

Causal Diagrams in R

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**Draw your causal
assumptions with causal
directed acyclic graphs
(DAGs)**

The basic idea

- 1 Specify your causal question
- 2 Use domain knowledge
- 3 Write variables as nodes
- 4 Write causal pathways as arrows
(edges)





dagitty

ggplot2
ggraph



dagitty

powerful,
robust
algorithms

ggplot2 ggraph

dagitty

powerful,
robust
algorithms

ggplot2
ggraph

unlimited
flexibility

beautiful
plots





dagitty

ggplot2
ggraph

Data
structure:
tidy DAGs

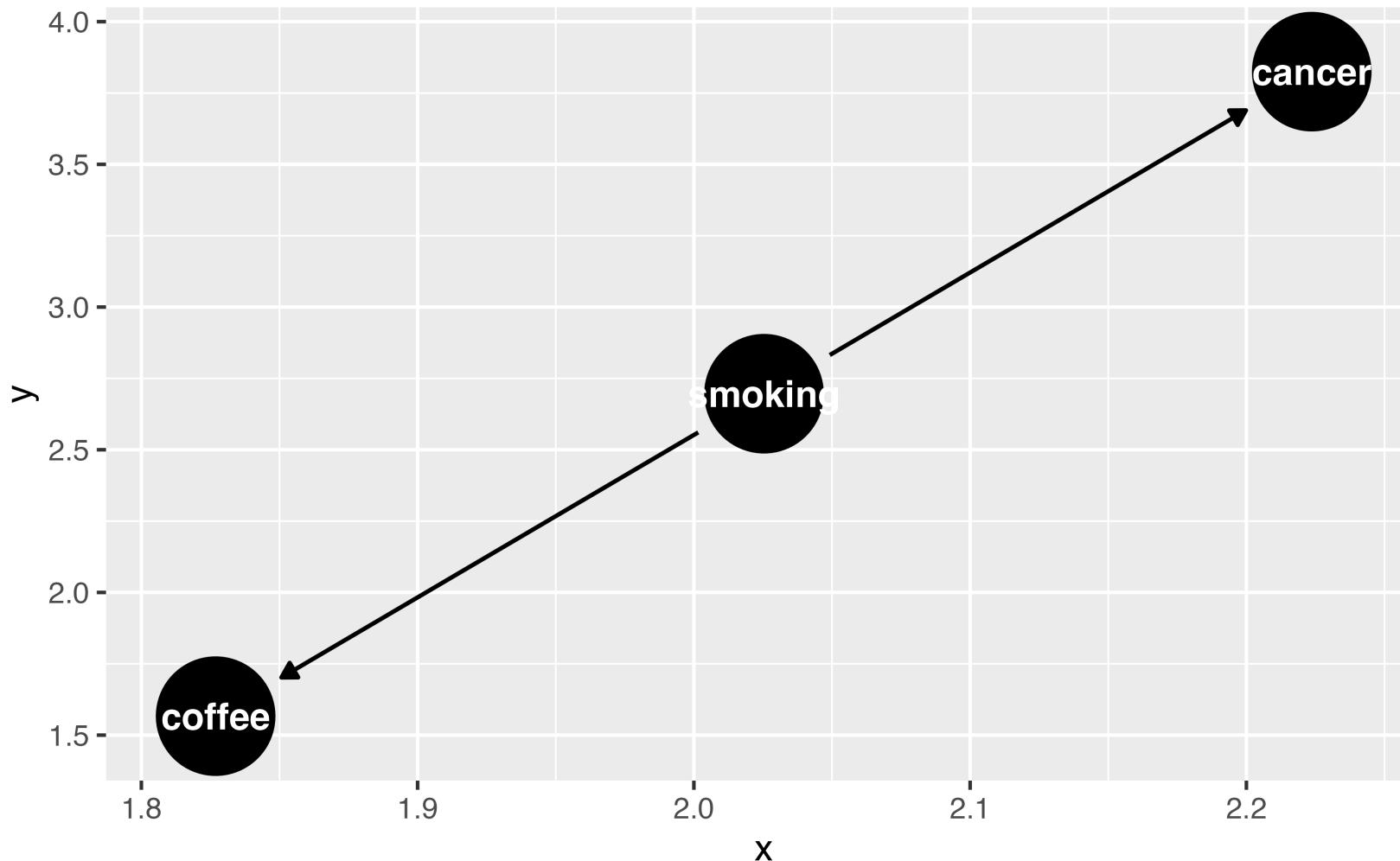
Step 1: Specify your DAG

```
1 library(ggdag)
2 dagify(
3   cancer ~ smoking,
4   coffee ~ smoking
5 )
```

Step 1: Specify your DAG

```
1 dagify(  
2   cancer ~ smoking,  
3   coffee ~ smoking  
4 ) |> ggdag()
```

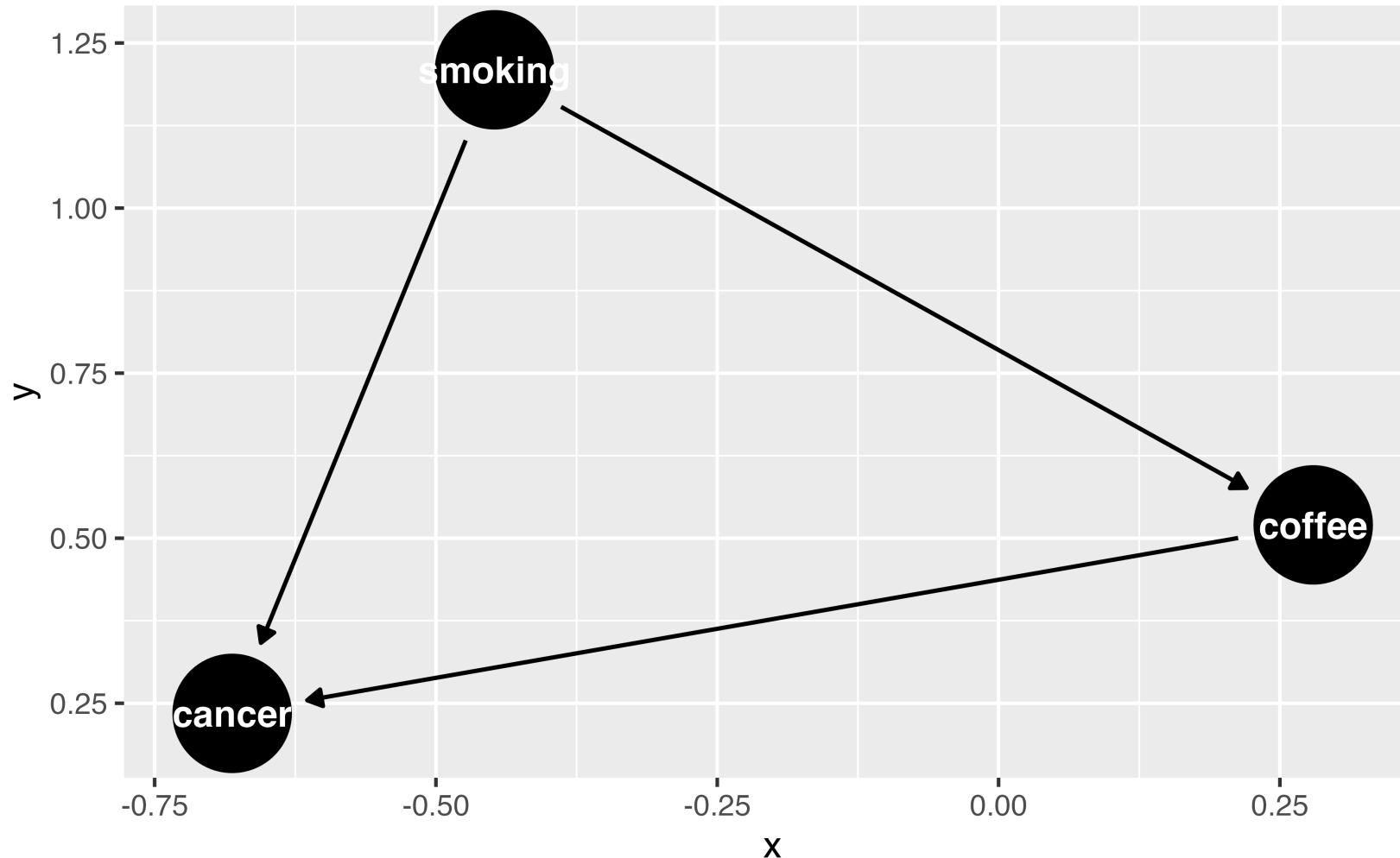
Step 1: Specify your DAG



Step 1: Specify your DAG

```
1 dagify(  
2   cancer ~ smoking + coffee,  
3   coffee ~ smoking  
4 ) |> ggdag()
```

Step 1: Specify your DAG



Your Turn 1 (04-dags-exercises.qmd)

Specify a DAG with `dagify()`. Write your assumption that `smoking` causes `cancer` as a formula.

We're going to assume that coffee does not cause cancer, so there's no formula for that. But we still need to declare our causal question.

Specify "coffee" as the exposure and "cancer" as the outcome (both in quotations marks).

