**Statistical code for our paper on social disadvantage and ageing:**

SAS (version 9.4), by Jaana Pentti:

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S3, S4, S5, S6, S13, S19B, S31, S32 \*\*;

\*\* (Incident diseases, HR) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* disease=dg, exposure=altiste, output file=resfile \*\*;

\*\* data sets: diseases, persons \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**%macro** coxit3 (dg,altiste,resfile);

data tauti;

set diseases;

IF dgnro=&dg;

data t1;

merge persons(in=i) tauti;

by id;

if i;

data t2;

set t1;

seurloppupvm=min(lostpvm,kuolinpvm,mdy(**11**,**12**,**2021**));

seuraika=(min(slaalkupvm,seurloppupvm)-alkupvm+**1**)/**365.25**;

if &altiste>**.** and seuraika>**0**;

if alkupvm<=slaalkupvm<=seurloppupvm then status=**1**; else status=**0**;

if (sex=**1** and &dg IN (**15**,**16**,**17**)) or (sex=**2** and &dg IN (**18**,**83**)) then do; status=**.**; seuraika=**.**; end;

status2=status;

if status=**0** and min(slaalkupvm,seurloppupvm)=kuolinpvm then status2=**2**; \*death\*;

proc phreg data=t2;

class ethnic &altiste(ref='1');

model seuraika\*status(**0**) = sex age ethnic &altiste / rl;

\* model seuraika\*status(0) = sex age ethnic education\_prs &altiste / rl;

\* model seuraika\*status2(0) = sex age ethnic &altiste / eventcode=1 rl; \*Fine & Gray -competing risk\*;

ods output ParameterEstimates=pe CensoredSummary=cs; run;

data pe; set pe; if Parameter='ses' and ClassVal0=**3**;

rename HazardRatio=HR\_trend HRLowerCL=HRlow\_trend HRUpperCL=HRupp\_trend ProbChiSq=P\_trend;

data res; merge pe cs; dgnro=&dg; ses='3 vs. 1';

keep ses dgnro Total Event HazardRatio HRLowerCL HRUpperCL ProbChiSq;

data res; merge res(in=i) lib.Dgnro\_labels; by dgnro; if i;

proc append base=&resfile data=res;

run;

**%mend**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* all diseases \*\*;

**proc** **datasets** lib=work memtype=data nolist; delete results\_all; **quit**;

**%MACRO** ***coxkaikki***;

%DO I = **1** %TO **83**;

%***coxit3***(&I,ses,results\_all);

%END;

**%MEND** coxkaikki;

%***coxkaikki***;

**proc** **print** data=results\_all;

id dgnro;

var label ses Total Event HazardRatio HRLowerCL HRUpperCL ProbChiSq;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* selected diseases \*\*;

**proc** **datasets** lib=work memtype=data nolist; delete results; **quit**;

%***coxit3***(**108**,ses,results);

%***coxit3***(**105**,ses,results);

%***coxit3***(**109**,ses,results);

%***coxit3***(**106**,ses,results);

%***coxit3***(**107**,ses,results);

%***coxit3***(**103**,ses,results);

%***coxit3***(**102**,ses,results);

%***coxit3***(**104**,ses,results);

%***coxit3***(**101**,ses,results);

%***coxit3***(**100**,ses,results);

**proc** **print** data=results;

id dgnro;

var label ses Total Event HazardRatio HRLowerCL HRUpperCL ProbChiSq;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S7, S8 \*\*;

\*\* (Number of hallmark-related diseases, Rate, RR) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**13**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**24**,**26**,**27**,**28**,**29**,**30**,**31**,**32**,**37**,**42**,**48**,**66**,**67**,**72**);

var slaalkupvm; class id;

output out=t101 n=dsum101;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**6**,**7**,**8**,**10**,**12**,**15**,**16**,**18**,**19**,**20**,**26**,**27**,**28**,**30**,**31**,**32**,**37**,**38**,**42**,**43**,**52**,**53**,**55**,**56**,**61**,**66**,**72**,**73**,**75**,**80**);

var slaalkupvm; class id;

output out=t102 n=dsum102;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**22**,**23**,**24**,**25**,**26**,**28**,**42**,**53**,**55**,**56**,**66**,**69**,**71**,**73**,**75**);

var slaalkupvm; class id;

output out=t103 n=dsum103;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**2**,**7**,**8**,**11**,**12**,**15**,**17**,**18**,**24**,**25**,**26**,**37**,**38**,**42**,**43**,**44**,**45**,**46**,**48**,**49**,**51**,**57**,**59**,**64**,**65**,**68**,**69**,**75**,**78**,**79**);

var slaalkupvm; class id;

output out=t104 n=dsum104;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**8**,**10**,**15**,**16**,**36**,**37**,**38**,**41**,**42**,**47**,**52**,**53**,**55**,**56**,**60**,**61**,**62**,**63**,**64**,**68**,**69**,**73**,**74**,**75**,**79**,**81**,**82**);

var slaalkupvm; class id;

output out=t105 n=dsum105;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**2**,**6**,**7**,**8**,**11**,**15**,**26**,**28**,**37**,**38**,**41**,**42**,**43**,**44**,**48**,**49**,**50**,**52**,**53**,**55**,**57**,**58**,**64**,**67**,**68**,**73**,**75**,**77**,**81**,**82**);

var slaalkupvm; class id;

output out=t106 n=dsum106;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**1**,**3**,**6**,**7**,**8**,**9**,**11**,**12**,**13**,**14**,**15**,**20**,**24**,**28**,**30**,**35**,**42**,**48**,**49**,**52**,**53**,**64**,**68**,**69**,**70**,**73**,**75**,**81**,**82**,**83**);

var slaalkupvm; class id;

output out=t107 n=dsum107;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**8**,**15**,**24**,**25**,**26**,**27**,**28**,**30**,**31**,**32**,**33**,**34**,**37**,**38**,**44**,**47**,**52**,**53**,**54**,**55**,**56**,**57**,**61**,**62**,**63**,**64**,**73**,**75**,**77**,**79**);

var slaalkupvm; class id;

output out=t108 n=dsum108;

