



```

1 .
2 . *****ALL INFECTIONS*****
3 .
4 . use "E:\16GBBACKUPUSB\BACKUP_USB_SEPTEMBER2014\May Baydoun_folder\UK_BIOBANK_PROJECT\UKB_PAPER3_LE8INFECTION\DATA\
5 .
6 .
7 . *****STSET FOR AD*****
8 . stset Age_AD if sample_final==1, failure(ad_diag==1) enter(baselineage) id(n_eid) scale(1)

```

Survival-time data settings

```

      ID variable: n_eid
      Failure event: ad_diag==1
Observed time interval: (Age_AD[_n-1], Age_AD]
Enter on or after: time baselineage
Exit on or before: failure
Keep observations
      if exp: sample_final==1

```

---

502,389 total observations

147,343 ignored at outset because of if exp

---

355,046 observations remaining, representing

355,046 subjects

2,665 failures in single-failure-per-subject data

4,364,749 total analysis time at risk and under observation

At risk from t = 0

Earliest observed entry t = 50.00137

Last observed exit t = 87.63313

```

9 .
10 .
11 .
12 . *****OVERALL*****
13 .
14 . **Model 1**
15 .
16 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES LE8_TOTALSCORE if sample_final==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
Enter on or after: time baselineage
      ID variable: n_eid

```

Iteration 0: log likelihood = -30701.579

Iteration 1: log likelihood = -30601.586

Iteration 2: log likelihood = -30601.4

Iteration 3: log likelihood = -30601.4

Refining estimates:

Iteration 0: log likelihood = -30601.4

Cox regression with Breslow method for ties

No. of subjects = 355,046

No. of failures = 2,665

Time at risk = 4,364,749.2

Number of obs = 355,046

LR chi2(7) = 200.36

Prob > chi2 = 0.0000

Log likelihood = -30601.4

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.000086</b>	<b>.0406064</b>	<b>0.00</b>	<b>0.998</b>	<b>.9235831</b>	<b>1.082925</b>
AGE	<b>.9442839</b>	<b>.0076126</b>	<b>-7.11</b>	<b>0.000</b>	<b>.9294806</b>	<b>.9593229</b>
SEX	<b>.9174315</b>	<b>.0357794</b>	<b>-2.21</b>	<b>0.027</b>	<b>.8499183</b>	<b>.9903076</b>
NonWhite	<b>1.063415</b>	<b>.1126751</b>	<b>0.58</b>	<b>0.562</b>	<b>.8639985</b>	<b>1.308858</b>
householdsize	<b>.9912657</b>	<b>.0194372</b>	<b>-0.45</b>	<b>0.655</b>	<b>.9538921</b>	<b>1.030104</b>
SES	<b>.7000345</b>	<b>.0205649</b>	<b>-12.14</b>	<b>0.000</b>	<b>.6608666</b>	<b>.7415239</b>
LE8_TOTALSCORE	<b>.9998458</b>	<b>.0002122</b>	<b>-0.73</b>	<b>0.467</b>	<b>.9994299</b>	<b>1.000262</b>

```

17 .
18 . **Model 2: Interaction with LE8 TOTAL SCORE**
19 . stcox c.infectionburdenbr##c.LE8_TOTALSCOREtert AGE SEX NonWhite householdsize SES if sample_final==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

Iteration 0: log likelihood = -30701.579
Iteration 1: log likelihood = -30601.441
Iteration 2: log likelihood = -30601.265
Iteration 3: log likelihood = -30601.265
Refining estimates:
Iteration 0: log likelihood = -30601.265

```

Cox regression with Breslow method for ties

```

No. of subjects =      355,046                Number of obs = 355,046
No. of failures =       2,665
Time at risk    = 4,364,749.2

LR chi2(8)      = 200.63
Prob > chi2     = 0.0000

Log likelihood = -30601.265

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.090359</b>	<b>.1142647</b>	<b>0.83</b>	<b>0.409</b>	<b>.8879071</b>	<b>1.338973</b>
LE8_TOTALSCOREtert	<b>1.018914</b>	<b>.0308553</b>	<b>0.62</b>	<b>0.536</b>	<b>.9601984</b>	<b>1.08122</b>
c.infectionburdenbr#c.LE8_TOTALSCOREtert	<b>.9561351</b>	<b>.0484855</b>	<b>-0.88</b>	<b>0.376</b>	<b>.8656751</b>	<b>1.056048</b>
AGE	<b>.9442525</b>	<b>.007612</b>	<b>-7.12</b>	<b>0.000</b>	<b>.9294505</b>	<b>.9592902</b>
SEX	<b>.9161586</b>	<b>.0357301</b>	<b>-2.25</b>	<b>0.025</b>	<b>.8487384</b>	<b>.9889343</b>
NonWhite	<b>1.065241</b>	<b>.1128679</b>	<b>0.60</b>	<b>0.551</b>	<b>.8654831</b>	<b>1.311104</b>
householdsize	<b>.9914984</b>	<b>.0194209</b>	<b>-0.44</b>	<b>0.663</b>	<b>.9541556</b>	<b>1.030303</b>
SES	<b>.6969527</b>	<b>.0203851</b>	<b>-12.34</b>	<b>0.000</b>	<b>.6581224</b>	<b>.7380741</b>