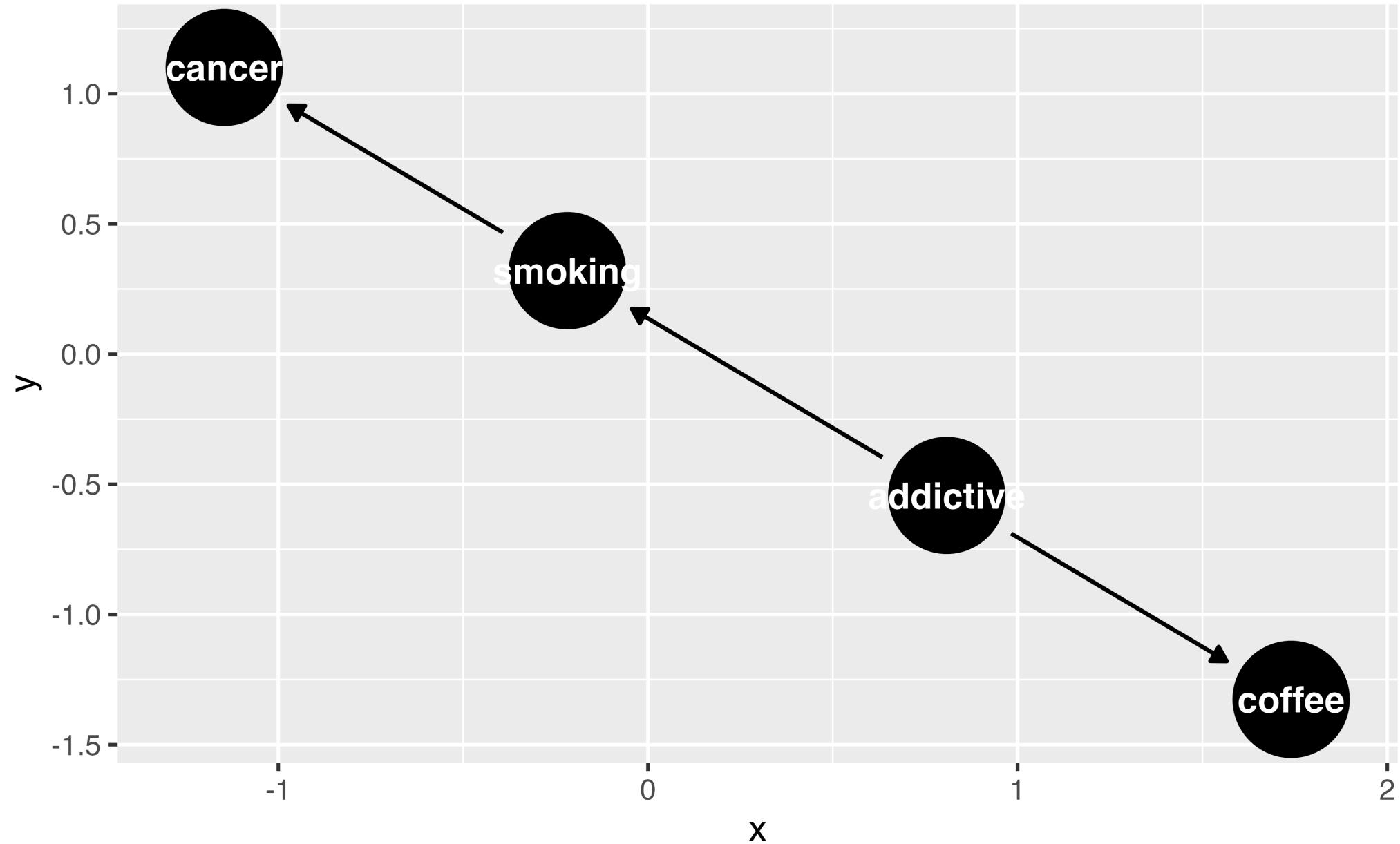
Plot the DAG using `ggdag()`

Finish early? Try the *stretch goals*

Your Turn 1 (02-dags-exercises.qmd)

```
1 coffee_cancer_dag <- dagify(  
2   cancer ~ smoking,  
3   smoking ~ addictive,  
4   coffee ~ addictive,  
5   exposure = "coffee",  
6   outcome = "cancer",  
7   labels = c(  
8     "coffee" = "Coffee",  
9     "cancer" = "Lung Cancer",  
10    "smoking" = "Smoking",  
11    "addictive" = "Addictive \nBehavior"  
12  )  
13 )
```

```
1 ggdag(coffee_cancer_dag)
```



Causal effects and backdoor paths

Ok, correlation != causation. But why not?

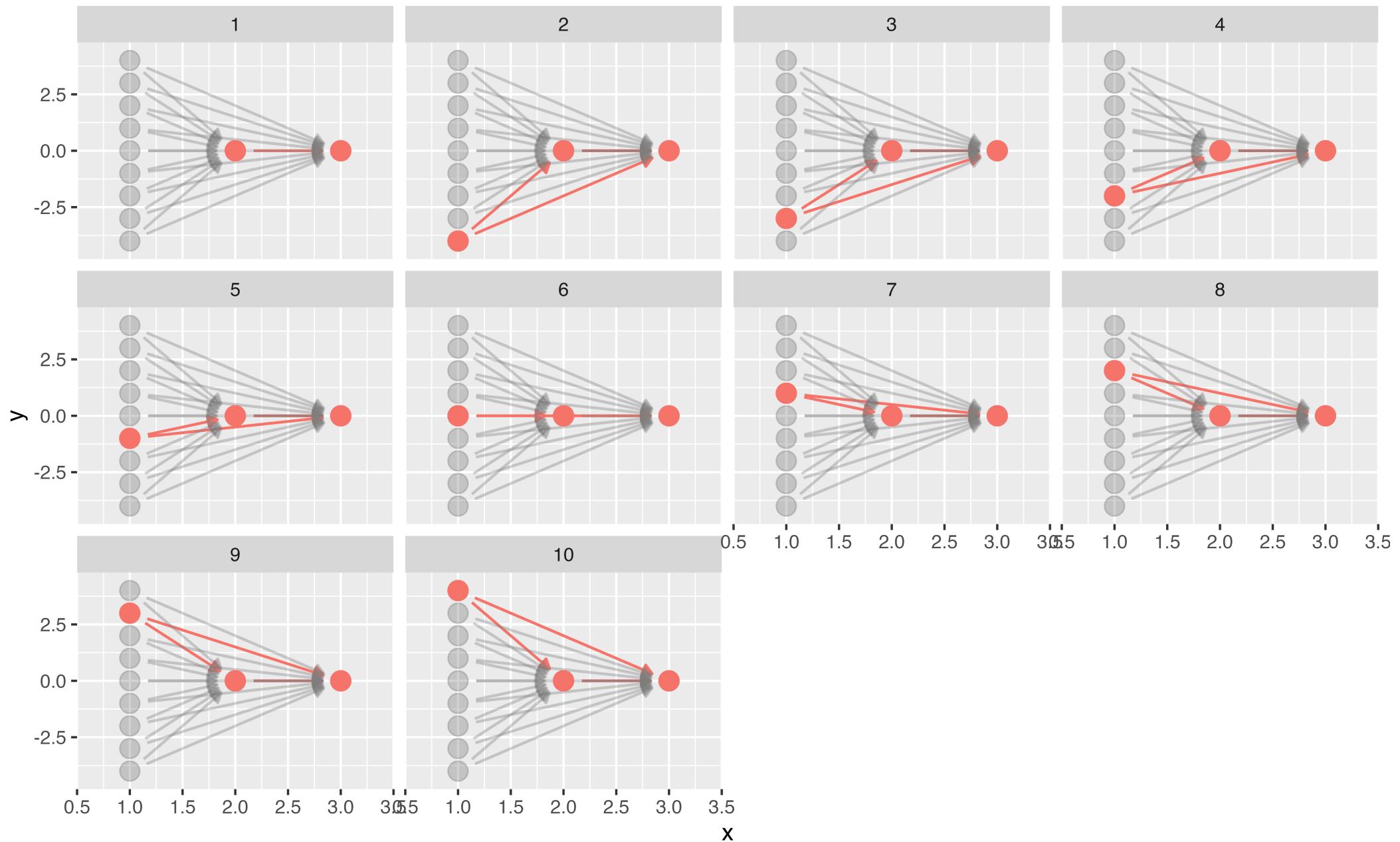
We want to know if $x \rightarrow y$...

But other paths also cause associations

ggdag_paths()

Identify “backdoor” paths

```
1 ggdag_paths(smk_wt_dag)
```



Your Turn 2

Call `tidy_dagitty()` on `coffee_cancer_dag` to create a tidy DAG, then pass the results to `dag_paths()`. What's different about these data?

Plot the open paths with `ggdag_paths()`. (Just give it `coffee_cancer_dag` rather than using `dag_paths()`; the quick plot function will do that for you.) Remember, since we assume there is *no* causal path from coffee to lung cancer, any open paths must be confounding pathways.

