# R-Code for Development and validation of Mild Cognitive Impairment to Dementia Risk (CIDER) score

**Abstract**

**Introduction**: This study aimed to develop and validate a 3-year dementia risk score in individuals with mild cognitive impairment (MCI) based on variables collected in routine clinical care.

**Methods**: The prediction score was developed using data from the National Alzheimer’s Coordinating Center. Selection criteria included aged 55 years and older with MCI. Cox models were validated internally via bootstrapping and externally using two independent cohorts from the PROspective Registry of Persons with Memory SyMPToms (PROMPT) registry and the Alzheimer’s Disease Neuroimaging Initiative (ADNI) database.

**Results**: Our Mild Cognitive Impairment to Dementia Risk (CIDER) score predicted dementia risk with c-indices of 0.69, 0.61, and 0.72, for the internally validated and the external validation PROMPT, and ADNI cohorts, respectively.

**Discussion**: The CIDER score could be used to inform clinicians and patients about the relative probabilities of developing dementia in patients with MCI.

**R codes script:**

## “rms” package variable selection process wasn’t included

#######plotting the scatterplot

#ggplot(outcome,aes(var1,var2,color=dem2))+geom\_point()

####### Model Development using PROMPT

# simple model, no interaction, no consideration of non-linearity

dtime <- dd$time

status <- dd$outcome

units(dtime) <- 'Month'

S <- Surv(dtime, status)

fit<- cph(S ~varlist

, data=dd, x=TRUE, y=TRUE, surv = T, time.inc = 24, units = "Month")

anova(fit)

plot(anova(fit)

###### bootrapping

set.seed(123)

validate(fit1, B=300)

######calibration

cal.km <- calibrate(fit1, cmethod='KM',method="boot",m=50, B=300,u=24,what="observed-predicted") # usually B=200 or 300

plot(cal.km, xlab = "Predicted 24 Months", ylab="Observed Survival", subtitles = FALSE)

cal.hare <- calibrate(fit1, cmethod='hare',method="boot",m=50, B=300,u=24,what="observed-predicted") # usually B=200 or 300

plot(cal.hare, add = TRUE)

###### points system

nom <- nomogram(fit1, maxscale = 100)

nom

plot(nom)

####external validation using an independent dataset

validated=val.surv(fit,newdata=test,S=S\_test, type="b", dxy=TRUE)

plot(validated, xlab="predcited", ylab="observed")

###Determine concordance

estimates=survest(fit,newdata=test,times=24)$surv

rcorr.cens(x=estimates,S=S\_test, outx = T)