```

20 .
21 . **Stratified analysis by LE8 TERTILES**

```

```

22 .
23 . **LOWEST TERTILE**
24 .
25 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if sample_final==1 & LE8_TOTALSCOREtert==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

Iteration 0: log likelihood = -10231.783
Iteration 1: log likelihood = -10183.01
Iteration 2: log likelihood = -10182.94
Iteration 3: log likelihood = -10182.94
Refining estimates:
Iteration 0: log likelihood = -10182.94

```

Cox regression with Breslow method for ties

```

No. of subjects =      124,912          Number of obs = 124,912
No. of failures =         977
Time at risk    = 1,516,657.3

LR chi2(6)      =    97.69
Prob > chi2     =    0.0000
Log likelihood = -10182.94

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	1.067016	.0704268	0.98	0.326	.9375375	1.214376
AGE	.935416	.0123801	-5.04	0.000	.9114634	.959998
SEX	.9661605	.0621012	-0.54	0.592	.8517991	1.095876
NonWhite	1.072603	.1731765	0.43	0.664	.781644	1.47187
householdsize	.9923868	.0302211	-0.25	0.802	.9348875	1.053422
SES	.6714983	.031144	-8.59	0.000	.6131494	.7353999

```

26 .
27 . **MIDDLE TERTILE**
28 .
29 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if sample_final==1 & LE8_TOTALSCOREtert==2

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

Iteration 0: log likelihood = -9607.1716
Iteration 1: log likelihood = -9572.6184
Iteration 2: log likelihood = -9572.5781
Iteration 3: log likelihood = -9572.5781
Refining estimates:
Iteration 0: log likelihood = -9572.5781

```

Cox regression with Breslow method for ties

```

No. of subjects =      120,827          Number of obs = 120,827
No. of failures =         915
Time at risk    = 1,489,440.1

LR chi2(6)      =    69.19
Prob > chi2     =    0.0000
Log likelihood = -9572.5781

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	.9354686	.0655928	-0.95	0.341	.8153517	1.073281
AGE	.9415752	.0129628	-4.37	0.000	.9165083	.9673276
SEX	.9820879	.0653795	-0.27	0.786	.8619543	1.118965
NonWhite	.785939	.1636573	-1.16	0.247	.5225668	1.18205
householdsize	.9961778	.0330907	-0.12	0.908	.9333874	1.063192
SES	.6909423	.0349157	-7.32	0.000	.6257885	.7628795

```

30 .
31 . **HIGHEST TERTILE**
32 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if sample_final==1 & LE8_TOTALSCOREtert==3

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

Iteration 0: log likelihood = -7944.0623
Iteration 1: log likelihood = -7921.9253
Iteration 2: log likelihood = -7921.7467
Iteration 3: log likelihood = -7921.7464
Refining estimates:
Iteration 0: log likelihood = -7921.7464

```

Cox regression with Breslow method for ties

```

No. of subjects =    109,307
No. of failures =     773
Time at risk   = 1,358,651.8

```

Number of obs = 109,307

Log likelihood = -7921.7464

```

LR chi2(6)      =    44.63
Prob > chi2     =    0.0000

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	.9920486	.0754877	-0.10	0.916	.8545996	1.151604
AGE	.9580657	.0144698	-2.84	0.005	.9301211	.98685
SEX	.7930086	.0576989	-3.19	0.001	.6876143	.9145573
NonWhite	1.441212	.2746483	1.92	0.055	.9920112	2.09382
householdsize	.9858911	.0393455	-0.36	0.722	.9117142	1.066103
SES	.7470317	.0424795	-5.13	0.000	.6682454	.835107

```

33 .
34 . *****AMONG MEN*****
35 .
36 .
37 .
38 .
39 . **Model 1**

