¶</strong></td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>141 TP (4.20%)</td>
<td>3209 FP (95.79%)</td>
<td>3350</td>
<td>PPV 4.20 %</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>8 FN (1.14%)</td>
<td>693 TN (98.29%)</td>
<td>701</td>
<td>NPV 98.85%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>94.63%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>17.76%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*‘Reduced’ HUNT model criteria.
†NLST criteria (>30 pack years of smoking, <15 years since quitting and ages between 55 and 74 years).
‡Total criteria positive selected by the ‘Reduced’ HUNT model includes those picked by the NLST.
§NELSON criteria age 50–75, >15 cigarettes a day >25 years, or >10 cigarettes a day >30 years, both with 10 or less years quit time.
¶NELSON2 criteria >10 cigarettes a day >30 years, both with 10 or less years quit time.
FN, false negative; FP, false positive; NPV, negative predictive value; PPV, positive predictive value; TN, true negative; TP, true positive.

Predicted. The NELSON2 criteria would select 3350/4051 (82.69%) people for screening detecting 141/149 (sensitivity 94.73%) cancers. The NELSON criteria, which is the union of the NELSON1 and NELSON2 criteria, would select 3590/4051 (88.62%) people for screening predicting 141/149 cancers (sensitivity 94.73%, p=0.018, in favour of HUNT) (table 3, figure 1).

To compare the NELSON criteria to the HUNT model on equal grounds we follow the same methodology described above. When the risk-threshold is set so that the two models suggest the same number of screenings (n=1668), the HUNT model outperforms the NELSON criteria in all metrics, namely sensitivity, specificity, PPV and NPV (table 5). In addition, for a risk threshold of the HUNT model so that the sensitivity achieved (percentage of detected cases out of all cases) equals the sensitivity of the NELSON criteria, the HUNT model requires the screening of a significantly smaller number of individuals, namely 1317 versus 1668 for the NELSON (p=2.2e-16, figure 2).

**DISCUSSION AND CONCLUSIONS**

The optimal selection of a high-risk population for lung cancer screening is still an unsolved issue. For example, simple age and smoking criteria, like the NLST, would fail to screen two-thirds of smokers that develop lung cancer.3

In this study, we used the validated 7-variable HUNT Lung Cancer Model to develop and apply a 5-variable ‘Reduced’ HUNT model, based on the five available variables in the Danish screening trial. This downgraded-to-5-variables, reduced model outperforms cut-off criteria such as the NLST and the NELSON. In addition, it outperforms these criteria on the high-risk subpopulations for which they were developed.

**Comparison of the ‘Reduced’ HUNT model with the NLST and NELSON**

The DLCST cohort was a high-risk cohort by itself and improving the selection further represented a difficult
### Table 4  Direct comparison of the ‘Reduced’ HUNT model against NLST criteria, for the same number of individuals as selected by the NLST \( (n=918) \), on the control group of DLCST \( (n=1999) \). The HUNT model shows increased predictive performance in all metrics (sensitivity, specificity, PPV, NPV)

<table>
<thead>
<tr>
<th>Population</th>
<th>LC (N)</th>
<th>Without LC (N)</th>
<th>Total (N)</th>
<th>Predictive value</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘Reduced’ HUNT</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>40 TP (4.36% )</td>
<td>878 FP (95.64%)</td>
<td>918†</td>
<td>PPV 4.36%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>12 FN (1.11%)</td>
<td>1069 TN (98.89%)</td>
<td>1081</td>
<td>NPV 98.89%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>76.92%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>54.90%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NLST‡</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>35 TP (3.81%)</td>
<td>883 FP (96.19%)</td>
<td>918*</td>
<td>PPV 3.81%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>17 FN 1.57%</td>
<td>1064 TN 98.43%</td>
<td>1081</td>
<td>NPV 98.43%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>67.31%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>54.65%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*‘Reduced’ HUNT model.  
“‘Reduced’ HUNT model criteria.  
†The number of those picked by the NLST, but with the top risk score by the ‘Reduced’ HUNT model.  
‡NLST criteria (≥30 pack years of smoking, <15 years since quitting and ages between 55 and 74 years).  
FN, false negative; FP , false positive; NPV, negative predictive value; PPV, positive predictive value; TN, true negative; TP, true positive.

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As we noted in our previous HUNT paper, and according to the original HUNT model, in a low-smoking population, one would need to screen only 22% of ever-smokers to identify 81.85% of all lung cancers within 6 years. In this highly selected cohort, using the same threshold excludes very few from screening (3.2%) and identifies almost the whole DLCT cohort as high-risk, which is logical, since most were heavy smokers and current smokers. However, it predicts 149 out of 150 cases, 99.3%.

