

# Advanced Medical Statistics – Answers lab 7

## Part 1: Building prediction models using backward elimination

### Step 1: Fit the initial linear regression model

Create an initial model for hospital length of stay (`los`) using the following predictors: `age`, `gender`, `hr`, `sysbp`, `diasbp`, `bmi`, `cvd`, `sho`. Run/summarize the model to inspect coefficients and p-values.

Call:

```
lm(formula = los ~ age + gender + hr + sysbp + diasbp + bmi +  
    cvd + sho, data = whas)
```

Residuals:

Min	1Q	Median	3Q	Max
-8.335	-2.653	-1.071	1.200	40.073

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.2648144	2.1394896	1.526	0.127659
age	0.0031994	0.0168850	0.189	0.849792
genderfemale	0.8575246	0.4489334	1.910	0.056698 .
hr	0.0190577	0.0090828	2.098	0.036396 *
sysbp	-0.0008358	0.0085656	-0.098	0.922304
diasbp	0.0141799	0.0128884	1.100	0.271780
bmi	-0.0304532	0.0427613	-0.712	0.476700
cvdyes	0.3903925	0.4981468	0.784	0.433600
shoyes	3.5265170	1.0329265	3.414	0.000693 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.632 on 491 degrees of freedom  
 Multiple R-squared: 0.04991, Adjusted R-squared: 0.03443  
 F-statistic: 3.224 on 8 and 491 DF, p-value: 0.001388

## Step 2: Eliminate the least significant predictor

Anova Table (Type III tests)

Response: los

	Sum Sq	Df	F value	Pr(>F)
(Intercept)	50.0	1	2.3286	0.1276592
age	0.8	1	0.0359	0.8497924
gender	78.3	1	3.6486	0.0566978 .
hr	94.5	1	4.4025	0.0363962 *
sysbp	0.2	1	0.0095	0.9223042
diasbp	26.0	1	1.2105	0.2717799
bmi	10.9	1	0.5072	0.4766997
cvd	13.2	1	0.6142	0.4336001
sho	250.1	1	11.6561	0.0006929 ***
Residuals	10535.8	491		

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The ANOVA table shows that the predictor with the highest p-value is **sysbp** ( $p = 0.92$ ). Systolic blood pressure is the least significant predictor and should be removed from the model.

## Step 3: Repeat the steps

The following variables are sequentially removed from the model (after initially removing **sysbp**):

1. **age**: p-value = 0.86
2. **cvd**: p-value = 0.41
3. **bmi**: p-value = 0.44
4. **diasbp**: p-value = 0.22

#### Step 4: Final model

Call:

```
lm(formula = los ~ gender + hr + sho, data = whas)
```

Residuals:

Min	1Q	Median	3Q	Max
-8.663	-2.661	-1.064	1.136	40.826

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	3.796075	0.799047	4.751	2.66e-06	***
genderfemale	0.910388	0.424827	2.143	0.032602	*
hr	0.020680	0.008843	2.339	0.019751	*
shoyes	3.550448	1.009081	3.518	0.000474	***