Finish early? Try the *stretch goals*

Your Turn 2

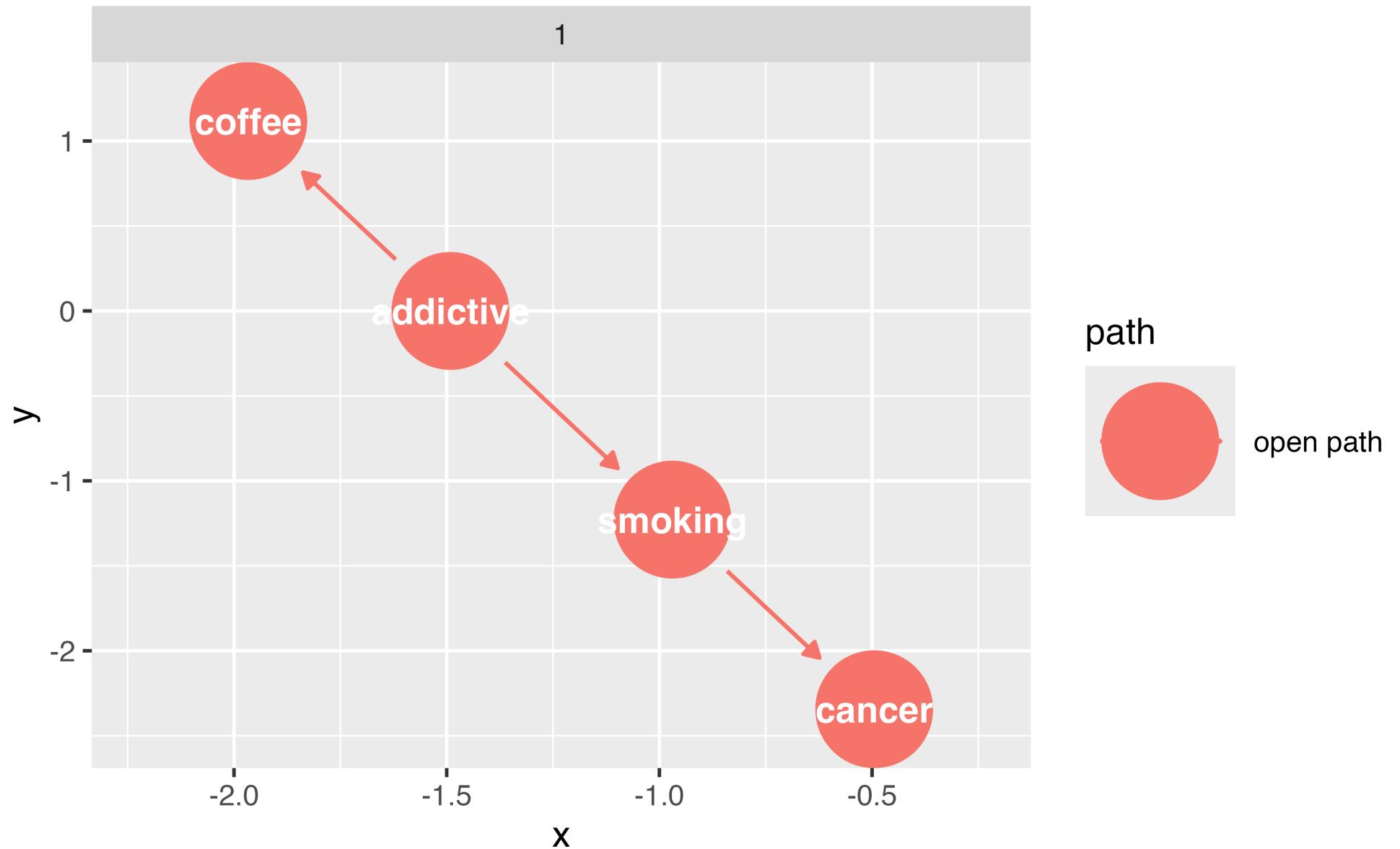
```
1 coffee_cancer_dag |>
2   tidy_dagitty() |>
3   dag_paths()
```

```

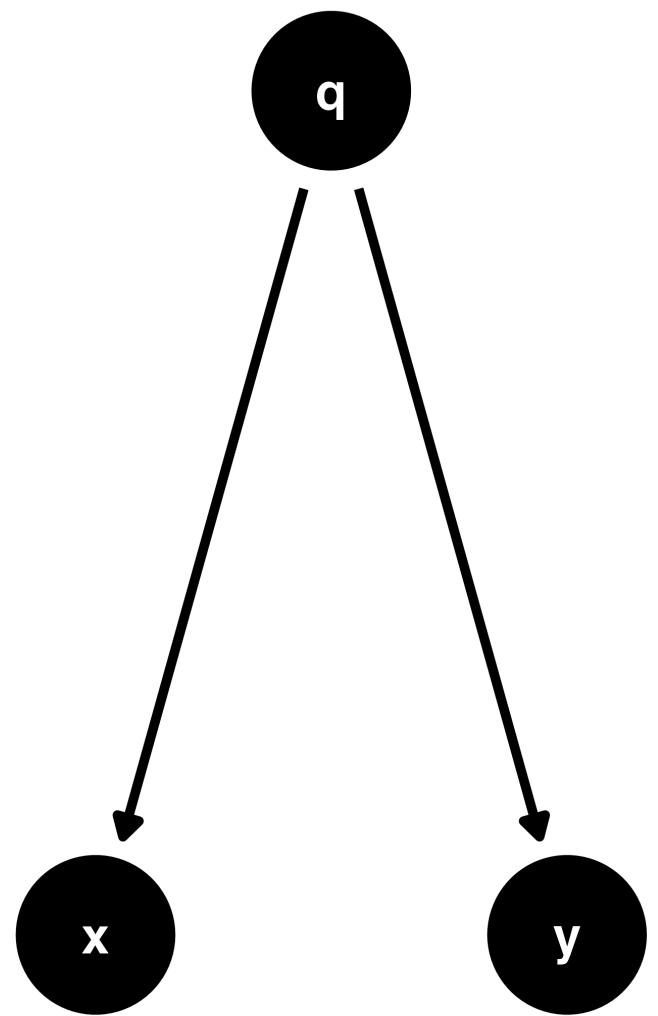
# A DAG with 4 nodes and 3 edges
#
# Exposure: coffee
# Outcome: cancer
#
# A tibble: 5 × 11
  set   name          x     y direction to      xend    yend
  <chr> <chr>     <dbl> <dbl> <fct>    <chr>    <dbl> <dbl>
1 1    addictive  -1.59  -2.26  -> coffee   -2.72  -1.83
2 1    addictive  -1.59  -2.26  -> smoki... -0.334 -2.73
3 1    cancer     0.801  -3.16  <NA>     <NA>     NA     NA
4 1    coffee     -2.72  -1.83  <NA>     <NA>     NA     NA
5 1    smoking    -0.334 -2.73  -> cancer   0.801  -3.16

```

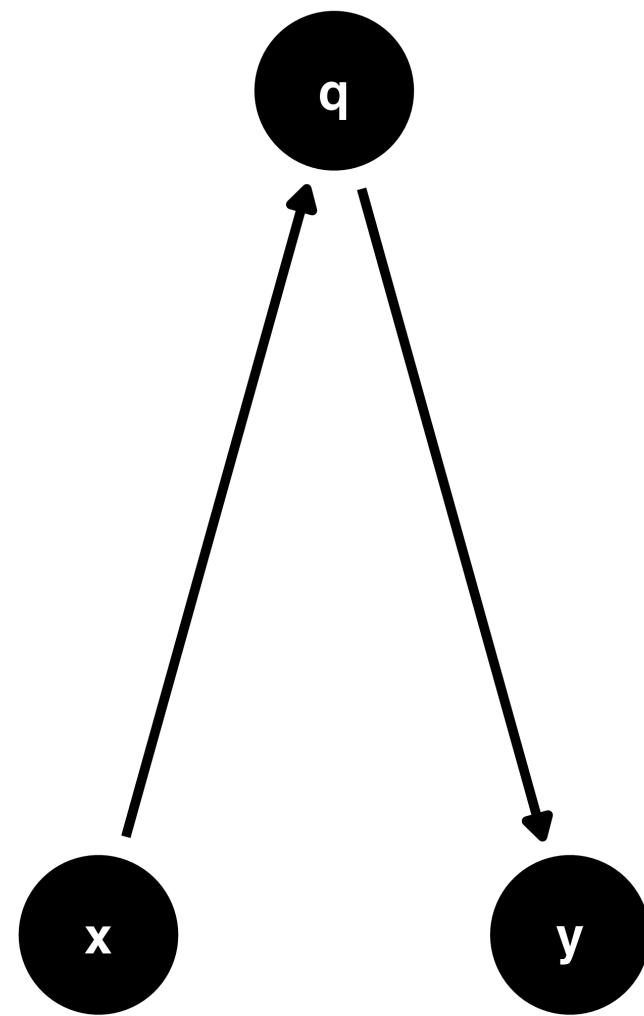
```
1 coffee_cancer_dag |>  
2 ggdag_paths()
```