```

40 .  
 41 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES LE8\_TOTALSCORE if SEX==1 & sample\_final==1

Failure \_d: ad\_diag==1  
 Analysis time \_t: Age\_AD  
 Enter on or after: time baselineage  
 ID variable: n\_eid

note: SEX omitted because of collinearity.  
 Iteration 0: log likelihood = -14222.856  
 Iteration 1: log likelihood = -14170.437  
 Iteration 2: log likelihood = -14170.334  
 Iteration 3: log likelihood = -14170.334  
 Refining estimates:  
 Iteration 0: log likelihood = -14170.334

Cox regression with Breslow method for ties

No. of subjects = 164,922 Number of obs = 164,922  
 No. of failures = 1,319  
 Time at risk = 2,004,595.1  
 Log likelihood = -14170.334  
 LR chi2(6) = 105.04  
 Prob > chi2 = 0.0000

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	1.006766	.0585098	0.12	0.908	.8983793	1.12823
AGE	.9446254	.010749	-5.01	0.000	.9237909	.9659298
SEX	1	(omitted)				
NonWhite	1.12278	.1620818	0.80	0.422	.8460915	1.489951
householdsize	.9790067	.0291653	-0.71	0.476	.9234805	1.037872
SES	.6939653	.0280626	-9.03	0.000	.6410869	.7512053
LE8_TOTALSCORE	1.000182	.0003065	0.59	0.552	.9995818	1.000783

42 .  
 43 . \*\*Model 2: Interaction with LE8 TOTAL SCORE\*\*  
 44 . stcox c.infectionburdenbr##c.LE8\_TOTALSCOREtert AGE SEX NonWhite householdsize SES if SEX==1 & sample\_final==1

Failure \_d: ad\_diag==1  
 Analysis time \_t: Age\_AD  
 Enter on or after: time baselineage  
 ID variable: n\_eid

note: SEX omitted because of collinearity.  
 Iteration 0: log likelihood = -14222.856  
 Iteration 1: log likelihood = -14168.297  
 Iteration 2: log likelihood = -14168.198  
 Iteration 3: log likelihood = -14168.198  
 Refining estimates:  
 Iteration 0: log likelihood = -14168.198

Cox regression with Breslow method for ties

No. of subjects = 164,922 Number of obs = 164,922  
 No. of failures = 1,319  
 Time at risk = 2,004,595.1  
 Log likelihood = -14168.198  
 LR chi2(7) = 109.32  
 Prob > chi2 = 0.0000

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.211571</b>	<b>.1832268</b>	<b>1.27</b>	<b>0.204</b>	<b>.9007848</b>	<b>1.629584</b>
LE8_TOTALSCOREtert	<b>1.096755</b>	<b>.0470793</b>	<b>2.15</b>	<b>0.031</b>	<b>1.008256</b>	<b>1.193022</b>
c.infectionburdenbr#c.LE8_TOTALSCOREtert	<b>.9081965</b>	<b>.0665008</b>	<b>-1.32</b>	<b>0.188</b>	<b>.7867782</b>	<b>1.048352</b>
AGE	<b>.9443583</b>	<b>.0107428</b>	<b>-5.03</b>	<b>0.000</b>	<b>.9235359</b>	<b>.9656502</b>
SEX	<b>1</b>	(omitted)				
NonWhite	<b>1.124123</b>	<b>.1622729</b>	<b>0.81</b>	<b>0.418</b>	<b>.8471072</b>	<b>1.491726</b>
householdsize	<b>.9793147</b>	<b>.0291563</b>	<b>-0.70</b>	<b>0.483</b>	<b>.9238047</b>	<b>1.03816</b>
SES	<b>.690076</b>	<b>.0278003</b>	<b>-9.21</b>	<b>0.000</b>	<b>.637684</b>	<b>.7467725</b>

```

45 .
46 . **Stratif SEX==1 by LE8 TERTILES**
47 .
48 . **LOWEST TERTILE**
49 .
50 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==1 & sample_final==1 & LE8_TOTALSCOREtert==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

note: SEX omitted because of collinearity.
Iteration 0: log likelihood = -4680.1601
Iteration 1: log likelihood = -4656.7141
Iteration 2: log likelihood = -4656.6898
Iteration 3: log likelihood = -4656.6898
Refining estimates:
Iteration 0: log likelihood = -4656.6898