---

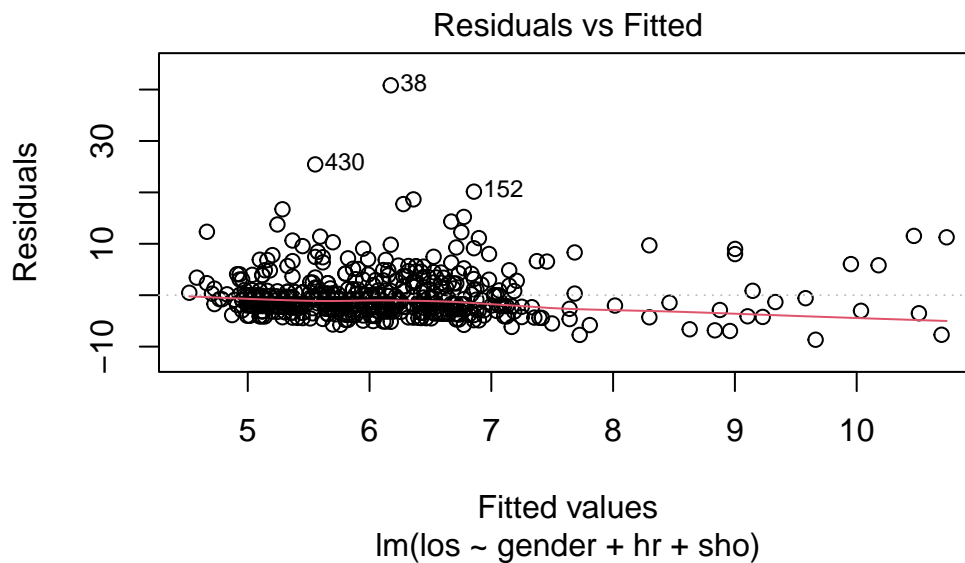
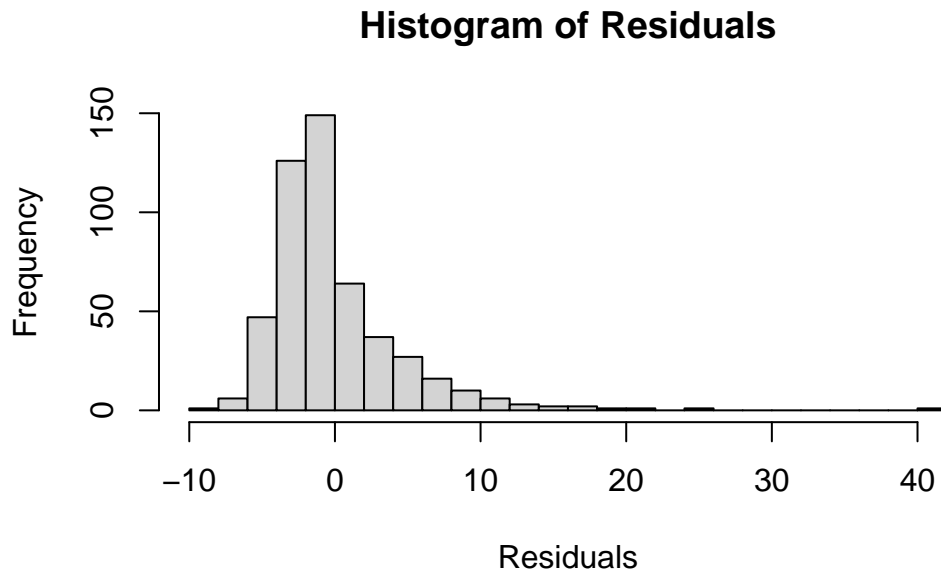
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.622 on 496 degrees of freedom

Multiple R-squared: 0.04443, Adjusted R-squared: 0.03865

F-statistic: 7.687 on 3 and 496 DF, p-value: 4.976e-05

#### Residual plots



The overall fit of the model appears reasonable, as the residuals are generally centered around zero with no major patterns suggesting severe violations of linearity. However, there are some outliers with very long lengths of stay (LOS) that are not adequately captured by the model. These outliers lead to a right skew in the residual distribution, as seen in the his-

togram, influencing model fit. While the current model seems to work reasonably well for most observations, further steps (e.g., transformations or robust regression techniques) could be considered to better account for these extreme cases.

## Part 2: Automated procedures for building prediction models

### Exercise: Automated procedures vs manual model

R

```
library(MASS)
fit <- lm(los ~ age + gender + hr + sysbp + diasbp + bmi + cvd + sho, data = whas)
step_model <- stepAIC(fit, direction = "backward")
```

Start: AIC=1541.96

los ~ age + gender + hr + sysbp + diasbp + bmi + cvd + sho

	Df	Sum of Sq	RSS	AIC
- sysbp	1	0.204	10536	1540.0
- age	1	0.770	10537	1540.0
- bmi	1	10.883	10547	1540.5
- cvd	1	13.179	10549	1540.6
- diasbp	1	25.974	10562	1541.2
<none>			10536	1542.0
- gender	1	78.292	10614	1543.7
- hr	1	94.469	10630	1544.4
- sho	1	250.115	10786	1551.7

Step: AIC=1539.97

los ~ age + gender + hr + diasbp + bmi + cvd + sho

	Df	Sum of Sq	RSS	AIC
- age	1	0.682	10537	1538.0
- bmi	1	11.109	10547	1538.5
- cvd	1	12.975	10549	1538.6
- diasbp	1	38.551	10575	1539.8
<none>			10536	1540.0
- gender	1	78.719	10615	1541.7
- hr	1	96.991	10633	1542.6
- sho	1	260.543	10797	1550.2