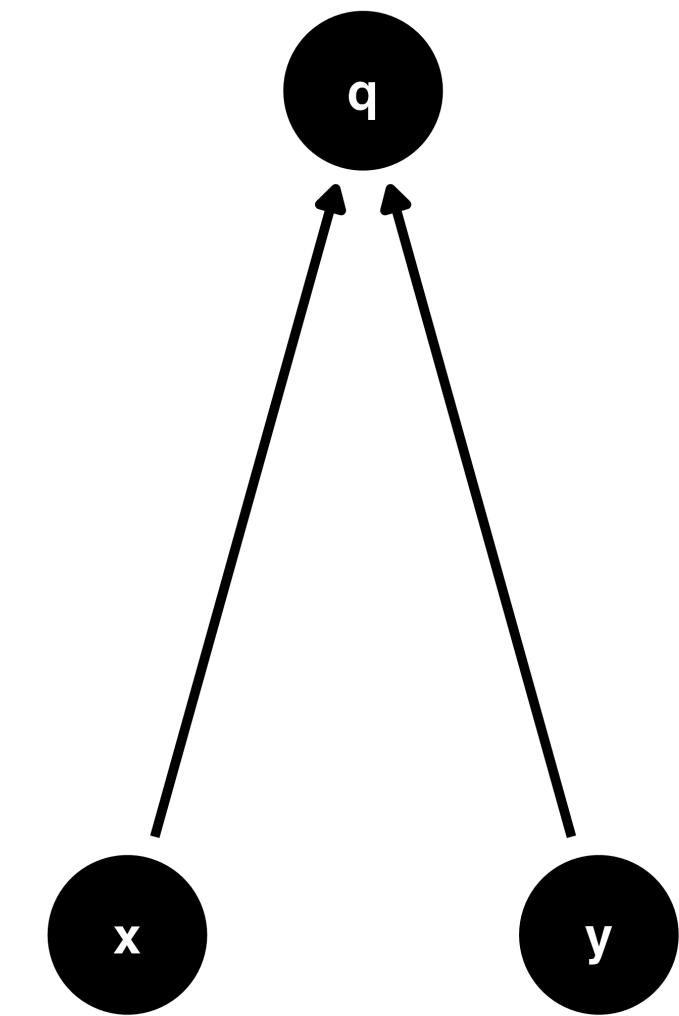
fork



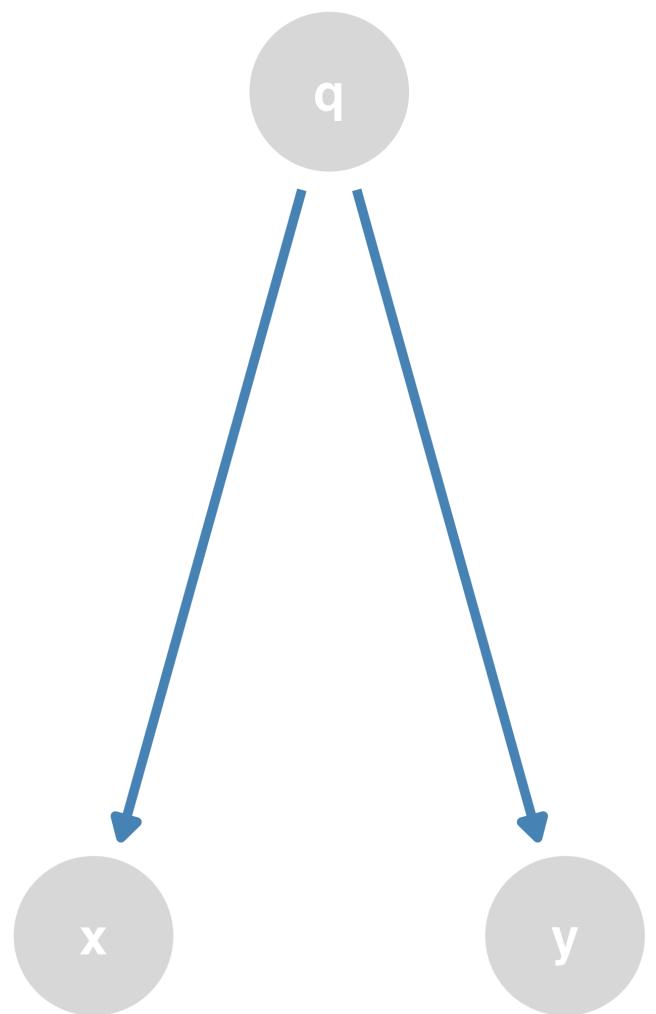
chain



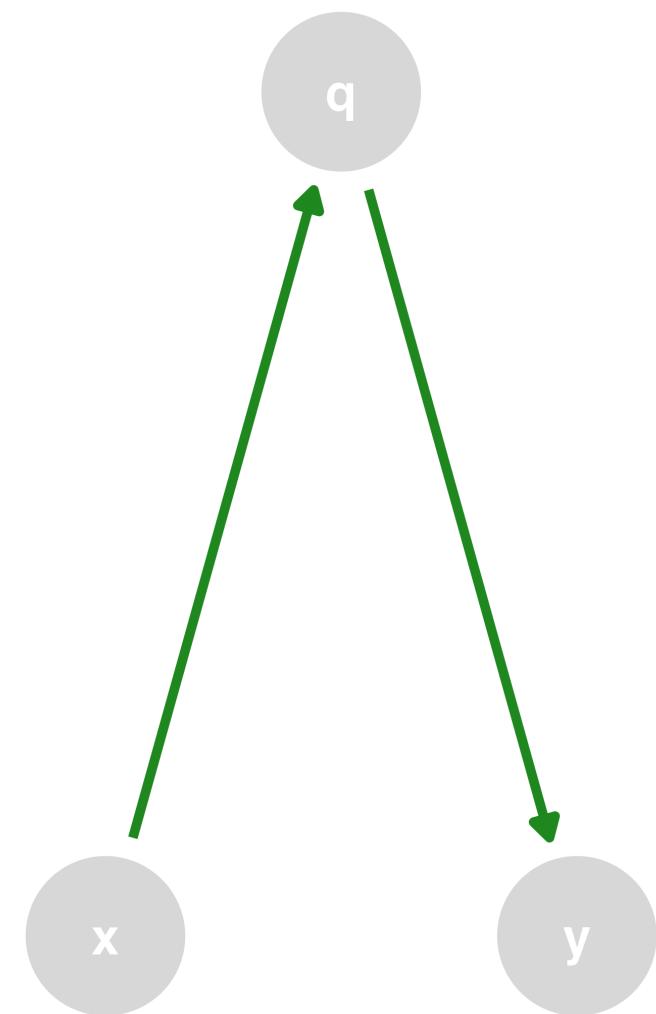
collider



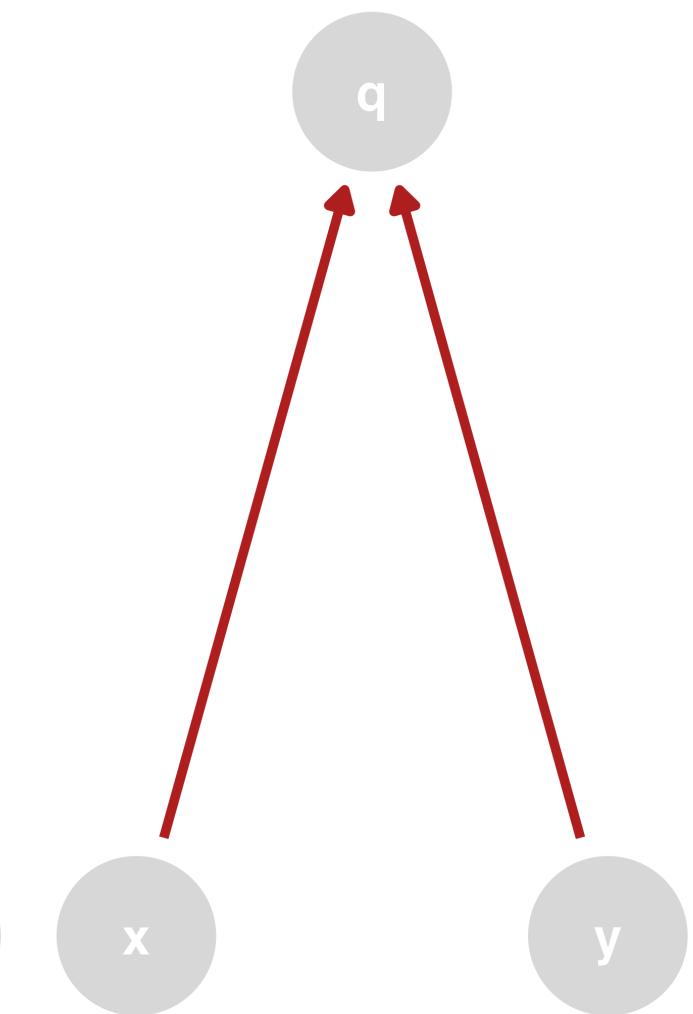
fork



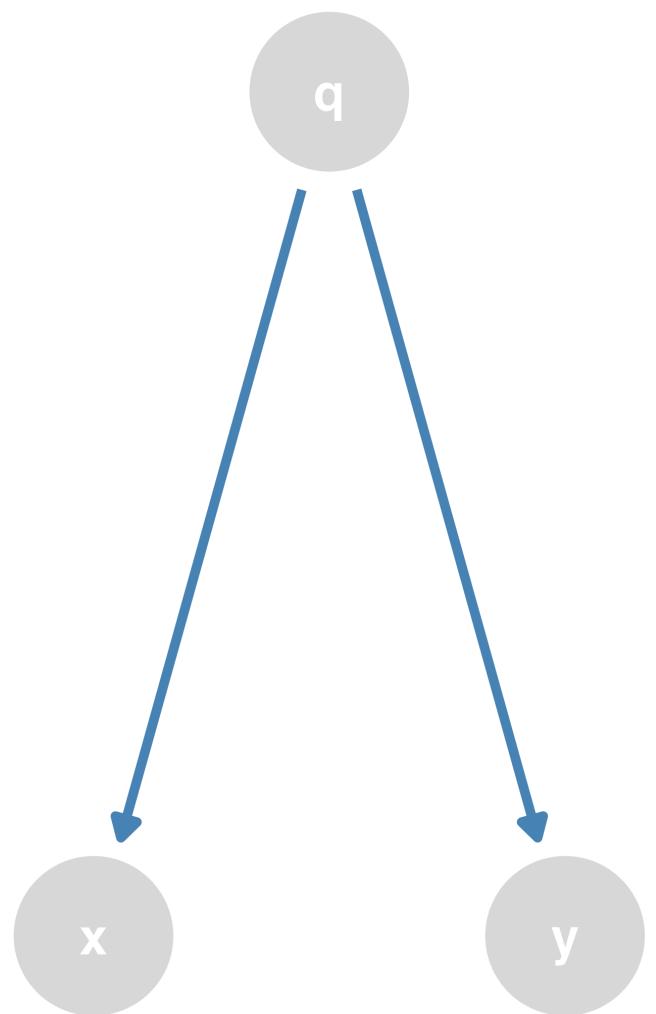
chain