```

Cox regression with Breslow method for ties

```

No. of subjects =      62,999           Number of obs = 62,999
No. of failures =       479
Time at risk    = 755,635.849

LR chi2(5)      = 46.94
Prob > chi2     = 0.0000
Log likelihood = -4656.6898

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.089995</b>	<b>.1033962</b>	<b>0.91</b>	<b>0.364</b>	<b>.9050653</b>	<b>1.31271</b>
AGE	<b>.9326647</b>	<b>.0174864</b>	<b>-3.72</b>	<b>0.000</b>	<b>.8990141</b>	<b>.9675748</b>
SEX	<b>1</b>	(omitted)				
NonWhite	<b>.916384</b>	<b>.2287418</b>	<b>-0.35</b>	<b>0.726</b>	<b>.5618314</b>	<b>1.494682</b>
householdsize	<b>1.001351</b>	<b>.0441915</b>	<b>0.03</b>	<b>0.976</b>	<b>.9183775</b>	<b>1.091821</b>
SES	<b>.6853658</b>	<b>.0440556</b>	<b>-5.88</b>	<b>0.000</b>	<b>.6042363</b>	<b>.7773883</b>

51 . **\*\*MIDDLE TERTILE\*\***

52 .

53 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==1 & sample\_final==1 & LE8\_TOTALSCOREtert==2

Failure \_d: ad\_diag==1  
 Analysis time \_t: Age\_AD  
 Enter on or after: time baselineage  
 ID variable: n\_eid

note: **SEX** omitted because of collinearity.  
 Iteration 0: log likelihood = **-4386.4545**  
 Iteration 1: log likelihood = **-4360.1511**  
 Iteration 2: log likelihood = **-4360.0964**  
 Iteration 3: log likelihood = **-4360.0964**  
 Refining estimates:  
 Iteration 0: log likelihood = **-4360.0964**

Cox regression with Breslow method for ties

No. of subjects = **58,075**  
 No. of failures = **449**  
 Time at risk = **709,399.763**

Number of obs = **58,075**

Log likelihood = **-4360.0964**

LR chi2(5) = **52.72**  
 Prob > chi2 = **0.0000**

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.012888</b>	<b>.1009014</b>	<b>0.13</b>	<b>0.898</b>	<b>.8332333</b>	<b>1.231277</b>
AGE	<b>.9326399</b>	<b>.0182536</b>	<b>-3.56</b>	<b>0.000</b>	<b>.897541</b>	<b>.9691114</b>
SEX	<b>1</b>	(omitted)				
NonWhite	<b>.7556967</b>	<b>.2226068</b>	<b>-0.95</b>	<b>0.342</b>	<b>.4242362</b>	<b>1.346131</b>
householdsize	<b>.9899155</b>	<b>.0453462</b>	<b>-0.22</b>	<b>0.825</b>	<b>.9049115</b>	<b>1.082904</b>
SES	<b>.6355388</b>	<b>.0438051</b>	<b>-6.58</b>	<b>0.000</b>	<b>.555229</b>	<b>.7274648</b>

54 .

55 . **\*\*HIGHEST TERTILE\*\***

56 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==1 & sample\_final==1 & LE8\_TOTALSCOREtert==3

Failure \_d: ad\_diag==1  
 Analysis time \_t: Age\_AD  
 Enter on or after: time baselineage  
 ID variable: n\_eid

note: **SEX** omitted because of collinearity.  
 Iteration 0: log likelihood = **-3710.2087**  
 Iteration 1: log likelihood = **-3699.7749**  
 Iteration 2: log likelihood = **-3698.9012**  
 Iteration 3: log likelihood = **-3698.8917**  
 Iteration 4: log likelihood = **-3698.8917**  
 Refining estimates:  
 Iteration 0: log likelihood = **-3698.8917**

Cox regression with Breslow method for ties

No. of subjects = **43,848**  
 No. of failures = **391**  
 Time at risk = **539,559.488**

Number of obs = **43,848**

Log likelihood = **-3698.8917**

LR chi2(5) = **22.63**  
 Prob > chi2 = **0.0004**

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	.9018013	.0987128	-0.94	0.345	.7276739	1.117596
AGE	.9727226	.020489	-1.31	0.189	.9333827	1.013721
SEX	1 (omitted)					
NonWhite	1.968217	.4377498	3.04	0.002	1.272793	3.043604
householdsize	.9293443	.0641186	-1.06	0.288	.8118006	1.063908
SES	.7775685	.0608406	-3.22	0.001	.6670166	.9064434