Step: AIC=1538.01  
 los ~ gender + hr + diasbp + bmi + cvd + sho

	Df	Sum of Sq	RSS	AIC
- cvd	1	14.624	10551	1536.7
- bmi	1	15.372	10552	1536.7
- diasbp	1	37.888	10575	1537.8
<none>			10537	1538.0
- gender	1	84.736	10621	1540.0
- hr	1	101.448	10638	1540.8
- sho	1	264.134	10801	1548.4

Step: AIC=1536.7  
 los ~ gender + hr + diasbp + bmi + sho

	Df	Sum of Sq	RSS	AIC
- bmi	1	12.883	10564	1535.3
- diasbp	1	38.599	10590	1536.5
<none>			10551	1536.7
- gender	1	97.518	10649	1539.3
- hr	1	99.732	10651	1539.4
- sho	1	266.183	10818	1547.2

Step: AIC=1535.31  
 los ~ gender + hr + diasbp + sho

	Df	Sum of Sq	RSS	AIC
- diasbp	1	32.352	10597	1534.8
<none>			10564	1535.3
- hr	1	104.369	10669	1538.2
- gender	1	108.564	10673	1538.4
- sho	1	273.160	10837	1546.1

Step: AIC=1534.84  
 los ~ gender + hr + sho

	Df	Sum of Sq	RSS	AIC
<none>			10597	1534.8
- gender	1	98.11	10695	1537.5
- hr	1	116.84	10713	1538.3
- sho	1	264.48	10861	1545.2

```
summary(step_model)
```

Call:

```
lm(formula = los ~ gender + hr + sho, data = whas)
```

Residuals:

Min	1Q	Median	3Q	Max
-8.663	-2.661	-1.064	1.136	40.826

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	3.796075	0.799047	4.751	2.66e-06	***
genderfemale	0.910388	0.424827	2.143	0.032602	*
hr	0.020680	0.008843	2.339	0.019751	*
shoyes	3.550448	1.009081	3.518	0.000474	***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.622 on 496 degrees of freedom

Multiple R-squared: 0.04443, Adjusted R-squared: 0.03865

F-statistic: 7.687 on 3 and 496 DF, p-value: 4.976e-05

The final model obtained from the automated procedure is identical to the manually created model in Part 1.

## SPSS

<b>Variables Entered/Removed<sup>a</sup></b>			
<b>Model</b>	<b>Variables Entered</b>	<b>Variables Removed</b>	<b>Method</b>
1	cardiogenic shock, gender, initial diastolic blood pressure, history of cardiovascular disease, initial heart rate, bmi, age at hospital admission, initial systolic blood pressure <sup>b</sup>	.	Enter
2	.	initial systolic blood pressure	Backward (criterion: Probability of F-to-remove $\geq$ , 100).
3	.	age at hospital admission	Backward (criterion: Probability of F-to-remove $\geq$ , 100).
4	.	history of cardiovascular disease	Backward (criterion: Probability of F-to-remove $\geq$ , 100).
5	.	bmi	Backward (criterion: Probability of F-to-remove $\geq$ , 100).
6	.	initial diastolic blood pressure	Backward (criterion: Probability of F-to-remove $\geq$ , 100).

a. Dependent Variable: length of hospital stay  
b. All requested variables entered.

Figure 1: SPSS results of the backward elimination procedure



The table above shows the variables eliminated at each step of the backward elimination procedure in SPSS. The final model obtained from the automated procedure is identical to the manually created model in Part 1.

### Part 3: Causal diagrams

For each of the exercises below:

- Try solving the diagrams by hand by using the recipe from the lecture (see lecture slides on Brightspace)
- Check your answer using the [DAGitty webtool](#)

#### Exercise 1

In the graph depicted below, for which variables do you need to adjust to assess the unconfounded effect of E on O (there may be several possibilities)?

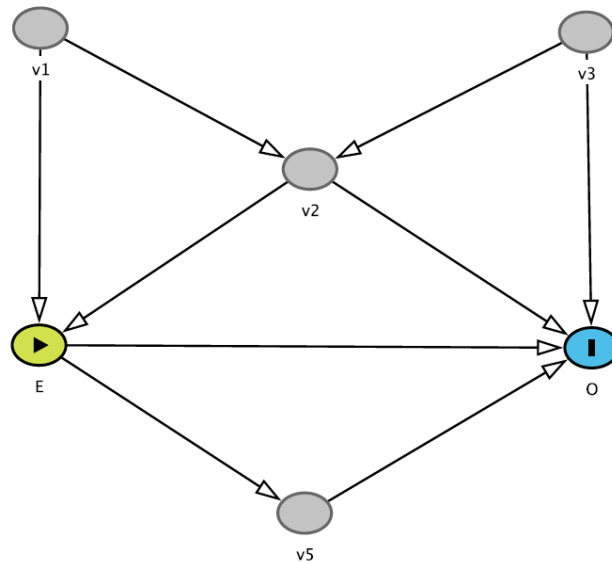


Figure 2: DAG exercise 1

**Answer:**

Following the recipe: after removing all arrows leaving E, there are several unblocked paths

