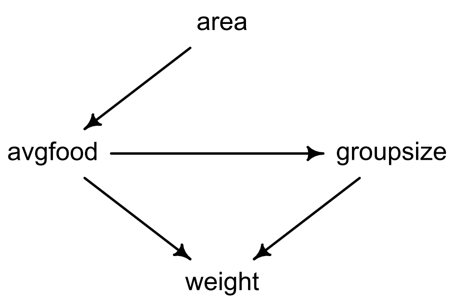
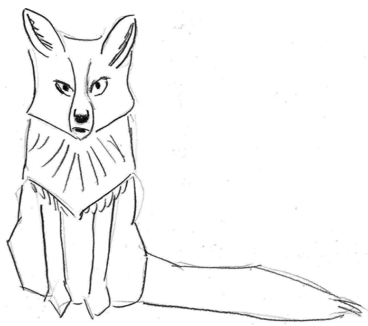
STATISTICAL RETHINKING WINTER 2019
HOMEWORK, WEEK 3 SOLUTIONS

As a reminder, here's the DAG (and FAX):





1. Because there are no back-door paths from `area` to `weight`, we only need to include `area`. No other variables are needed. Here is a model using standardized versions of the variables and those standardized priors from the book:

```
library(rethinking)
data(foxes)
d <- foxes
d$W <- standardize(d$weight)
d$A <- standardize(d$area)
m1 <- 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 )
precis(m1)
```

```
      mean   sd  5.5% 94.5%
a     0.00 0.08 -0.13  0.13
bA    0.02 0.09 -0.13  0.16
sigma 0.99 0.06  0.89  1.09
```

Territory size seems to have no total causal influence on weight, at least not in this sample.

2. To infer the causal influence of `avgfood` on `weight`, we need to close any back-door paths. There are no back-door paths in the DAG. So again, just use a model with a single predictor. If you include `groupsize`, to block the indirect path, then you won't get the total causal influence of food. You'll just get the direct influence. But I asked for the effect of adding food, and that would mean through all forward paths.

```
d$F <- standardize(d$avgfood)
m2 <- 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 )
precis(m2)
```

```
       mean   sd  5.5% 94.5%
a      0.00 0.08 -0.13  0.13
bF    -0.02 0.09 -0.17  0.12
sigma  0.99 0.06  0.89  1.09
```

Again nothing. Adding food does not change weight. This shouldn't surprise you, if the DAG is correct, because `area` is upstream of `avgfood`.

3. The variable `groupsize` does have a back-door path, passing through `avgfood`. So to infer the causal influence of `groupsize`, we need to close that path. This implies a model with both `groupsize` and `avgfood` as predictors.

```
d$G <- standardize(d$groupsize)
m3 <- 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 )
precis(m3)
```

```
       mean   sd  5.5% 94.5%
a      0.00 0.08 -0.13  0.13
bF     0.48 0.18  0.19  0.76
bG    -0.57 0.18 -0.86 -0.29
sigma  0.94 0.06  0.84  1.04
```

It looks like group size is negatively associated with weight, controlling for food. Similarly, food is positively associated with weight, controlling for group size. So the causal influence of group size is to reduce weight—less food for each fox. And the direct causal influence of food is positive, of course. But the total causal influence of food is still nothing, since it causes larger groups. This is a masking effect, like in the milk energy example. But the causal explanation here is that more foxes move into a territory until the food available to each is no better than the food in a neighboring territory. Every territory ends up equally good/bad on average. This is known in behavioral ecology as an *ideal free distribution*.