**proc** **means** data=diseases nway noprint;

where dgnro IN (**2**,**4**,**7**,**15**,**16**,**17**,**18**,**21**,**30**,**36**,**37**,**38**,**39**,**40**,**42**,**52**,**53**,**55**,**61**,**64**,**67**,**68**,**69**,**73**,**75**,**76**,**79**,**81**,**82**,**83**);

var slaalkupvm; class id;

output out=t109 n=dsum109;

**run**;

**data** tsum;

merge t101 t102 t103 t104 t105 t106 t107 t108 t109;

by id;

drop \_TYPE\_ \_freq\_;

**run**;

**data** persons2;

merge persons(in=i) tsum;

by id;

if i;

array tau{**9**} dsum101-dsum109;

do l=**1** to **9**;

if tau{l}=**.** then tau{l}=**0**;

end;

age\_end=age+maxseura;

lnage=log(age\_end/**7000**); \*\* Rate per 100\*70yrs \*\*;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**proc** **means** data=persons2;

var age\_end;

**run**;

**proc** **format**;

value dik **1**-**10**='1+';

**proc** **freq** data=persons2;

tables dsum101-dsum109;

tables educ \*(dsum108 dsum105 dsum109 dsum106 dsum107

dsum103 dsum102 dsum104 dsum101) / nopercent nocol norow;

format dsum108 dsum105 dsum109 dsum106 dsum107

dsum103 dsum102 dsum104 dsum101 dik.;

**run**;

**proc** **genmod** data=persons2;

class educ;

model dsum108 = sex educ / dist=poisson offset=lnage;

\* model dsum105 = sex educ / dist=poisson offset=lnage;

\* model dsum109 = sex educ / dist=poisson offset=lnage;

\* model dsum106 = sex educ / dist=poisson offset=lnage;

\* model dsum107 = sex educ / dist=poisson offset=lnage;

\* model dsum103 = sex educ / dist=poisson offset=lnage;

\* model dsum102 = sex educ / dist=poisson offset=lnage;

\* model dsum104 = sex educ / dist=poisson offset=lnage;

\* model dsum101 = sex educ / dist=poisson offset=lnage;

lsmeans educ / exp cl; \*Rate per 100\*70yrs\*;

estimate 'educ 2 vs 1' educ -**1** **1** **0**;

estimate 'educ 3 vs 1' educ -**1** **0** **1**;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S9, S10 \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* 1. INCIDENT HALLMARK-RELATED DISEASE (HR, Rate per 1000 py) \*\*;

**data** persons3b;

set persons3;

seurloppupvm=min(lostpvm,kuolinpvm,mdy(**11**,**12**,**2021**));

seuraika=(seurloppupvm-alkupvm+**1**)/**365.25**;

if seurv108=**.** then seurv108=seuraika;

if dis108=**.** then dis108=**0**;

if **.**<slaalkupvm108<alkupvm then delete;

lnseuraika=log((min(seurloppupvm)-alkupvm+**1**)/**365.25**/**1000**);

**run**;

**proc** **phreg** data=persons3b;

class ethnic ses(ref='1');

model seurv108\*dis108(**0**) = sex age ethnic ses / rl;

**run**;

**proc** **genmod** data=persons3b;

class ethnic ses;

model dis108 = sex age ethnic ses / dist=poisson offset=lnseuraika;

lsmeans ses / exp cl;

estimate 'Low vs High' ses -**1** **0** **1**;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* 2. DISEASE \*\*;

**data** diseases3;

merge diseases persons3;

by id;

**run**;

**proc** **means** data=diseases3 nway noprint;

where dgnro<=**83** and

slaalkupvm>slaalkupvm100 and dis100=**1**;

var slaalkupvm; class id;

output out=t100 min=slaalkupvm2\_100;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**13**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**24**,**26**,**27**,**28**,**29**,**30**,**31**,**32**,**37**,**42**,**48**,**66**,**67**,**72**) and

slaalkupvm>slaalkupvm101 and dis101=**1**;

var slaalkupvm; class id;

output out=t101 min=slaalkupvm2\_101;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**6**,**7**,**8**,**10**,**12**,**15**,**16**,**18**,**19**,**20**,**26**,**27**,**28**,**30**,**31**,**32**,**37**,**38**,**42**,**43**,**52**,**53**,**55**,**56**,**61**,**66**,**72**,**73**,**75**,**80**) and

slaalkupvm>slaalkupvm102 and dis102=**1**;

var slaalkupvm; class id;

output out=t102 min=slaalkupvm2\_102;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**22**,**23**,**24**,**25**,**26**,**28**,**42**,**53**,**55**,**56**,**66**,**69**,**71**,**73**,**75**) and

slaalkupvm>slaalkupvm103 and dis103=**1**;

var slaalkupvm; class id;

output out=t103 min=slaalkupvm2\_103;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**2**,**7**,**8**,**11**,**12**,**15**,**17**,**18**,**24**,**25**,**26**,**37**,**38**,**42**,**43**,**44**,**45**,**46**,**48**,**49**,**51**,**57**,**59**,**64**,**65**,**68**,**69**,**75**,**78**,**79**) and

slaalkupvm>slaalkupvm104 and dis104=**1**;

var slaalkupvm; class id;

output out=t104 min=slaalkupvm2\_104;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**8**,**10**,**15**,**16**,**36**,**37**,**38**,**41**,**42**,**47**,**52**,**53**,**55**,**56**,**60**,**61**,**62**,**63**,**64**,**68**,**69**,**73**,**74**,**75**,**79**,**81**,**82**) and

