Biostatistics I: Variable Selection

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Chapter 1 Variable Selection



Scientific questions revolve around the *understanding* of phenomena

- ▷ How does the age of patients affect their blood pressure?
- > Are patients with gene mutations more likely to develop cancer?

▷...



- These questions translate to the understanding of random variables
 - > however, the relationships between these variables are quite complex

To make progress, we make a simplification of reality

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Statistical Regression Models



- Regression models describe the relationships between
 - ▷ an outcome variable
 - \triangleright a set of explanatory variables / predictors / covariates
- The outcome defines the model
 - \triangleright continuous outcomes \rightarrow linear regression model
 - \triangleright binary outcomes \rightarrow logistic regression model
 - \triangleright count outcomes \rightarrow Poisson regression model
 - \triangleright survival outcomes \rightarrow proportional hazards models

 $\triangleright \dots$



- Statistical models are developed for three main purposes
 - ▷ etiology
 - \triangleright prediction
 - ▷ description

Explanatory models:

- used in etiology research to explain differences in outcome values by differences in explanatory variables
 - ▷ estimate (causal) effects of risk factors or exposures
 - ▷ confounders, colliders and mediators

 \triangleright aim to minimize bias



Predictive Models: aim to accurately predict an outcome using a set of predictors ▷ expected prediction error is the quantity of main concern

Descriptive Models:

- capture the association between covariates and an outcome
 - ▷ elements of both explanatory and predictive models
 - ▷ focus on size of effects, but not causal relationships



• For all three types of models, a relevant and difficult question is

Which explanatory variables / predictors / covariates to include in the model?



- Secondary question: How to include these variables in the model?
- Linearity: Including a continuous variable as-is in a model assumes linearity \Rightarrow Many times not reasonable
 - ▷ polynomials & splines
 - \triangleright transformations
- <u>Additivity</u>: Including two variables in a model assumes that their effects on the outcome are independent

▷ interaction terms



- Fitting too complex models (i.e., models with too many parameters) may result in *Overfitting*
- Overfitting has two important consequences
 - \triangleright estimated effects have increased variance \Rightarrow influences confidence intervals and p-values
 - ▷ predicted values from the model do not agree with observed values from future data sets (from the same population) ⇒ the model does not validate well



- To avoid overfitting, we need to restrict the model's complexity
 b the number of coefficients to estimate
- Note: the number of coefficients is not, in general, equal to the number of covariates
 ▷ categorical covariates with k levels are represented by k 1 dummy variables
 ▷ nonlinear & interaction terms



• A *rule of thumb* is to include up to

Effective Sample Size
$$=$$
 $\frac{n^*}{10}$

coefficients in a model

• The value of n^* depends on the information available in the outcome



▷ Continuous outcome / linear regression:

 $n^* = n$, the sample size

▷ Dichotomous outcomes / logistic regression:

 $n^* = \min\{\# \text{ number of 0s}, \# \text{ number of 1s}\}$

▷ Event times / Cox regression:

 $n^* = \{ \# \text{ number of events} \}$



• For all three types of models, a relevant and difficult question is

Which explanatory variables / predictors / covariates to include in the model?



Due to its practical importance, this question has received a lot of attention

- There are many algorithms available to tackle this problem, ranging from
 - \triangleright automatic: the computer does the work for you
 - \triangleright manual: the user/researcher needs to do the work



Automatic Algorithms

- ▷ Backward elimination
 - * Start: a global model
 - * Repeat: remove the most insignificant covariate and re-estimate the model
 - * Stop: if no insignificant covariate is left

▷ Forward Selection

- * Start: the most significant univariable model
- * Repeat: Evaluate the added value of each covariate that is currently not in the model; include the most significant covariate and re-estimate the model
- * Stop: if no significant covariate is left to include



Automatic Algorithms

- ▷ Stepwise flavors
 - * Combinations of backward elimination & forward selection
- ▷ Univariable selection
 - * Estimate all univariable models
 - * Fit a multivariable model including only the significant covariates from the previous step



- Automatic Algorithms Advantages
 - \triangleright we don't have to think \Rightarrow the computer does the work for us automatically
 - \triangleright we can consider as many variables as we like



- Automatic Algorithms **Disadvantages**
 - \triangleright we don't have to think \Rightarrow the computer does the work for us automatically
 - ▷ we can consider as many variables as we like



• Automatic Algorithms – **Disadvantages**

▷ yield coefficients that biased high in absolute value

▷ yield p-values that are too small

▷ provide confidence intervals that are too narrow

▷ they suffer even more from collinearity



- ▷ Make a list of candidate variables using background knowledge
 - * critically question the role and further properties of each variable, i.e.,
 - * chronology of measurement collection, costs of collection, quality of measurement, availability
- > Make a grouping of variables of primary and secondary interest
- \triangleright For the variables of primary interest consider
 - * nonlinear terms for continuous variables
 - * relevant interaction terms