```

57 .
58 .
59 .
60 . *****AMONG WOMEN*****
61 .
62 .
63 .
64 .
65 . **Model 1**
66 .
67 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES LE8_TOTALSCORE if SEX==2 & sample_final==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

note: SEX omitted because of collinearity.
Iteration 0:  log likelihood = -14628.876
Iteration 1:  log likelihood = -14580.981
Iteration 2:  log likelihood = -14580.91
Iteration 3:  log likelihood = -14580.91
Refining estimates:
Iteration 0:  log likelihood = -14580.91

```

Cox regression with Breslow method for ties

```

No. of subjects =    190,124          Number of obs = 190,124
No. of failures =     1,346
Time at risk    = 2,360,154.1

LR chi2(6)      =    95.93
Prob > chi2     =    0.0000
Log likelihood = -14580.91

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	.9940999	.0564193	-0.10	0.917	.8894484	1.111065
AGE	.9430186	.0107823	-5.13	0.000	.9221207	.9643901
SEX	1 (omitted)					
NonWhite	1.005011	.1570843	0.03	0.974	.739822	1.365258
householdsize	1.001867	.0255274	0.07	0.942	.9530625	1.05317
SES	.7074039	.0302698	-8.09	0.000	.6504959	.7692904
LE8_TOTALSCORE	.9995556	.0002948	-1.51	0.132	.998978	1.000133



```

68 .
69 . **Model 2: Interaction with LE8 TOTAL SCORE**
70 . stcox c.infectionburdenbr#c.LE8_TOTALSCOREtert AGE SEX NonWhite householdsize SES if SEX==2 & sample_final==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

note: SEX omitted because of collinearity.
Iteration 0: log likelihood = -14628.876
Iteration 1: log likelihood = -14581.097
Iteration 2: log likelihood = -14581.032
Iteration 3: log likelihood = -14581.032
Refining estimates:
Iteration 0: log likelihood = -14581.032

```

Cox regression with Breslow method for ties

```

No. of subjects =      190,124      Number of obs = 190,124
No. of failures =       1,346
Time at risk    = 2,360,154.1

LR chi2(7)      =    95.69
Prob > chi2     =    0.0000
Log likelihood = -14581.032

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	.9795455	.1424104	-0.14	0.887	.7366706	1.302494
LE8_TOTALSCOREtert	.9496636	.0406222	-1.21	0.227	.8732917	1.032714
c.infectionburdenbr#c.LE8_TOTALSCOREtert	1.008112	.0709292	0.11	0.909	.8782527	1.157172
AGE	.9430177	.0107831	-5.13	0.000	.9221183	.9643908
SEX	1	(omitted)				
NonWhite	1.004959	.1570904	0.03	0.975	.739763	1.365225
householdsize	1.001875	.0255226	0.07	0.941	.9530797	1.053168
SES	.705713	.0300499	-8.19	0.000	.649207	.7671372

```

71 .
72 . **Stratif SEX==2 by LE8 TERTILES**
73 .
74 . **LOWEST TERTILE**
75 .
76 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==2 & sample_final==1 & LE8_TOTALSCOREtert==1