slaalkupvm>slaalkupvm105 and dis105=**1**;

var slaalkupvm; class id;

output out=t105 min=slaalkupvm2\_105;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**2**,**6**,**7**,**8**,**11**,**15**,**26**,**28**,**37**,**38**,**41**,**42**,**43**,**44**,**48**,**49**,**50**,**52**,**53**,**55**,**57**,**58**,**64**,**67**,**68**,**73**,**75**,**77**,**81**,**82**) and

slaalkupvm>slaalkupvm106 and dis106=**1**;

var slaalkupvm; class id;

output out=t106 min=slaalkupvm2\_106;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**1**,**3**,**6**,**7**,**8**,**9**,**11**,**12**,**13**,**14**,**15**,**20**,**24**,**28**,**30**,**35**,**42**,**48**,**49**,**52**,**53**,**64**,**68**,**69**,**70**,**73**,**75**,**81**,**82**,**83**) and

slaalkupvm>slaalkupvm107 and dis107=**1**;

var slaalkupvm; class id;

output out=t107 min=slaalkupvm2\_107;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**8**,**15**,**24**,**25**,**26**,**27**,**28**,**30**,**31**,**32**,**33**,**34**,**37**,**38**,**44**,**47**,**52**,**53**,**54**,**55**,**56**,**57**,**61**,**62**,**63**,**64**,**73**,**75**,**77**,**79**) and

slaalkupvm>slaalkupvm108 and dis108=**1**;

var slaalkupvm; class id;

output out=t108 min=slaalkupvm2\_108;

**proc** **means** data=diseases3 nway noprint;

where dgnro IN (**2**,**4**,**7**,**15**,**16**,**17**,**18**,**21**,**30**,**36**,**37**,**38**,**39**,**40**,**42**,**52**,**53**,**55**,**61**,**64**,**67**,**68**,**69**,**73**,**75**,**76**,**79**,**81**,**82**,**83**) and

slaalkupvm>slaalkupvm109 and dis109=**1**;

var slaalkupvm; class id;

output out=t109 min=slaalkupvm2\_109;

**run**;

**data** tpvm;

merge t100 t101 t102 t103 t104 t105 t106 t107 t108 t109;

by id;

drop \_TYPE\_ \_freq\_;

**run**;

**data** ppersons2;

merge persons3(in=i) tpvm;

by id;

if i;

array tau1{**10**} slaalkupvm100-slaalkupvm1000;

array tau2{**10**} slaalkupvm2\_100-slaalkupvm2\_1000;

array seu{**10**} seurv2\_100-seurv2\_1000;

array ero{**10**} seurv12\_100-seurv12\_1000;

array ik{**10**} age2\_h100-age2\_h1000;

do l=**1** to **10**;

seu{l}=(tau2{l}-alkupvm+**1**)/**365.25**;

ero{l}=(tau2{l}-tau1{l})/**365.25**;

ik{l}=age+(tau2{l}-alkupvm+**1**)/**365.25**;

end;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**data** ppersons2b;

set ppersons2;

seurloppupvm=min(lostpvm,kuolinpvm,mdy(**11**,**12**,**2021**));

seuraika=(seurloppupvm-slaalkupvm108+**1**)/**365.25**;

if seurv12\_108>**.** then status=**1**; else status=**0**;

if seurv12\_108=**.** then seurv12\_108=seuraika;

if **.**<slaalkupvm108<alkupvm or dis108=**0** then delete;

age2=age\_h108;

lnseuraika=log(seuraika/**1000**);

**run**;

**proc** **phreg** data=ppersons2b;

class ethnic ses(ref='1');

model seurv12\_108\*status(**0**) = sex age2 ethnic ses / rl;

**run**;

**proc** **genmod** data=ppersons2b;

class ethnic ses;

model status = sex age2 ethnic ses / dist=poisson offset=lnseuraika;

lsmeans ses / exp cl;

estimate 'Low vs High' ses -**1** **0** **1**;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* 3. DISEASE \*\*;

**data** diseases4;

merge diseases ppersons2;

by id;

**run**;

**proc** **means** data=diseases4 nway noprint;

where dgnro<=**83** and

slaalkupvm>slaalkupvm2\_100 and slaalkupvm2\_100>**.**;

var slaalkupvm; class id;

output out=tt100 min=slaalkupvm3\_100;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**13**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**24**,**26**,**27**,**28**,**29**,**30**,**31**,**32**,**37**,**42**,**48**,**66**,**67**,**72**) and

slaalkupvm>slaalkupvm2\_101 and slaalkupvm2\_101>**.**;

var slaalkupvm; class id;

output out=tt101 min=slaalkupvm3\_101;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**6**,**7**,**8**,**10**,**12**,**15**,**16**,**18**,**19**,**20**,**26**,**27**,**28**,**30**,**31**,**32**,**37**,**38**,**42**,**43**,**52**,**53**,**55**,**56**,**61**,**66**,**72**,**73**,**75**,**80**) and

slaalkupvm>slaalkupvm2\_102 and slaalkupvm2\_102>**.**;

var slaalkupvm; class id;

output out=tt102 min=slaalkupvm3\_102;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**5**,**6**,**7**,**8**,**10**,**11**,**12**,**14**,**15**,**16**,**17**,**18**,**19**,**20**,**21**,**22**,**23**,**24**,**25**,**26**,**28**,**42**,**53**,**55**,**56**,**66**,**69**,**71**,**73**,**75**) and

slaalkupvm>slaalkupvm2\_103 and slaalkupvm2\_103>**.**;

var slaalkupvm; class id;