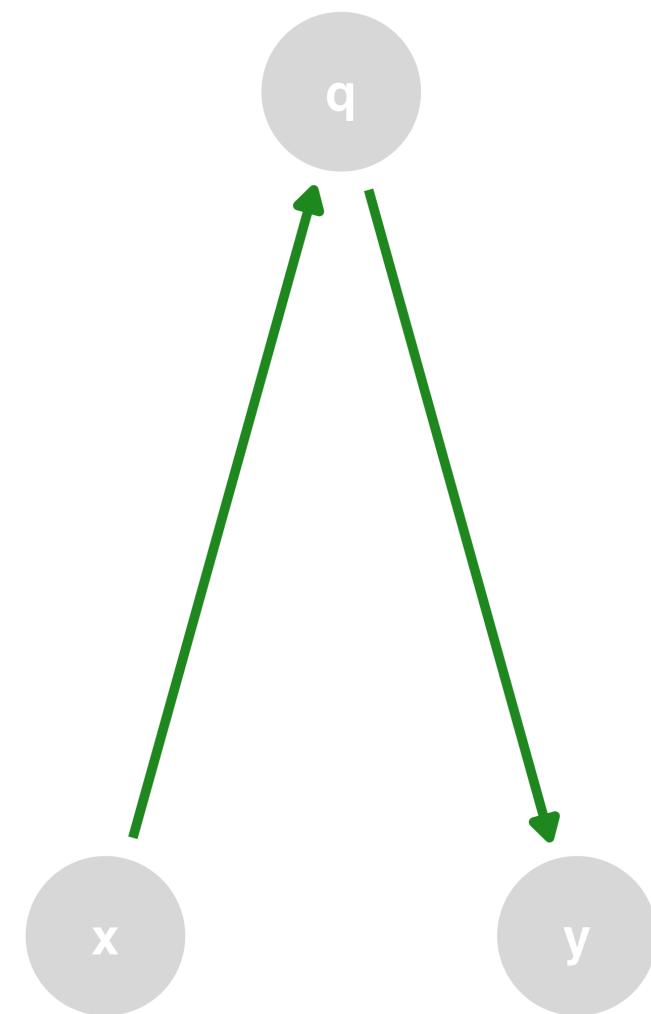
collider



fork



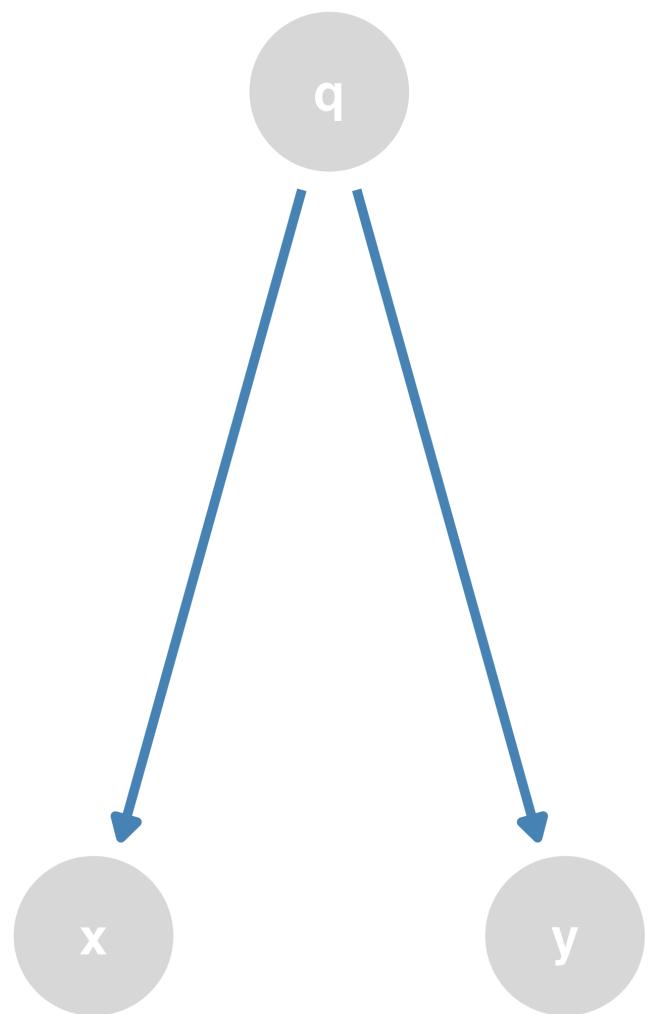
chain



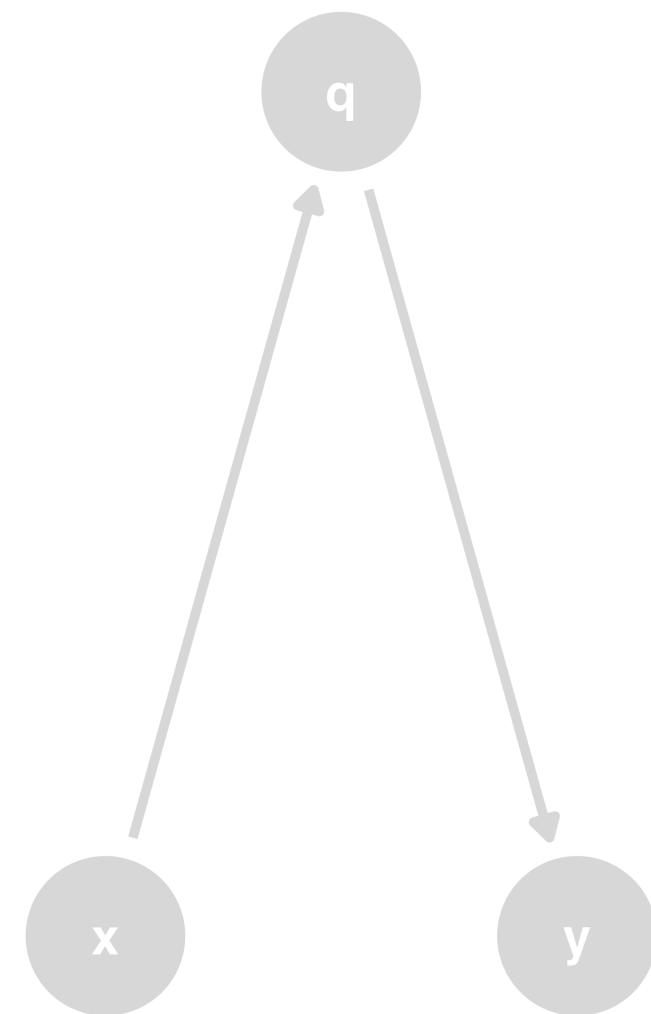
collider



fork



chain



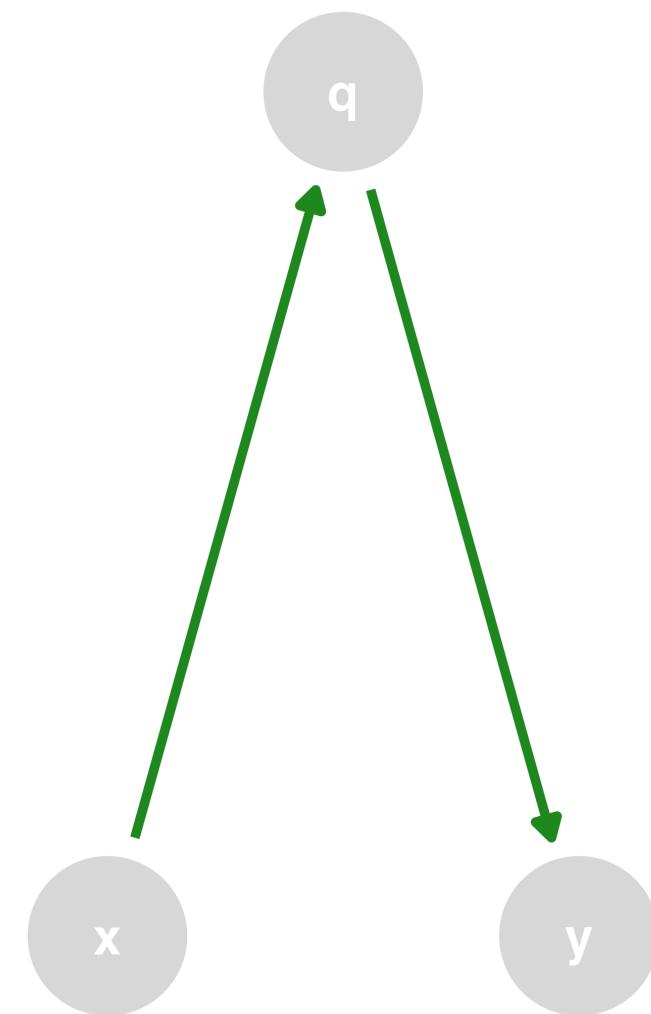
collider



fork



chain



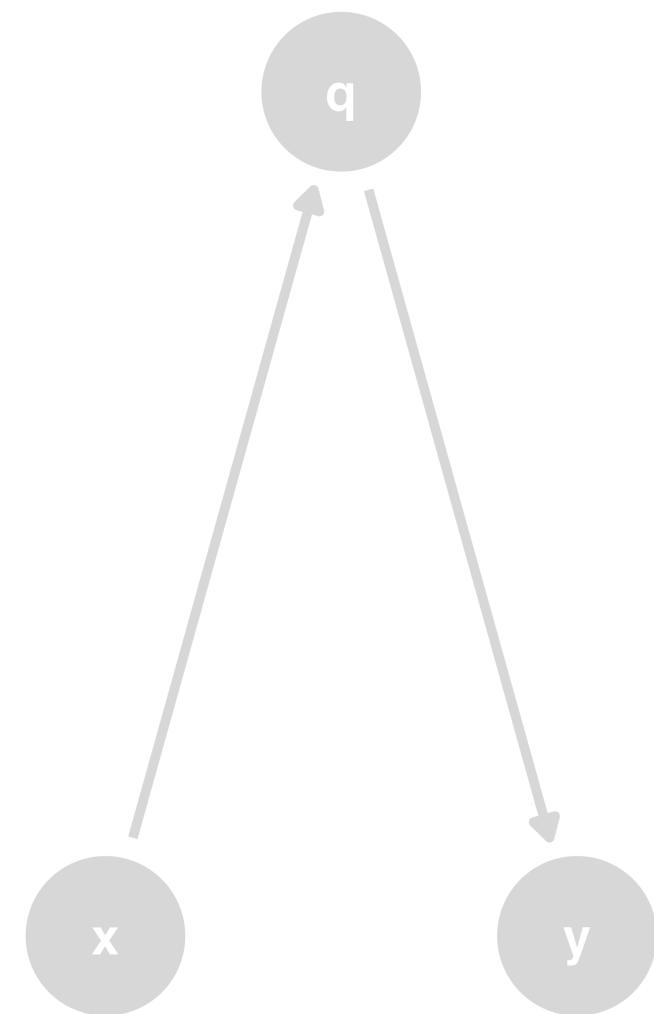