In contrast, applying the NLST selection criteria on the DLCST cohort is so strict that 53.8% of this population would be excluded and one would fail to screen 40.2% of the cases within this cohort (figure 1, table 3). Similarly, applying the NELSON study criteria on the DLCST, one would exclude from screening 17.4% of the population failing to identify 5.3% of the cancer cases (table 3).

A major difference between the HUNT model and fixed criteria sets, like the NELSON and the NLST, is that the former produces a ranking of individuals according to risk. To decide which individuals to screen, one needs to set a risk threshold above which screening should take place. The threshold should be set in the most cost-effective way, as a consensus, considering all public health factors (eg, screening capacity, risk due to screening, predictive performance of the model).

One may question whether these models are developed in a population with a representative spectrum of all lung cancer subtypes. The cancer subtypes in the DLCST were...
can be fivefold more common than correct diagnosis. 17

reasons, such as estrangement, death, or adoption from
may not know details of their family history due to several
that may be hard to obtain accurately as some people
Similarly, ‘family history of lung cancer’ is also a variable
misdiagnosis is very common : under- and over-
in biassed predictions. Specifically, in the case of COPD,
‘family history of lung cancer’, correspondingly reflected
that are susceptible to bias, namely ‘history of COPD’ and
Moreover, there are two variables used in the PLCO m2012
as well as combinations of all those are not represented.11
of smoking, people younger than 55 or older than 74 and
≈
count of
30 high, and thus light smokers with many years
in a population of age 55–74 and with a mean pack year

Previous studies have previously published and include the whole spectrum of
lung cancers, including 38% adenocarcinoma, 15% squa-

-60000
-
potential danger of transferring a population-
histor
documented in medical records did not report a family
one-
factor to a personal risk prediction model.19 20

Model was developed in a total adult population of all
degrees of smoking burden with 199 clinical variables to
choose among, an ideal population to learn which are
suitable to high-

Moreover, there are two variables used in the PLCO m2012
that are susceptible to bias, namely ‘history of COPD’ and
‘family history of lung cancer’, correspondingly reflected
in biassed predictions. Specifically, in the case of COPD,
misdiagnosis is very common : under- and over-diagnosis
can be fivefold more common than correct diagnosis. 17
Similarly, ‘family history of lung cancer’ is also a variable
that may be hard to obtain accurately as some people
may not know details of their family history due to several
reasons, such as estrangement, death, or adoption from
unknown donors.16 18 Some studies showed that about
one-quarter of those who had blood relatives with cancer
documented in medical records did not report a family
history. Such studies demonstrate the weakness and
potential danger of transferring a population-based risk
factor to a personal risk prediction model.19 20

Study limitations
The present study, analysis, and model exhibit several
limitations. The original HUNT Lung Cancer Risk
Model was developed in a total adult population of all
degrees of smoking burden with 199 clinical variables to
choose among, an ideal population to learn which are
independent and interdependent risk factors.11
Out of the 199 variables, 36 were manually selected based
on expert knowledge; the data-driven feature selection
ended up with seven clinical variables, out of which five
were employed in the HUNT model presented here. The
manual feature selection was performed so that the Cox
model had enough statistical power to enable a back-
ward feature selection methodology. However, one could
potentially employ other feature selection method, more
suitable to high-dimensional data, to perform feature
selection directly with the original set of the 199 vari-
ables, possibly leading to better predictive models. In addi-
tion, other modelling techniques could be employed to
try to improve the predictive power, for example, using
Random Survival Forests, Support Vector Machines for
censored time-to-event outcomes, and others.

To apply the HUNT model to a clinical setting, as
mentioned above, one should choose a risk threshold
for defining the high-risk population to screen. Such
a threshold is not trivial to determine as it depends on
several factors and public health issues.

<table>
<thead>
<tr>
<th>Population</th>
<th>LC (N)</th>
<th>Without LC (N)</th>
<th>Total (N)</th>
<th>Predictive value</th>
</tr>
</thead>
<tbody>
<tr>
<td>‘Reduced’ HUNT*</td>
<td>52</td>
<td>1947</td>
<td>1999</td>
<td></td>
</tr>
<tr>
<td>Criteria positive</td>
<td>50 TP (3.00%)</td>
<td>1618 FP (97.00%)</td>
<td>1668†</td>
<td>PPV 3.00%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>2 FN (0.60%)</td>
<td>329 TN (99.40%)</td>
<td>331</td>
<td>NPV 99.40%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>96.15%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>16.90%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NELSON‡</td>
<td>47 TP (2.82%)</td>
<td>1621 FP (97.18%)</td>
<td>1668*</td>
<td>PPV 2.82%</td>
</tr>
<tr>
<td>Criteria negative</td>
<td>5 FN (1.51%)</td>
<td>326 TN (98.45%)</td>
<td>331</td>
<td>NPV 98.45%</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>90.38%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Specificity</td>
<td>16.74%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*‘Reduced’ HUNT model.
†‘Reduced’ HUNT model criteria.
‡NELSON criteria age 50–75, >15 cigarettes a day >25 years, or >10 cigarettes a day >30 years, both with 10 or less years quit time.
FN, false negative; FP, false positive; NPV, negative predictive value; PPV, positive predictive value; TN, true negative; TP, true positive.