output out=tt103 min=slaalkupvm3\_103;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**2**,**7**,**8**,**11**,**12**,**15**,**17**,**18**,**24**,**25**,**26**,**37**,**38**,**42**,**43**,**44**,**45**,**46**,**48**,**49**,**51**,**57**,**59**,**64**,**65**,**68**,**69**,**75**,**78**,**79**) and

slaalkupvm>slaalkupvm2\_104 and slaalkupvm2\_104>**.**;

var slaalkupvm; class id;

output out=tt104 min=slaalkupvm3\_104;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**8**,**10**,**15**,**16**,**36**,**37**,**38**,**41**,**42**,**47**,**52**,**53**,**55**,**56**,**60**,**61**,**62**,**63**,**64**,**68**,**69**,**73**,**74**,**75**,**79**,**81**,**82**) and

slaalkupvm>slaalkupvm2\_105 and slaalkupvm2\_105>**.**;

var slaalkupvm; class id;

output out=tt105 min=slaalkupvm3\_105;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**2**,**6**,**7**,**8**,**11**,**15**,**26**,**28**,**37**,**38**,**41**,**42**,**43**,**44**,**48**,**49**,**50**,**52**,**53**,**55**,**57**,**58**,**64**,**67**,**68**,**73**,**75**,**77**,**81**,**82**) and

slaalkupvm>slaalkupvm2\_106 and slaalkupvm2\_106>**.**;

var slaalkupvm; class id;

output out=tt106 min=slaalkupvm3\_106;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**1**,**3**,**6**,**7**,**8**,**9**,**11**,**12**,**13**,**14**,**15**,**20**,**24**,**28**,**30**,**35**,**42**,**48**,**49**,**52**,**53**,**64**,**68**,**69**,**70**,**73**,**75**,**81**,**82**,**83**) and

slaalkupvm>slaalkupvm2\_107 and slaalkupvm2\_107>**.**;

var slaalkupvm; class id;

output out=tt107 min=slaalkupvm3\_107;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**8**,**15**,**24**,**25**,**26**,**27**,**28**,**30**,**31**,**32**,**33**,**34**,**37**,**38**,**44**,**47**,**52**,**53**,**54**,**55**,**56**,**57**,**61**,**62**,**63**,**64**,**73**,**75**,**77**,**79**) and

slaalkupvm>slaalkupvm2\_108 and slaalkupvm2\_108>**.**;

var slaalkupvm; class id;

output out=tt108 min=slaalkupvm3\_108;

**proc** **means** data=diseases4 nway noprint;

where dgnro IN (**2**,**4**,**7**,**15**,**16**,**17**,**18**,**21**,**30**,**36**,**37**,**38**,**39**,**40**,**42**,**52**,**53**,**55**,**61**,**64**,**67**,**68**,**69**,**73**,**75**,**76**,**79**,**81**,**82**,**83**) and

slaalkupvm>slaalkupvm2\_109 and slaalkupvm2\_109>**.**;

var slaalkupvm; class id;

output out=tt109 min=slaalkupvm3\_109;

**run**;

**data** ttpvm;

merge tt100 tt101 tt102 tt103 tt104 tt105 tt106 tt107 tt108 tt109;

by id;

drop \_TYPE\_ \_freq\_;

**run**;

**data** ppersons3;

merge ppersons2(in=i) ttpvm;

by id;

if i;

array tau2{**10**} slaalkupvm2\_100-slaalkupvm2\_1000;

array tau3{**10**} slaalkupvm3\_100-slaalkupvm3\_1000;

array seu{**10**} seurv3\_100-seurv3\_1000;

array ero{**10**} seurv23\_100-seurv23\_1000;

array ik{**10**} age3\_h100-age3\_h1000;

do l=**1** to **10**;

seu{l}=(tau3{l}-alkupvm+**1**)/**365.25**;

ero{l}=(tau3{l}-tau2{l})/**365.25**;

ik{l}=age+(tau3{l}-alkupvm+**1**)/**365.25**;

end;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**data** ppersons3b;

set ppersons3;

seurloppupvm=min(lostpvm,kuolinpvm,mdy(**11**,**12**,**2021**));

seuraika=(seurloppupvm-slaalkupvm2\_108+**1**)/**365.25**;

if seurv23\_108>**.** then status=**1**; else status=**0**;

if seurv23\_108=**.** then seurv23\_108=seuraika;

if **.**<slaalkupvm108<alkupvm or slaalkupvm2\_108=**.** then delete;

age3=age2\_h108;

lnseuraika=log(seuraika/**1000**);

**run**;

**proc** **phreg** data=ppersons3b;

class ethnic ses(ref='1');

model seurv23\_108\*status(**0**) = sex age3 ethnic ses / rl;

**run**;

**proc** **genmod** data=ppersons3b;

class ethnic ses;

model status = sex age3 ethnic ses / dist=poisson offset=lnseuraika;

lsmeans ses / exp cl;

estimate 'Low vs High' ses -**1** **0** **1**;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S11, S19C \*\*;

\*\* (Multivariable/multilevel model) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* disease=dg, exposures=altiste1, altiste2 \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**%macro** coxit3m (dg,altiste1,altiste2);

data tauti;

set diseases;

IF dgnro=&dg;

data t1;

merge persons(in=i) tauti;

by id;

if i;

data t2;

set t1;

seurloppupvm=min(lostpvm,kuolinpvm,mdy(**11**,**12**,**2021**));

seuraika=(min(slaalkupvm,seurloppupvm)-alkupvm+**1**)/**365.25**;

if &altiste1>**.** and &altiste2>**.** and seuraika>**0**;

if alkupvm<=slaalkupvm<=seurloppupvm then status=**1**; else status=**0**;

if (sex=**1** and &dg IN (**15**,**16**,**17**)) or (sex=**2** and &dg IN (**18**,**83**)) then do; status=**.**; seuraika=**.**; end;

proc phreg data=t2;

class ethnic &altiste1(ref='1') &altiste2(ref='1');

model seuraika\*status(**0**) = sex age ethnic &altiste1 &altiste2 / rl;

run;