collider



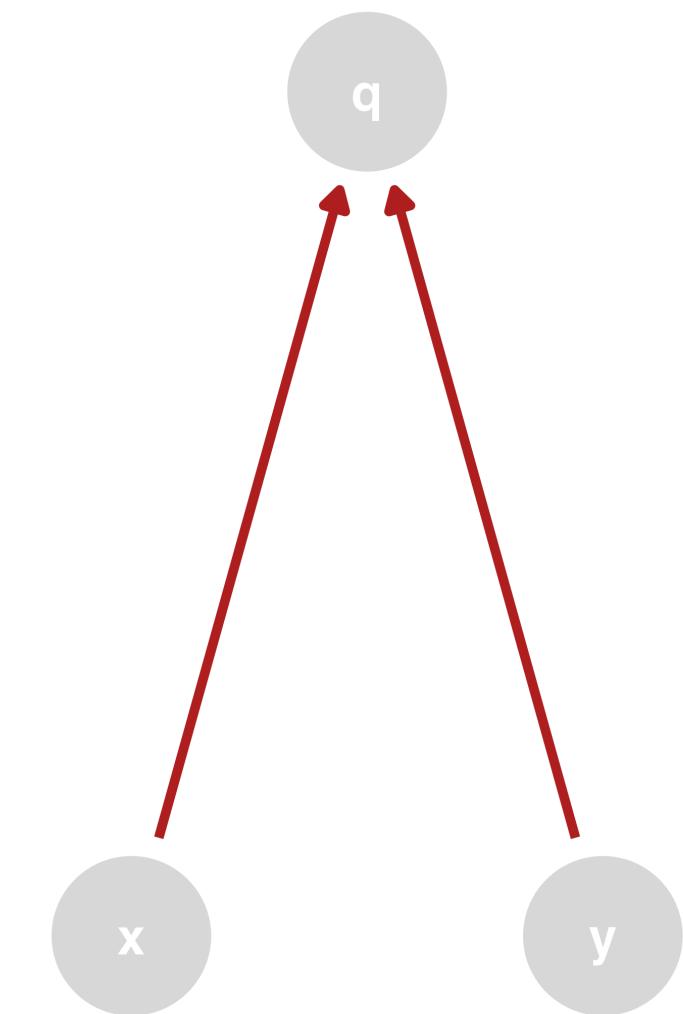
fork



chain



collider



Closing backdoor paths

We need to account for these open, non-causal paths

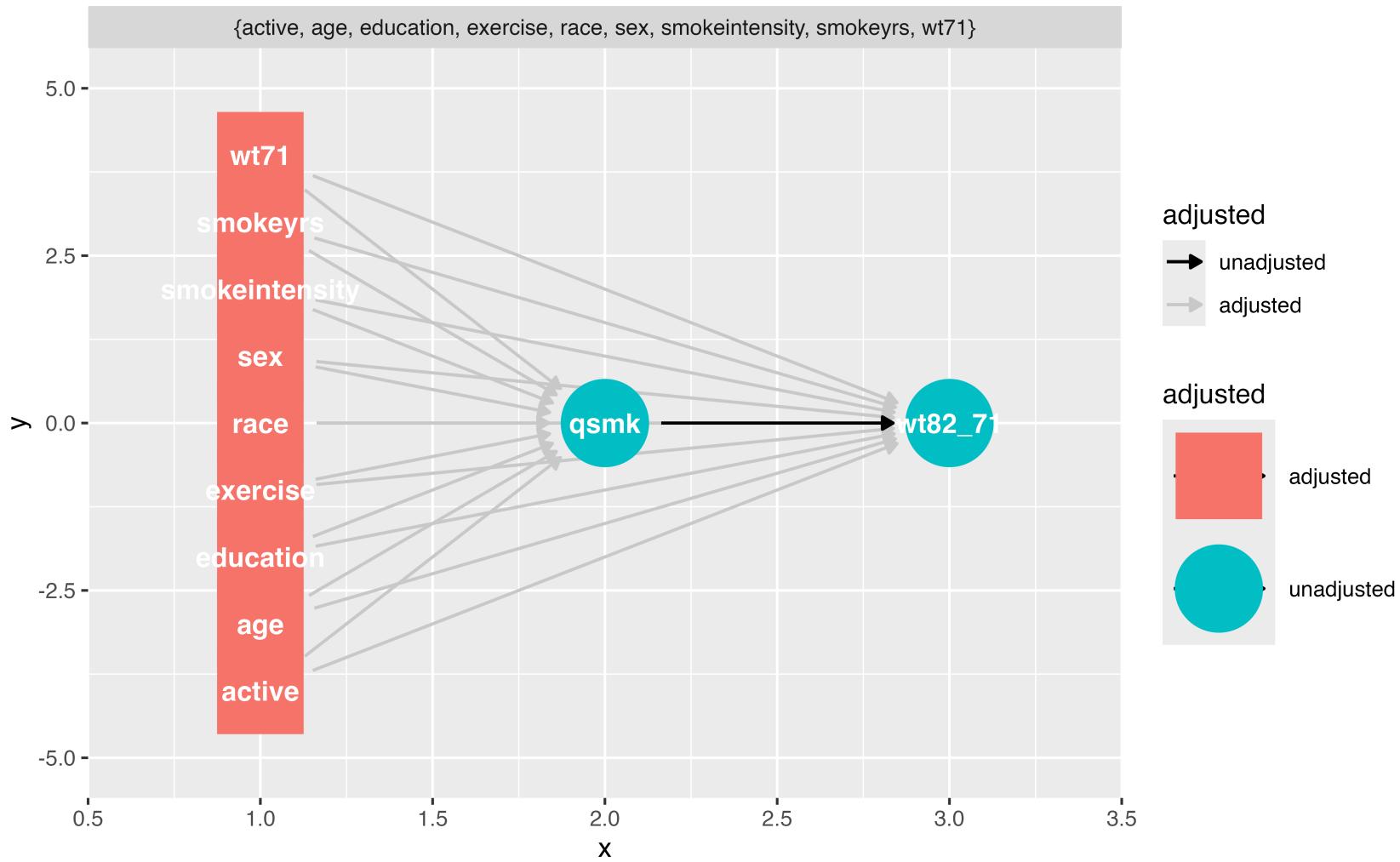
Randomization

Stratification, adjustment, weighting, matching,
etc.

