STATISTICAL RETHINKING 2025
WEEK 4 SOLUTIONS

1. I won't repeat the models here. They are in the text. Model `m6.9` contains both marriage status and age. Model `m6.10` contains only age. Model `m6.9` produces a confounded inference about the relationship between age and happiness, due to opening a collider path. To compare these models using PSIS and WAIC:

```
compare( m6.9 , m6.10 , func=PSIS )
compare( m6.9 , m6.10 , func=WAIC )
```

```
        PSIS    SE dPSIS  dSE pPSIS weight
m6.9  2714.0 37.57   0.0   NA   3.8      1
m6.10 3101.9 27.76 387.9 35.4   2.4      0

        WAIC    SE dWAIC   dSE pWAIC weight
m6.9  2714.3 37.51   0.0    NA   3.9      1
m6.10 3101.9 27.68 387.6 35.34   2.3      0
```

The model that produces the invalid inference, `m6.9`, is expected to predict much better. And it would. This is because the collider path does convey actual association. We simply end up mistaken about the causal inference. We should not use PSIS or WAIC to choose among models, unless we have some clear sense of the causal model. These criteria will happily favor confounded models.

So what about the coefficients in the confounded model?

```
precis( m6.9 , depth=2 )
```

```
       mean   sd  5.5% 94.5%
a[1]  -0.24 0.06 -0.34 -0.13
a[2]   1.26 0.08  1.12  1.39
bA    -0.75 0.11 -0.93 -0.57
sigma  0.99 0.02  0.95  1.03
```

We cannot interpret these estimates without reference to the causal model. So let's remember that the causal model is just:

$$H \rightarrow M \leftarrow A$$

where H is happiness, M is married, and A is age.

Okay, you know that the bA parameter is bias by the collider relationship. This model suffers from collider bias, and so bA is not anything but a conditional association. It isn't any kind of causal effect.

The parameters a[1] and a[2] are intercepts for unmarried and married, respectively. But do they correctly estimate the effect of marriage on happiness? No, because marriage in this example does not influence happiness. It is a consequence of happiness.

So what do they estimate? They measure the association between marriage and happiness. But they do it with bias, because the model also includes age. To prove this to yourself, fit a model that stratifies happiness by marriage status but ignore age. You'll see that the a[1] and a[2] estimates you get are different, once you omit age from the model.

In sum, every parameter in the model is a non-causal association.

2. Here are five models with different combinations of predictors:

```
library(rethinking)
data(foxes)
d <- foxes
d$W <- standardize(d$weight)
d$A <- standardize(d$area)
d$F <- standardize(d$avgfood)
d$G <- standardize(d$groupsize)

m1 <- quap(
    alist(
        W ~ dnorm( mu , sigma ),
        mu <- a + bF*F + bG*G + bA*A,
        a ~ dnorm(0,0.2),
        c(bF,bG,bA) ~ dnorm(0,0.5),
        sigma ~ dexp(1)
    ), data=d )
m2 <- quap(
    alist(
        W ~ dnorm( mu , sigma ),
        mu <- a + bF*F + bG*G,
        a ~ dnorm(0,0.2),
        c(bF,bG) ~ dnorm(0,0.5),
        sigma ~ dexp(1)
    ), data=d )
m3 <- quap(
    alist(
        W ~ dnorm( mu , sigma ),
```

```
        mu <- a + bG*G + bA*A,
        a ~ dnorm(0,0.2),
        c(bG,bA) ~ dnorm(0,0.5),
        sigma ~ dexp(1)
    ), data=d )
m4 <- quap(
    alist(
        W ~ dnorm( mu , sigma ),
        mu <- a + bF*F,
        a ~ dnorm(0,0.2),
        bF ~ dnorm(0,0.5),
        sigma ~ dexp(1)
    ), data=d )
m5 <- quap(
    alist(
        W ~ dnorm( mu , sigma ),
        mu <- a + bA*A,
        a ~ dnorm(0,0.2),
        bA ~ dnorm(0,0.5),
        sigma ~ dexp(1)
    ), data=d )
```

Comparing with PSIS:

```
compare( m1 , m2 , m3 , m4 , m5 , func=PSIS )
```

```
    PSIS    SE dPSIS  dSE pPSIS weight
m1 323.6 16.40   0.0   NA   5.0   0.35
m2 323.7 16.09   0.1 3.63   3.6   0.34
m3 323.9 15.85   0.3 2.92   3.8   0.30
m4 333.6 13.83  10.0 7.26   2.5   0.00
m5 333.8 13.99  10.2 7.28   2.7   0.00
```

So the model with all three predictors is very slightly better than the model with only F and G. To remind you, the DAG from last week is:

$$
\begin{array}{ccc}
 & A & \\
\swarrow & & \\
F & \longrightarrow & G \\
\searrow & & \swarrow \\
 & W &
\end{array}
$$

The estimates are:

```
precis(m1)
```

```
       mean   sd  5.5% 94.5%
a      0.00 0.08 -0.13  0.13
bF     0.30 0.21 -0.04  0.63
bG    -0.64 0.18 -0.93 -0.35
bA     0.28 0.17  0.01  0.55
sigma  0.93 0.06  0.83  1.03
```

We don't know the true causal effects in this example. The goal is just to use the DAG to reason what these coefficients are estimating, if anything.

First consider F and `bF`. Since G is in the model, the indirect causal effect of F on W is missing. So `bF` only measures the direct path. But it doesn't even do that completely, because A is also in the model. You saw in an earlier lecture that including a cause of the exposure is usually a bad idea, because it statistical reduces variation in the exposure. So `bF` is probably less accurate than if we omitted A. But it estimates the direct causal effect of F on W.

Second consider G. `bG` estimates the direct effect of G on W.

Now what about A? This is a weird one. From the perspective of A, including its mediator F should block all of its association with W. So it isn't a measure of anything, but it is a kind of test of test of the DAG structure. There may be unobserved confounding or more causal paths that explain why A and W remain associated even after stratifying by F. However, since the model without A has almost the same PSIS score as the one with it, maybe there isn't much statistical support for A being associated with W here anyway. A regression that includes only A and F shows no association really between A and W. Why does including G strengthen the association between A and W? It could just be a fluke of the sample, or it could indicate something is wrong with the causal structure.