/\*

proc phreg data=t2; \*multilevel\*;

class city &altiste1(ref='1') &altiste2(ref='1');

model seuraika\*status(0) = sex age &altiste1 &altiste2 / rl;

random city / dist=lognormal; \*log-normal frailty distribution\*;

run;

\*/

**%mend**;

\*\* selected diseases \*\*;

%***coxit3m***(**108**,educ,ases);

%***coxit3m***(**105**,educ,ases);

%***coxit3m***(**109**,educ,ases);

%***coxit3m***(**106**,educ,ases);

%***coxit3m***(**107**,educ,ases);

%***coxit3m***(**103**,educ,ases);

%***coxit3m***(**102**,educ,ases);

%***coxit3m***(**104**,educ,ases);

%***coxit3m***(**101**,educ,ases);

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Table S12 \*\*;

\*\* (Reverse causality) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**proc** **logistic** data=f2; where mover5=**1**;

model nhood\_diff5(ref='0') = sex age nhood0 disease / link=glogit;

**proc** **logistic** data=f2; where mover10=**1**;

model ases\_diff10(ref='0') = sex age nhood0 disease / link=glogit;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Table S15 \*\*;

\*\* (Organ age) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

/\*

CAgeGap\_zscored\_Artery

CAgeGap\_zscored\_Brain

CAgeGap\_zscored\_Heart

CAgeGap\_zscored\_Immune

CAgeGap\_zscored\_Intestine

CAgeGap\_zscored\_Kidney

CAgeGap\_zscored\_Liver

CAgeGap\_zscored\_Lung

CAgeGap\_zscored\_Pancreas

CAgeGap\_zscored\_Organismal

\*/

**proc** **logistic** data=wh1; \*multinomial logistic regression\*;

class ses5(ref='3');

model ses5 = sex\_F age ETHN\_DS CAgeGap\_zscored\_Artery / link=glogit;

\* model ses5 = sex\_F age ETHN\_DS education\_prs\_std CAgeGap\_zscored\_Artery / link=glogit;

\* model educ5 = sex\_F age ETHN\_DS CAgeGap\_zscored\_Artery / link=glogit;

\* model educ5 = sex\_F age ETHN\_DS education\_prs\_std CAgeGap\_zscored\_Artery / link=glogit;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Table S16 \*\*;

\*\* Inverse Odds Ratio Weighted (IORW) mediation \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**data** wh4;

set wh3;

ses=ses5;

\* ses=educ5;

IF nmiss(of ses Artery Brain Heart Immune Intestine Kidney Liver Lung Pancreas)=**0**;

**run**;

\*\*\* weights \*\*\*;

**proc** **logistic** data=wh4;

model ses(ref='3') = sex age ETHN\_DS

Artery Brain Heart Immune Intestine Kidney Liver Lung Pancreas / link=glogit;

ods output ParameterEstimates=beta;

**proc** **transpose** data=beta out=beta; id Variable Response;

**data** beta; set beta; if \_NAME\_='Estimate'; all=**1**;

estimate11=Artery1; estimate12=Artery2;

estimate21=Brain1; estimate22=Brain2;

estimate31=Heart1; estimate32=Heart2;

estimate41=Immune1; estimate42=Immune2;

estimate51=Intestine1; estimate52=Intestine2;

estimate61=Kidney1; estimate62=Kidney2;

estimate71=Liver1; estimate72=Liver2;

estimate81=Lung1; estimate82=Lung2;

estimate91=Pancreas1; estimate92=Pancreas2;

keep all estimate11--estimate92;

**data** idt; set wh4; all=**1**; keep all STNO;

**data** beta2; merge idt beta; by all;

**data** wh5; merge wh4 beta2; by STNO;

**data** wh5; set wh5;

if ses=**3** then IORW=**1**;

if ses=**2** then

IORW=**1**/exp(estimate12\*Artery+estimate22\*Brain+estimate32\*Heart+estimate42\*Immune+

estimate52\*Intestine+estimate62\*Kidney+estimate72\*Liver+estimate82\*Lung+

estimate92\*Pancreas);

if ses=**1** then

IORW=**1**/exp(estimate11\*Artery+estimate21\*Brain+estimate31\*Heart+estimate41\*Immune+

estimate51\*Intestine+estimate61\*Kidney+estimate71\*Liver+estimate81\*Lung+

estimate91\*Pancreas);

**run**;

\*\*\* Cox model (hallmark diseases 100-109) \*\*\*;

**proc** **phreg** data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

ods output ParameterEstimates=te; \*\* Total effect \*\*;

**proc** **phreg** data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

weight IORW;

ods output ParameterEstimates=de; \*\* Direct effect \*\*;

**run**;

**data** te; set te; if Parameter='ses' and ClassVal0='1'; TE\_est=Estimate; TE\_HR=HazardRatio;

TE\_HR\_low=HRLowerCL; TE\_HR\_upp=HRUpperCL; keep TE\_est TE\_HR TE\_HR\_low TE\_HR\_upp;

**data** de; set de; if Parameter='ses' and ClassVal0='1'; DE\_est=Estimate; DE\_HR=HazardRatio;

DE\_HR\_low=HRLowerCL; DE\_HR\_upp=HRUpperCL; keep DE\_est DE\_HR DE\_HR\_low DE\_HR\_upp;

**data** est; merge te de; \*\* Indirect effect \*\*;

IE\_est=TE\_est-DE\_est;

IE\_percent=IE\_est/TE\_est\***100**;

**proc** **print** data=est;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S19A, S20, S21, S22, S33, S34 \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* protein \*\*;