leading from E to O. Just like in the lecture, adjusting for v2 opens a backdoor path ( $E - v1 - v3 - O$ ) This newly opened backdoor path needs to be closed by also conditioning on v1 or v3, or both. Hence, there are 3 options: (v1, v2, v3) ; (v1, v2) ; and finally, (v2, v3).

## Exercise 2

In the graph depicted below, what happens when you additionally adjust for **v5**?

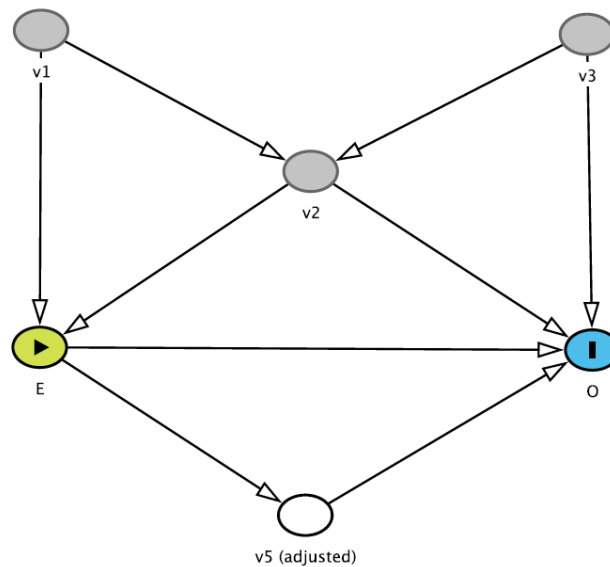


Figure 3: DAG exercise 2

**Answer:** When adjusting for v5, we are blocking the effect through this indirect path from E to O (v5 is a mediator between E and O). Instead of the total effect of E on O, we will be estimating the direct effect.

In DAGitty, when you set v5 to ‘adjusted’, the algorithm will say the following: “The total effect cannot be estimated due to adjustment for an intermediate or a descendant of an intermediate.”

### Exercise 3

This diagram is slightly different: **v1** now is the exposure. For which variables do you need to adjust to assess the unconfounded effect of **v1** on **O**?

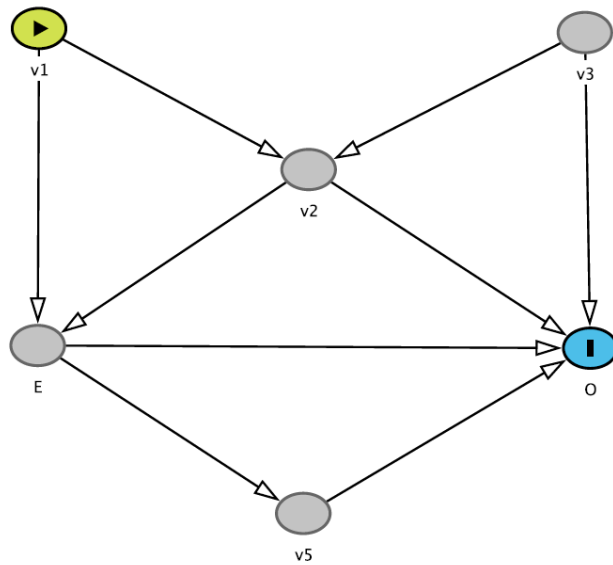


Figure 4: DAG exercise 3

**Answer:** No adjustment is needed: there are no backdoor paths (removing all arrows leaving v1 reveals no remaining unblocked path from v1 to O).

### Exercise 4

Now, **v2** is the exposure. For which variables do you need to adjust to assess the total unconfounded effect of **v2** on **O**?