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

note: SEX omitted because of collinearity.
Iteration 0: log likelihood = -4875.2137
Iteration 1: log likelihood = -4849.3838
Iteration 2: log likelihood = -4849.3
Iteration 3: log likelihood = -4849.2999
Refining estimates:
Iteration 0: log likelihood = -4849.2999

```

Cox regression with Breslow method for ties

No. of subjects = **61,913**  
 No. of failures = **498**  
 Time at risk = **761,021.438**

Number of obs = **61,913**

Log likelihood = **-4849.2999**

LR chi2(5) = **51.83**  
 Prob > chi2 = **0.0000**

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>1.047779</b>	<b>.0962527</b>	<b>0.51</b>	<b>0.611</b>	<b>.8751356</b>	<b>1.254481</b>
AGE	<b>.9386499</b>	<b>.017545</b>	<b>-3.39</b>	<b>0.001</b>	<b>.9048846</b>	<b>.9736751</b>
SEX	<b>1</b>	(omitted)				
NonWhite	<b>1.219434</b>	<b>.2585958</b>	<b>0.94</b>	<b>0.350</b>	<b>.8047306</b>	<b>1.847846</b>
householdsize	<b>.9851869</b>	<b>.0422125</b>	<b>-0.35</b>	<b>0.728</b>	<b>.9058307</b>	<b>1.071495</b>
SES	<b>.6569078</b>	<b>.044049</b>	<b>-6.27</b>	<b>0.000</b>	<b>.576006</b>	<b>.7491725</b>

77 .

78 . **\*\*MIDDLE TERTILE\*\***

79 .

80 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==2 & sample\_final==1 & LE8\_TOTALSCOREtert==2

Failure \_d: **ad\_diag==1**  
 Analysis time \_t: **Age\_AD**  
 Enter on or after: **time baselineage**  
 ID variable: **n\_eid**

note: **SEX** omitted because of collinearity.  
 Iteration 0: log likelihood = **-4585.9404**  
 Iteration 1: log likelihood = **-4575.3792**  
 Iteration 2: log likelihood = **-4575.3742**  
 Iteration 3: log likelihood = **-4575.3742**  
 Refining estimates:  
 Iteration 0: log likelihood = **-4575.3742**

Cox regression with Breslow method for ties

No. of subjects = **62,752**  
 No. of failures = **466**  
 Time at risk = **780,040.34**

Number of obs = **62,752**

Log likelihood = **-4575.3742**

LR chi2(5) = **21.13**  
 Prob > chi2 = **0.0008**

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	<b>.8698974</b>	<b>.0858524</b>	<b>-1.41</b>	<b>0.158</b>	<b>.7169037</b>	<b>1.055541</b>
AGE	<b>.9506943</b>	<b>.018404</b>	<b>-2.61</b>	<b>0.009</b>	<b>.9152989</b>	<b>.9874584</b>
SEX	<b>1</b>	(omitted)				
NonWhite	<b>.8324457</b>	<b>.2452224</b>	<b>-0.62</b>	<b>0.534</b>	<b>.4673135</b>	<b>1.482871</b>
householdsize	<b>1.004924</b>	<b>.04856</b>	<b>0.10</b>	<b>0.919</b>	<b>.9141164</b>	<b>1.104753</b>
SES	<b>.7591684</b>	<b>.0564562</b>	<b>-3.71</b>	<b>0.000</b>	<b>.6562023</b>	<b>.8782911</b>

```

81 .
82 . **HIGHEST TERTILE**
83 . stcox infectionburdenbr AGE SEX NonWhite householdsize SES if SEX==2 & sample_final==1 & LE8_TOTALSCOREtert==3

```

```

      Failure _d: ad_diag==1
      Analysis time _t: Age_AD
      Enter on or after: time baselineage
      ID variable: n_eid

```

```

note: SEX omitted because of collinearity.
Iteration 0:  log likelihood = -3693.7989
Iteration 1:  log likelihood = -3682.1991
Iteration 2:  log likelihood = -3682.1804
Iteration 3:  log likelihood = -3682.1804
Refining estimates:
Iteration 0:  log likelihood = -3682.1804

```

Cox regression with Breslow method for ties

```

No. of subjects =      65,459
No. of failures =       382
Time at risk   = 819,092.295

```

Number of obs = 65,459

Log likelihood = -3682.1804

```

LR chi2(5)      = 23.24
Prob > chi2     = 0.0003

```

_t	Haz. ratio	Std. err.	z	P> z	[95% conf. interval]	
infectionburdenbr	1.087905	.1155507	0.79	0.428	.883449	1.339678
AGE	.9390493	.0204816	-2.88	0.004	.899752	.980063
SEX	1	(omitted)				
NonWhite	.8086685	.3091941	-0.56	0.579	.3822204	1.71091
householdsize	1.022298	.0450783	0.50	0.617	.9376567	1.114581
SES	.7179521	.0595072	-4.00	0.000	.6103009	.844592

```

84 .
85 .
86 .
87 . save "E:\16GBBACKUPUSB\BACKUP_USB_SEPTEMBER2014\May Baydoun_folder\UK_BIOBANK_PROJECT\UKB_PAPER3_LE8INFECTDEM\DATA\
file E:\16GBBACKUPUSB\BACKUP_USB_SEPTEMBER2014\May Baydoun_folder\UK_BIOBANK_PROJECT\UKB_PAPER3_LE8INFECTDEM\DATA\UK
88 .
89 . *****HOSPITAL TREATED INFECTIONS: TABLES S2-S3*****
90 .
91 . capture log close

```