Identifying adjustment sets

```
1 ggdag_adjustment_set(smk_wt_dag)
```

Identifying adjustment sets



Identifying adjustment sets

```
1 library(dagitty)  
2 adjustmentSets(smk_wt_dag)
```

```
{ active, age, education, exercise, race, sex, smokeintensity,  
smokeyrs, wt71 }
```

Your Turn 3

Now that we know the open, confounding pathways (sometimes called “backdoor paths”), we need to know how to close them! First, we’ll ask `{ggdag}` for adjustment sets, then we would need to do something in our analysis to account for at least one adjustment set (e.g. multivariable regression, weighting, or matching for the adjustment sets).

Use `ggdag_adjustment_set()` to visualize the adjustment sets. Add the arguments `use_labels = "label"` and `text = FALSE`.

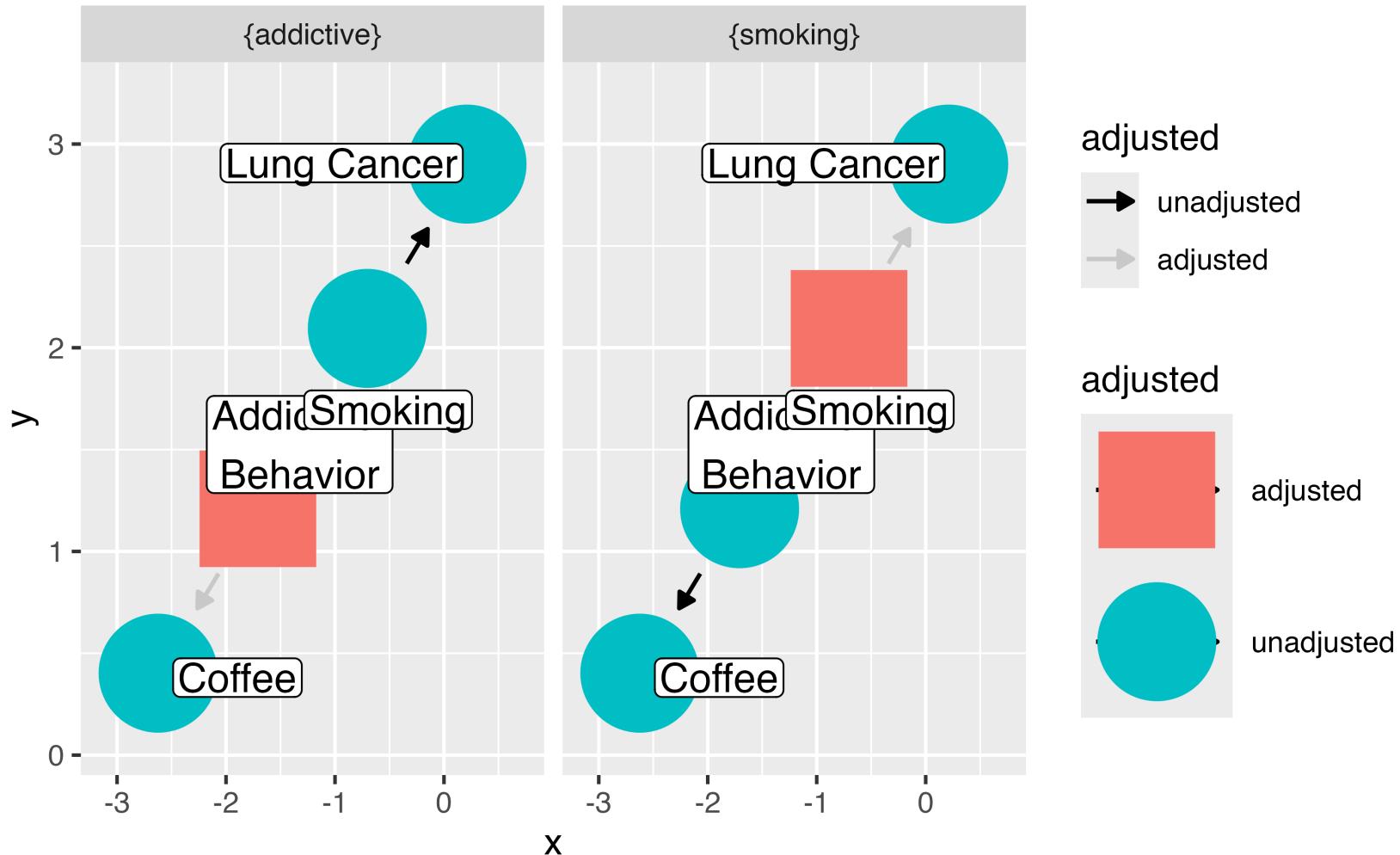
Write an R formula for each adjustment set, as you might if you were fitting a model in `lm()` or `glm()`

Finish early? Try the *stretch goals*

Your Turn 3

```
1 ggdag_adjustment_set(  
2   coffee_cancer_dag,  
3   use_labels = "label",  
4   text = FALSE  
5 )
```

Your Turn 3



Your Turn 3

- 1 cancer ~ coffee + addictive
- 2 cancer ~ coffee + smoking

Let's prove it!

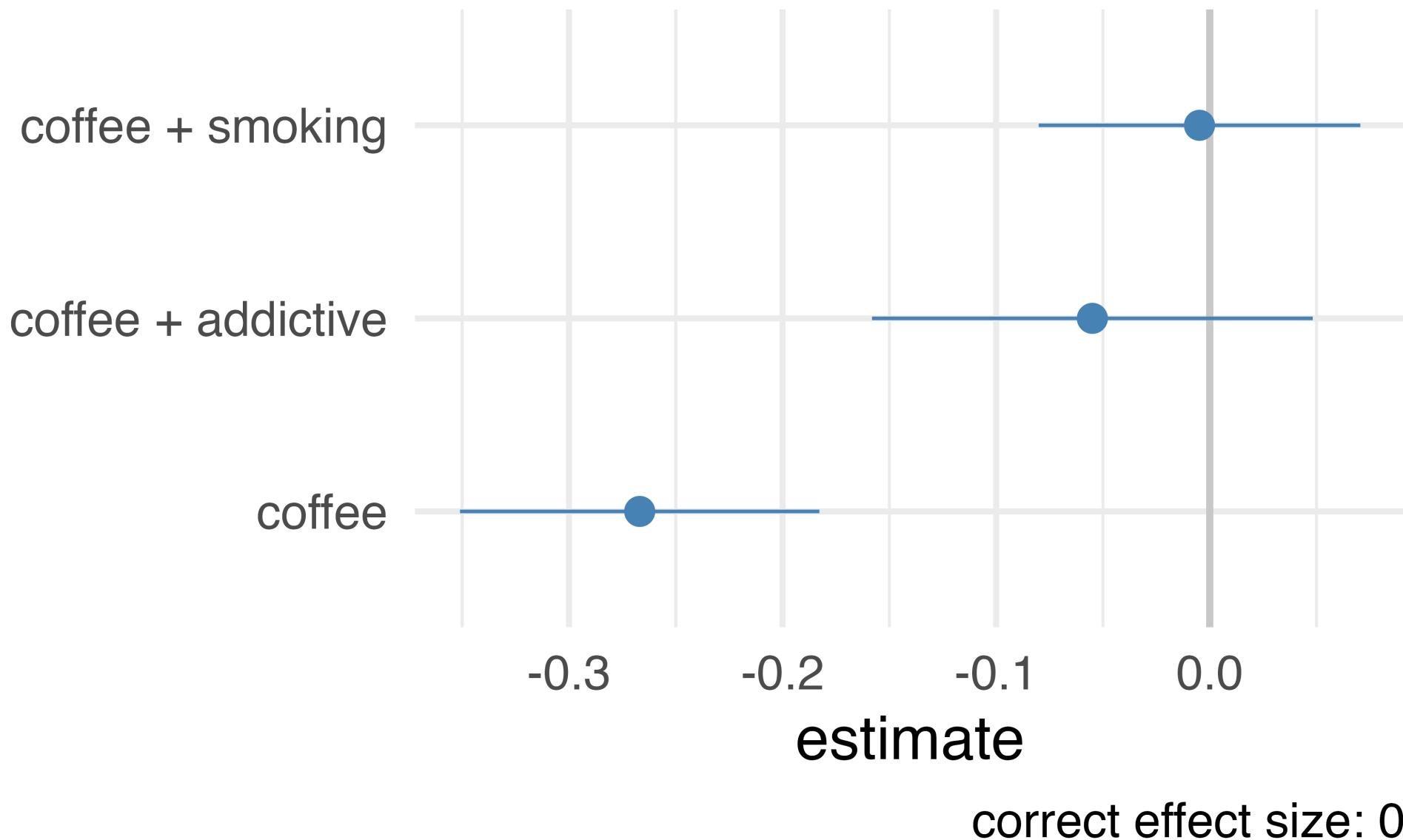
```
1 set.seed(1234)
2 dag_data <- coffee_cancer_dag |>
3   simulate_data(-.6)
```