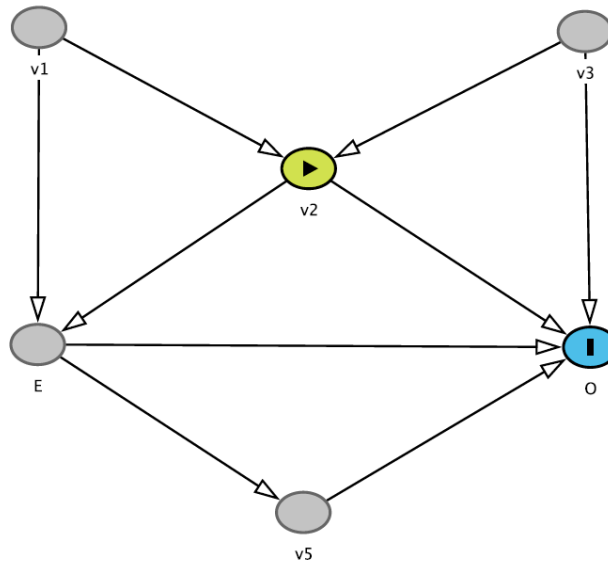


Figure 5: DAG exercise 4

**Answer:** Following the recipe, there are three unblocked paths left after removing the arrows leaving v2:

- a)  $v2 - v3 - O$  and
- b)  $v2 - v1 - E - O$
- c)  $v2 - v1 - E - v5 - O$

Backdoor path a) can be closed by conditioning on v3.

Backdoor path b) can be closed by conditioning on v1 (but not by conditioning on E, as you would no longer be estimating the total effect by blocking the paths from v2 to O mediated by E).

In this case, you should therefore condition on v1 and v3.

### Exercise 5

Back to the first DAG. However, **v2** is now unmeasured. Can we still obtain an unconfounded estimate of the effect of **E** on **O**?

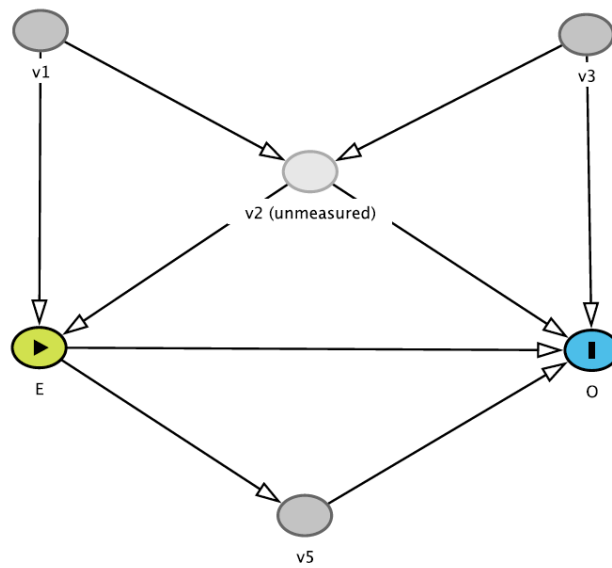


Figure 6: DAG exercise 5

**Answer:** No, we cannot close the backdoor path between E and O since v2 is unmeasured and cannot be corrected for.

### Exercise 6

See the DAG below: you adjusted for **v5**. What would be the consequence of this action?

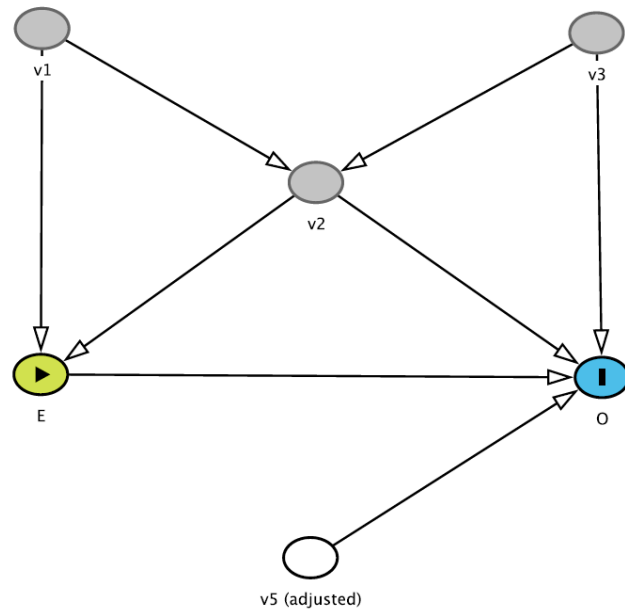


Figure 7: DAG exercise 6

**Answer:** There is no consequence: conditioning on  $v_5$  cannot alter any of the estimated effects in the DAG (it is neither a confounder, collider, nor a mediator in the E-O relationship).