**data** wh3;

set wh2;

format varname $20.;

array pro{**7596**} seq1000028--seq99991;

do v=**1** to **7596**;

varname=vname(pro{v});

protein=pro{v};

output;

end;

drop seq1000028--seq99991;

**run**;

**proc** **sort** data=wh3;

by varname;

**run**;

**data** wh4;

set wh3;

if variable IN ('seq1080322','seq1121440','seq1369026','seq1890126','seq2111848','seq41572','seq433749',

'seq491378','seq533949','seq543763','seq58526','seq598250','seq606971','seq627616');

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* age \*\*;

**proc** **reg** data=wh4 plots=none;

model age5 = sex eth soma\_batch protein;

by varname;

ods output ParameterEstimates=pe;

**run**;

**quit**;

**data** results\_age;

set pe;

if variable='protein';

keep varname estimate stderr tValue Probt;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* ses, educ, nhood, dadsoc \*\*;

**proc** **logistic** data=wh4;

model ses5 = age5 sex eth soma\_batch protein;

\* model ses5 = age5 sex eth soma\_batch education\_prs protein;

by varname;

ods output ParameterEstimates=pe;

**run**;

**data** results\_ses;

set pe;

if variable='protein';

keep varname estimate stderr WaldChiSq ProbChiSq;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* mortality \*\*;

**proc** **phreg** data=wh4;

model futime\_mort\*status\_mort(**0**)= sex age eth protein / rl;

by varname;

ods output ParameterEstimates=pe;

**run**;

**data** results\_mort;

set pe;

if parameter='protein';

keep varname Estimate StdErr HazardRatio HRLowerCL HRUpperCL ProbChiSq;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* hallmark-related diseases \*\*;

**proc** **phreg** data=wh4;

model futime\_hall\*status\_hall(**0**)= sex age eth protein / rl;

\* model futime\_hall\*status\_hall(0)= sex age eth education\_prs protein / rl;

by varname;

ods output ParameterEstimates=pe;

**run**;

**data** results\_hall;

set pe;

if parameter='protein';

keep varname Estimate StdErr HazardRatio HRLowerCL HRUpperCL ProbChiSq;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S23, S24 \*\*;

\*\* Inverse Odds Ratio-Weighted (IORW) mediation \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**%macro** mediation (prot,resfile);

data wh4; set wh3;

ses=ses5;

\* ses=educ5;

IF ses>**.** and &prot>**.**;

run;

\*\*\* weights \*\*\*;

proc logistic data=wh4;

model ses(ref='3') = &prot sex age ETHN\_DS / link=glogit;

ods output ParameterEstimates=beta;

data med; set beta; if \_n\_=**3**; format Protein $20.; Protein=Variable; keep Protein;

proc transpose data=beta out=beta;

data beta; set beta; if \_NAME\_='Estimate'; all=**1**;

estimate1=COL3; estimate2=COL4;

keep all estimate1 estimate2;

data idt; set wh4; all=**1**; keep all STNO;

data beta2; merge idt beta; by all;

data wh5; merge wh4 beta2; by STNO;

data wh5; set wh5;

if ses=**3** then IORW=**1**;

if ses=**2** then IORW=**1**/exp(estimate2\*&prot);

if ses=**1** then IORW=**1**/exp(estimate1\*&prot);

run;

\*\*\* Cox model (hallmark diseases 100-109) \*\*\*;

proc phreg data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

ods output ParameterEstimates=te; \*\* Total effect \*\*;

proc phreg data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

weight IORW;

ods output ParameterEstimates=de; \*\* Direct effect \*\*;

run;

data te; set te; if Parameter='ses' and ClassVal0='1'; TE\_est=Estimate; TE\_HR=HazardRatio;

TE\_HR\_low=HRLowerCL; TE\_HR\_upp=HRUpperCL; keep TE\_est TE\_HR TE\_HR\_low TE\_HR\_upp;

data de; set de; if Parameter='ses' and ClassVal0='1'; DE\_est=Estimate; DE\_HR=HazardRatio;

DE\_HR\_low=HRLowerCL; DE\_HR\_upp=HRUpperCL; keep DE\_est DE\_HR DE\_HR\_low DE\_HR\_upp;

data res; merge med te de; \*\* Indirect effect \*\*;

IE\_est=TE\_est-DE\_est;

IE\_percent=IE\_est/TE\_est\***100**;

proc append base=&resfile data=res;

run;

**%mend**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**proc** **datasets** lib=work memtype=data nolist; delete results; **quit**;

%***mediation***(seq58526,results);

%***mediation***(seq2111848,results);

%***mediation***(seq491378,results);

%***mediation***(seq433749,results);

%***mediation***(seq598250,results);

%***mediation***(seq41572,results);

%***mediation***(seq533949,results);

%***mediation***(seq543763,results);

%***mediation***(seq1369026,results);

%***mediation***(seq1121440,results);

%***mediation***(seq627616,results);

%***mediation***(seq606971,results);

%***mediation***(seq1080322,results);

%***mediation***(seq1890126,results);

**proc** **print** data=results;

id Protein;

var TE\_est TE\_HR TE\_HR\_low TE\_HR\_upp DE\_est DE\_HR DE\_HR\_low DE\_HR\_upp IE\_est IE\_percent;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* 14 protein mediators \*\*;

**data** wh4;

set wh3;

ses=ses5;

\* ses=educ5;

IF nmiss(of ses seq58526 seq2111848 seq491378 seq433749 seq598250 seq41572 seq533949 seq543763

seq1369026 seq1121440 seq627616 seq606971 seq1080322 seq1890126)=**0**;

**run**;

\*\*\* weights \*\*\*;