> Setting I: The number of coefficients is *smaller* than the effective sample size

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Fit the multivariable model containing all terms



- > Setting II: The number of coefficients is *larger* than the effective sample size
 - * reduce the set of secondary variables by eliminating variables with narrow distributions and large number of missing data
 - * use data reduction methods (e.g., principal component analysis, clustering)

Fit the multivariable model containing the reduced terms



- evaluate the model assumptions using residuals, and appropriately refit the model
 * e.g., consider transformations of the outcome variable
- ▷ consider dropping the complex terms, i.e., the interaction and nonlinear terms
 - * perform an omnibus test for all interaction (nonlinear) terms
 - * if the p-value > 0.15, you could eliminate all of them
 - * otherwise, find which of them seem to play a role



- \triangleright if you build a Descriptive Model \Rightarrow stop
 - * you do **not** need to drop non-significant variables
 - * p-values and confidence from the full model (containing non-significant variables) are of better quality
- ▷ if you build a Predictive Model
 - * you could drop variables, provided that the predictive accuracy is not compromised
 - * the model needs to be 'practical', i.e., easy to use in clinical practice



- \triangleright present the results of the analysis
 - * interpret the size (i.e., point estimate) and uncertainty (95% CIs) of the coefficients
 - * if necessary (i.e., when you have interaction and nonlinear terms), use effect plots to communicate the results



We have presented a procedure with general guidelines for model-building.

It should be stressed that in some settings, adaptations and exceptions of some of these steps could be relevant.



When we compare (two) statistical models, an important consideration is whether these models are **nested** or **non-nested**

- <u>Note</u>: Model A is nested in Model B, when Model A is a special case of Model B
 - \triangleright i.e., by setting some of the parameters of Model B at some specific value we obtain Model A



• Example 1:

$$M_A : \log(\texttt{serBilir}_i) = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \beta_3 \texttt{Age}_i^2 + \varepsilon_i$$
$$M_B : \log(\texttt{serBilir}_i) = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \varepsilon_i$$

• Model M_B is nested in model M_A

 \triangleright because if we set $\beta_3 = 0$ in model M_A , we get model M_B



• Example 2:

$$M_A : \log(\texttt{serBilir}_i) = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \beta_3 \texttt{Age}_i^2 + \varepsilon_i$$
$$M_B : \log(\texttt{serBilir}_i) = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \beta_3 \texttt{BMI}_i + \varepsilon_i$$

- \bullet Models M_A and M_B are not nested
 - ▷ we cannot set some coefficients to a particular value in the one model to get the other



• Example 3:

$$M_A : \texttt{serBilir}_i = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \beta_3 \texttt{Age}_i^2 + \varepsilon_i$$
$$M_B : \log(\texttt{serBilir}_i) = \beta_0 + \beta_1 \texttt{Sex}_i + \beta_2 \texttt{Age}_i + \varepsilon_i$$

- Models M_A and M_B are not nested
 - \triangleright if we set $\beta_3 = 0$ in the linear predictor of M_A , we get the linear predictor of M_B
 - \triangleright *however*, model M_A has outcome variable serBilir_i while model model M_B has outcome variable $\log(\text{serBilir}_i)$



• Most often we compare **nested** models using the likelihood ratio test (LRT):

$$\mathsf{LRT} = -2 \times \{\ell(\hat{\theta}_0) - \ell(\hat{\theta}_a)\} \sim \chi_p^2$$

where

- $\triangleright \ell(\hat{\theta}_0)$ the value of the log-likelihood function under the null hypothesis, i.e., the special case model
- $\triangleright \ell(\hat{\theta}_a)$ the value of the log-likelihood function under the alternative hypothesis, i.e., the general model
- $\triangleright p$ denotes the number of parameters being tested

<u>Note:</u> We can also compare nested model using the Wald and Score tests



- When we have **non-nested** models we **cannot** use standard tests anymore
- As an alternative for this case we use information criteria the two standard ones are:

$$AIC = -2\ell(\hat{\theta}) + 2n_{par}$$

$$BIC = -2\ell(\hat{\theta}) + n_{par}\log(n)$$

where

 $\triangleright \ell(\hat{\theta})$ is the value of the log-likelihood function $\triangleright n_{par}$ the number of parameters in the model $\triangleright n$ the number of subjects (independent units)



When we compare two **non-nested** models we choose the model that has the **lowest** AIC/BIC value