Let's prove it!

```
1 dag_data
```

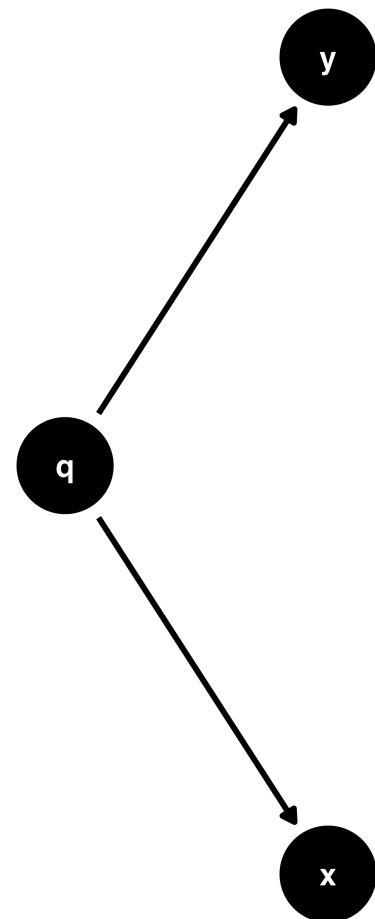
```
# A tibble: 500 × 4
  addictive cancer coffee smoking
  <dbl>     <dbl>    <dbl>    <dbl>
1 0.0708    2.87   -0.565   -1.79
2 0.626     1.63    0.434   -1.35
3 1.98      1.43   -0.182   -1.62
4 -0.198    -0.223   0.133    0.960
5 1.66      0.0696   0.437    0.0954
6 1.37      0.765   -2.18    -1.41
7 0.791     0.0460   -0.745   -0.876
8 0.531     0.813   -1.44    -0.432
9 -0.861    0.708    0.415    0.220
10 -1.40     0.801    0.439    0.472
# ... with 490 more rows
```

Let's prove it!

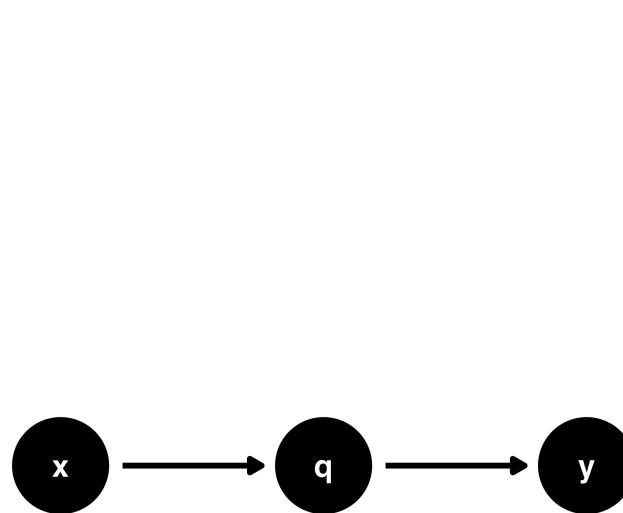


Time-ordering

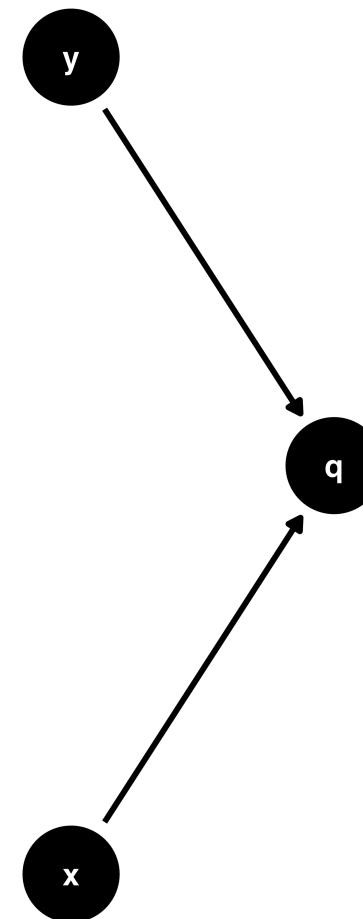
fork



chain



collider



don't adjust for the future!

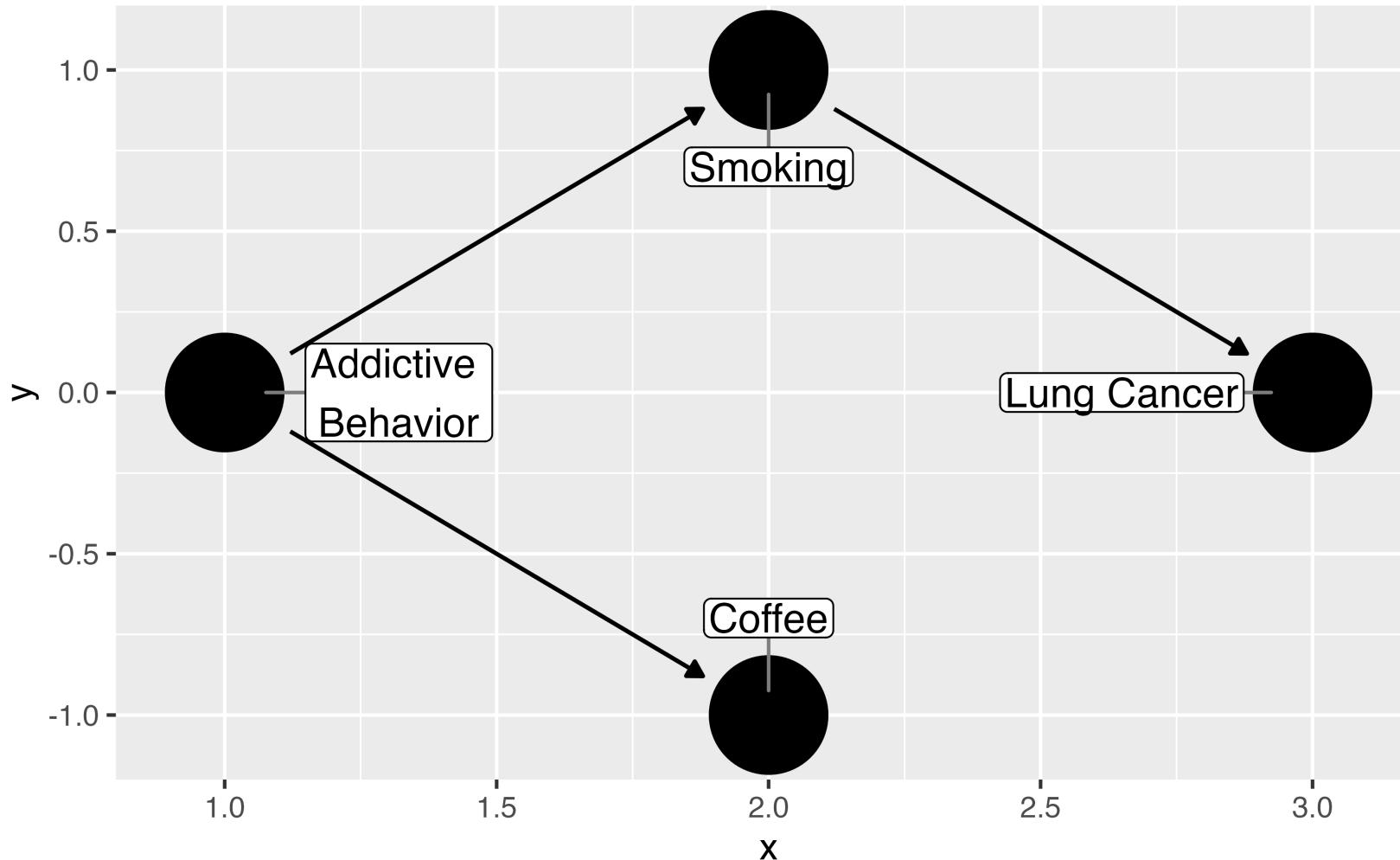
Your Turn 4

Recreate the DAG we've been working with using `time_ordered_coords()`, then visualize the DAG. You don't need to use any arguments for this function, so `coords = time_ordered_coords()` will do.

Your Turn 4

```
1 coffee_cancer_dag_to <- dagify(  
2   cancer ~ smoking,  
3   smoking ~ addictive,  
4   coffee ~ addictive,  
5   exposure = "coffee",  
6   outcome = "cancer",  
7   coords = time_ordered_coords(),  
8   labels = c(  
9     "coffee" = "Coffee",  
10    "cancer" = "Lung Cancer",  
11    "smoking" = "Smoking",  
12    "addictive" = "Addictive \nBehavior"  
13  )  
14 )  
15  
16 ggdag(coffee_cancer_dag_to, use_labels = "label", text = FALSE)
```

Your Turn 4



Choosing what variables to include

Adjustment sets and domain knowledge

Conduct sensitivity analysis if you don't have something important

Common trip ups

Using prediction metrics

The 10% rule

Predictors of the outcome, predictors of the exposure

Forgetting to consider time-ordering (something has to happen before something else to cause it!)

Selection bias and colliders (more later!)

Incorrect functional form for confounders (e.g. BMI often non-linear)

Resources: ggdag vignettes

An Introduction to ggdag

An Introduction to Directed Acyclic Graphs

Common Structures of Bias