**proc** **logistic** data=wh4;

model ses(ref='3') = sex age ETHN\_DS

seq58526 seq2111848 seq491378 seq433749 seq598250 seq41572 seq533949 seq543763

seq1369026 seq1121440 seq627616 seq606971 seq1080322 seq1890126 / link=glogit;

ods output ParameterEstimates=beta;

**proc** **transpose** data=beta out=beta; id Variable Response;

**data** beta; set beta; if \_NAME\_='Estimate'; all=**1**;

estimate11=seq585261; estimate12=seq585262;

estimate21=seq21118481; estimate22=seq21118482;

estimate31=seq4913781; estimate32=seq4913782;

estimate41=seq4337491; estimate42=seq4337492;

estimate51=seq5982501; estimate52=seq5982502;

estimate61=seq415721; estimate62=seq415722;

estimate71=seq5339491; estimate72=seq5339492;

estimate81=seq5437631; estimate82=seq5437632;

estimate91=seq13690261; estimate92=seq13690262;

estimate101=seq11214401; estimate102=seq11214402;

estimate111=seq6276161; estimate112=seq6276162;

estimate121=seq6069711; estimate122=seq6069712;

estimate131=seq10803221; estimate132=seq10803222;

estimate141=seq18901261; estimate142=seq18901262;

keep all estimate11--estimate142;

**data** idt; set wh4; all=**1**; keep all STNO;

**data** beta2; merge idt beta; by all;

**data** wh5; merge wh4 beta2; by STNO;

**data** wh5; set wh5;

if ses=**3** then IORW=**1**;

if ses=**2** then

IORW=**1**/exp(estimate12\*seq58526+estimate22\*seq2111848+estimate32\*seq491378+estimate42\*seq433749+

estimate52\*seq598250+estimate62\*seq41572+estimate72\*seq533949+estimate82\*seq543763+

estimate92\*seq1369026+estimate102\*seq1121440+estimate112\*seq627616+estimate122\*seq606971+

estimate132\*seq1080322+estimate142\*seq1890126);

if ses=**1** then

IORW=**1**/exp(estimate11\*seq58526+estimate21\*seq2111848+estimate31\*seq491378+estimate41\*seq433749+

estimate51\*seq598250+estimate61\*seq41572+estimate71\*seq533949+estimate81\*seq543763+

estimate91\*seq1369026+estimate101\*seq1121440+estimate111\*seq627616+estimate121\*seq606971+

estimate131\*seq1080322+estimate141\*seq1890126);

**run**;

\*\*\* Cox model \*\*\*;

**proc** **phreg** data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

ods output ParameterEstimates=te; \*\* Total effect \*\*;

**proc** **phreg** data=wh5;

class ses(ref='3');

model futime\_hall\*status\_hall(**0**)= sex age ETHN\_DS ses / rl;

weight IORW;

ods output ParameterEstimates=de; \*\* Direct effect \*\*;

**run**;

**data** te; set te; if Parameter='ses' and ClassVal0='1'; TE\_est=Estimate; TE\_HR=HazardRatio;

TE\_HR\_low=HRLowerCL; TE\_HR\_upp=HRUpperCL; keep TE\_est TE\_HR TE\_HR\_low TE\_HR\_upp;

**data** de; set de; if Parameter='ses' and ClassVal0='1'; DE\_est=Estimate; DE\_HR=HazardRatio;

DE\_HR\_low=HRLowerCL; DE\_HR\_upp=HRUpperCL; keep DE\_est DE\_HR DE\_HR\_low DE\_HR\_upp;

**data** est; merge te de; \*\* Indirect effect \*\*;

IE\_est=TE\_est-DE\_est;

IE\_percent=IE\_est/TE\_est\***100**;

**proc** **print** data=est;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Tables S19D, S25, S26 \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Socioeconomic disadvantage \*\*;

/\* educses=educ5+ses5;

if educ5=1 and ses5=1 then educses3=1;

if educ5=1 and ses5 IN (2,3) then educses3=2;

if educ5=2 and ses5>. then educses3=3;

if educ5=3 and ses5 IN (1,2) then educses3=4;

if educ5=3 and ses5=3 then educses3=5; \*/

**proc** **genmod** data=wh4;

class educses; \*educses, educses3\*;

model protein = age5 sex eth educses;

lsmeans educses / cl;

by varname;

ods output LSMeans=lsm;

**run**;

**data** results\_educses;

set lsm;

keep varname nro educses Estimate Lower Upper;

**run**;

**proc** **genmod** data=wh4;

class educ5 nhood3;

model protein = age5 sex eth educ5 nhood3;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Extended Data Figure 4 (Phi Coefficients) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**data** t101; set diseases; if dgnro=**101**; rename slaalkupvm=slaalkupvm101;

**data** t102; set diseases; if dgnro=**102**; rename slaalkupvm=slaalkupvm102;

**data** t103; set diseases; if dgnro=**103**; rename slaalkupvm=slaalkupvm103;

**data** t104; set diseases; if dgnro=**104**; rename slaalkupvm=slaalkupvm104;

**data** t105; set diseases; if dgnro=**105**; rename slaalkupvm=slaalkupvm105;

**data** t106; set diseases; if dgnro=**106**; rename slaalkupvm=slaalkupvm106;

**data** t107; set diseases; if dgnro=**107**; rename slaalkupvm=slaalkupvm107;

**data** t108; set diseases; if dgnro=**108**; rename slaalkupvm=slaalkupvm108;

**data** t109; set diseases; if dgnro=**109**; rename slaalkupvm=slaalkupvm109;

**data** diseases2;

merge t101 t102 t103 t104 t105 t106 t107 t108 t109;

by id;

**data** persons2;

merge persons(in=i) diseases2;

by id;

if i;