Comparison of HUNT with the PLCO m2012 model
The five variables in this HUNT model were also found
in another high-performing model, the PLCO m2012, that
consists of 10 variables, including COPD, family history
of lung cancer and educational status.16 The PLCO m2012
was also found more sensitive than the NLST criteria in the
NLST study, and showed how ranking of risk is superior
to fixed criteria, like in our study. However, in contrast to
the original HUNT model the PLCO m2012 was developed
in a population of age 55–74 and with a mean pack year
count of =30 high, and thus light smokers with many years
of smoking, people younger than 55 or older than 74 and
as well as combinations of all those are not represented.11

Moreover, there are two variables used in the PLCO m2012
that are susceptible to bias, namely ‘history of COPD’ and
‘family history of lung cancer’, correspondingly reflected
in biassed predictions. Specifically, in the case of COPD,
misdiagnosis is very common : under- and over-diagnosis
can be fivefold more common than correct diagnosis. 17
Similarly, ‘family history of lung cancer’ is also a variable
that may be hard to obtain accurately as some people
may not know details of their family history due to several
reasons, such as estrangement, death, or adoption from
unknown donors.16 18 Some studies showed that about
one-quarter of those who had blood relatives with cancer
documented in medical records did not report a family
history. Such studies demonstrate the weakness and
potential danger of transferring a population-based risk
factor to a personal risk prediction model.19 20

Table 5 Direct comparison of the ‘Reduced’ HUNT model against NELSON criteria, for the same number of individuals (n=1668), on the control group of DLCST. The HUNT model shows increased predictive performance in all metrics (sensitivity, specificity, PPV, NPV)
A shortcoming of the present study is that the DLCST lacked two variables of the original HUNT model, namely, periodical daily cough and hours of exposure to indoor smoke. Thus, the current study serves only as a proxy of a direct comparison of the original HUNT model with the NLST and the NELSON criteria. Nevertheless, it is reasonable to expect that the inclusion of these extra sources of information would prove beneficial and not detrimental to the predictive power of the model.

Moreover, as much as we would like to compare the PLCO model against the HUNT model on the Danish cohort, unfortunately, this is not possible as the PLCO model requires variables not measured in that cohort. Specifically, the variables needed for the PLCO model not included in the Danish trial are: race, education, COPD yes/no, personal history of cancer yes/no, family history of lung cancer yes/no. Nevertheless, an aggregate comparison between the original HUNT model and the PLCO, that is, a comparison on their average predictive metrics and not individual predictions on the same cohort, was performed in the HUNT original paper in EBiomedicine.11

Regarding the cohorts used in this study, both the training data (HUNT cohort) and the validation data (DLCST) are of European ancestry; it is thus untested, how well the model generalises to populations of other ancestries such as, African, Asian and South American that are under-represented in both cohorts. The generalisation of the model to populations that are either genetically or socially (lifestyle) quite different deserves further study. In addition, the training cohort lacked some quantities, not included in our original 36 considered variables. Clinical quantities such as significant comorbidities and employment exposures could possibly improve the predictive power of the model. Of course, molecular measurements could provide a wealth of predictive information that is not employed in the current work.

CONCLUSIONS

The HUNT model outperforms the NLST and the NELSON criteria in all predictive performance metrics, as demonstrated on the DLCST study, a screening trial in Denmark with a 10-year follow-up period. Unlike cut-off criteria regarding age, pack years and quit time, a risk prediction model ranks individuals according to a weighted average of many variables, permitting the medical community and public health authorities to determine the risk threshold that is most cost-effective for screening. This is the first study that directly compares favourably against the NELSON criteria. The results support the original HUNT Lung Cancer Model and indicate that this should be used prospectively in a screening study or programme. Data-driven, multivariable predictive models, when trained with state-of-the-art methods in statistics and machine learning, seem to outperform current criteria and provide a potentially fruitful research direction that could be clinically important. Our hope is that public health authorities will consider this fact when determining screening guidelines.

REFERENCES


4 De Koning H, Van Der Aalst C, Ten Haaf K, et al. PL02.05 effects of volume CT lung cancer screening: mortality results of the Nelson