**data** persons3;

merge persons2;

dis101=**0**; dis102=**0**; dis103=**0**; dis104=**0**; dis105=**0**; dis106=**0**; dis107=**0**; dis108=**0**; dis109=**0**;

if slaalkupvm101>=alkupvm then do; dis101=**1**; age\_h101=age+(year(slaalkupvm101)-year(alkupvm)); seurv101=(slaalkupvm101-alkupvm+**1**)/**365.25**; end;

if slaalkupvm102>=alkupvm then do; dis102=**1**; age\_h102=age+(year(slaalkupvm102)-year(alkupvm)); seurv102=(slaalkupvm102-alkupvm+**1**)/**365.25**; end;

if slaalkupvm103>=alkupvm then do; dis103=**1**; age\_h103=age+(year(slaalkupvm103)-year(alkupvm)); seurv103=(slaalkupvm103-alkupvm+**1**)/**365.25**; end;

if slaalkupvm104>=alkupvm then do; dis104=**1**; age\_h104=age+(year(slaalkupvm104)-year(alkupvm)); seurv104=(slaalkupvm104-alkupvm+**1**)/**365.25**; end;

if slaalkupvm105>=alkupvm then do; dis105=**1**; age\_h105=age+(year(slaalkupvm105)-year(alkupvm)); seurv105=(slaalkupvm105-alkupvm+**1**)/**365.25**; end;

if slaalkupvm106>=alkupvm then do; dis106=**1**; age\_h106=age+(year(slaalkupvm106)-year(alkupvm)); seurv106=(slaalkupvm106-alkupvm+**1**)/**365.25**; end;

if slaalkupvm107>=alkupvm then do; dis107=**1**; age\_h107=age+(year(slaalkupvm107)-year(alkupvm)); seurv107=(slaalkupvm107-alkupvm+**1**)/**365.25**; end;

if slaalkupvm108>=alkupvm then do; dis108=**1**; age\_h108=age+(year(slaalkupvm108)-year(alkupvm)); seurv108=(slaalkupvm108-alkupvm+**1**)/**365.25**; end;

if slaalkupvm109>=alkupvm then do; dis109=**1**; age\_h109=age+(year(slaalkupvm109)-year(alkupvm)); seurv109=(slaalkupvm109-alkupvm+**1**)/**365.25**; end;

**run**;

**proc** **corr** data=persons3;

var dis108 dis105 dis109 dis106 dis107 dis103 dis102 dis104 dis101;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

\*\* Figure (Kaplan-Meier) \*\*;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*;

**data** apu1;

set wh3;

futime\_hall=round(futime\_hall,**0.1**);

rename futime\_hall=time educses=group;

**run**;

**proc** **phreg** data=apu1;

where ses>**.**;

model time\*status\_hall(**0**)= ;

strata group;

baseline out=apu2 survival=survival;

**run**;

**data** apu3;

set apu2;

by group;

retain prehazard **0**;

hazard=**1**-survival;

if (hazard>**.** and hazard NE prehazard) or first.group;

prehazard=hazard;

keep group time hazard;

**data** apu4;

set apu3;

retain prehazard pregroup **0**;

if group=pregroup then do;

cumhazard=prehazard; output; end;

cumhazard=hazard; output;

pregroup=group;

prehazard=hazard;

keep group time cumhazard;

**data** apu4;

set apu4;

cumhazard=**100**\*cumhazard; \*\* % \*\*;

**run**;

**proc** **print** data=apu4; \*\* => Excel figure \*\*;

**run**;

\*\* Number at risk, new cases \*\*;

**data** n1;

set apu1;

f0n=**0**; f5n=**0**; f10n=**0**; f15n=**0**; f20n=**0**;

if time>=**0** then do; f0n=**1**; timecl=**5**; end;

if time>=**5** then do; f5n=**1**; timecl=**10**; end;

if time>=**10** then do; f10n=**1**; timecl=**15**; end;

if time>=**15** then do; f15n=**1**; timecl=**20**; end;

if time>=**20** then do; f20n=**1**; timecl=**25**; end;

**run**;

**proc** **means** data=n1 sum;

var f0n f5n f10n f15n f20n;

class group;

**proc** **freq** data=n1; where status\_hall=**1**;

tables group\*timecl / list;

**run**;

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

**Fig. 3E**, by Joni V. Lindbohm**:**

library(igraph)

library(STRINGdb)

library(AnnotationDbi)

library(clusterProfiler)

library(enrichplot)

library(ggplot2)

organism = "org.Hs.eg.db"

library(organism, character.only = TRUE)

keytypes(org.Hs.eg.db)

require(DOSE)

### Run enrichment analyses for main proteins that are

main\_proteins\_ids = Cs(S100A12, GCHFR, CCL16, CRP, CFHR1, F2, S100A9, FABP3, BGN, DNAJB9, FURIN, SUMF2, HSPA1A, HSPA1B)

### Load identifiers for other proteins

all\_proteins = read.xlsx("all\_analyzed\_ses\_proteins.xlsx")

head(all\_proteins)

dim(all\_proteins)

all\_protein\_ids = all\_proteins %>% pull(EntrezGeneSymbol)

ego <- enrichGO(gene = main\_proteins\_ids,

universe = all\_protein\_ids,

OrgDb = org.Hs.eg.db,

keyType = "SYMBOL",

ont = "ALL",

pAdjustMethod = "BH",

qvalueCutoff = 0.05,

readable = TRUE)

ego@result$Description = firstup(ego@result$Description )

dplot = (dotplot(ego))

dplot = dplot + xlab("Gene ratio")

pdf(paste0("SES\_proteins\_enrichment\_plot.pdf"), width=9, height=10)

print(dplot)

dev.off()

**Fig 3F**, by Joni Lindbohm**:**

### String analyses were done with STRINGdb online tool:

https://string-db.org/cgi/input?sessionId=b5a1h76WOaR7&input\_page\_show\_search=on