

# 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



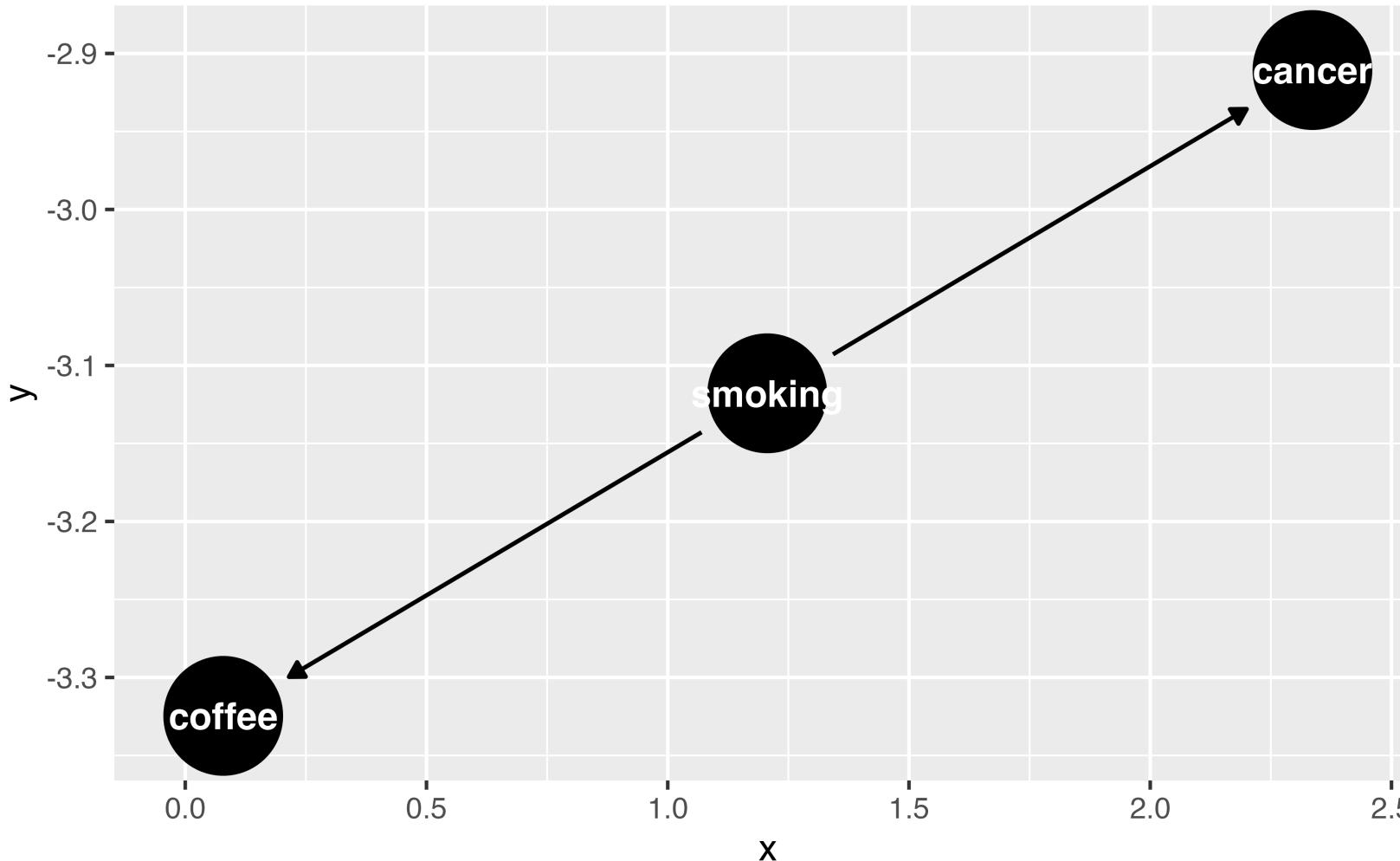
# Step 1: Specify your DAG

```
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()
```

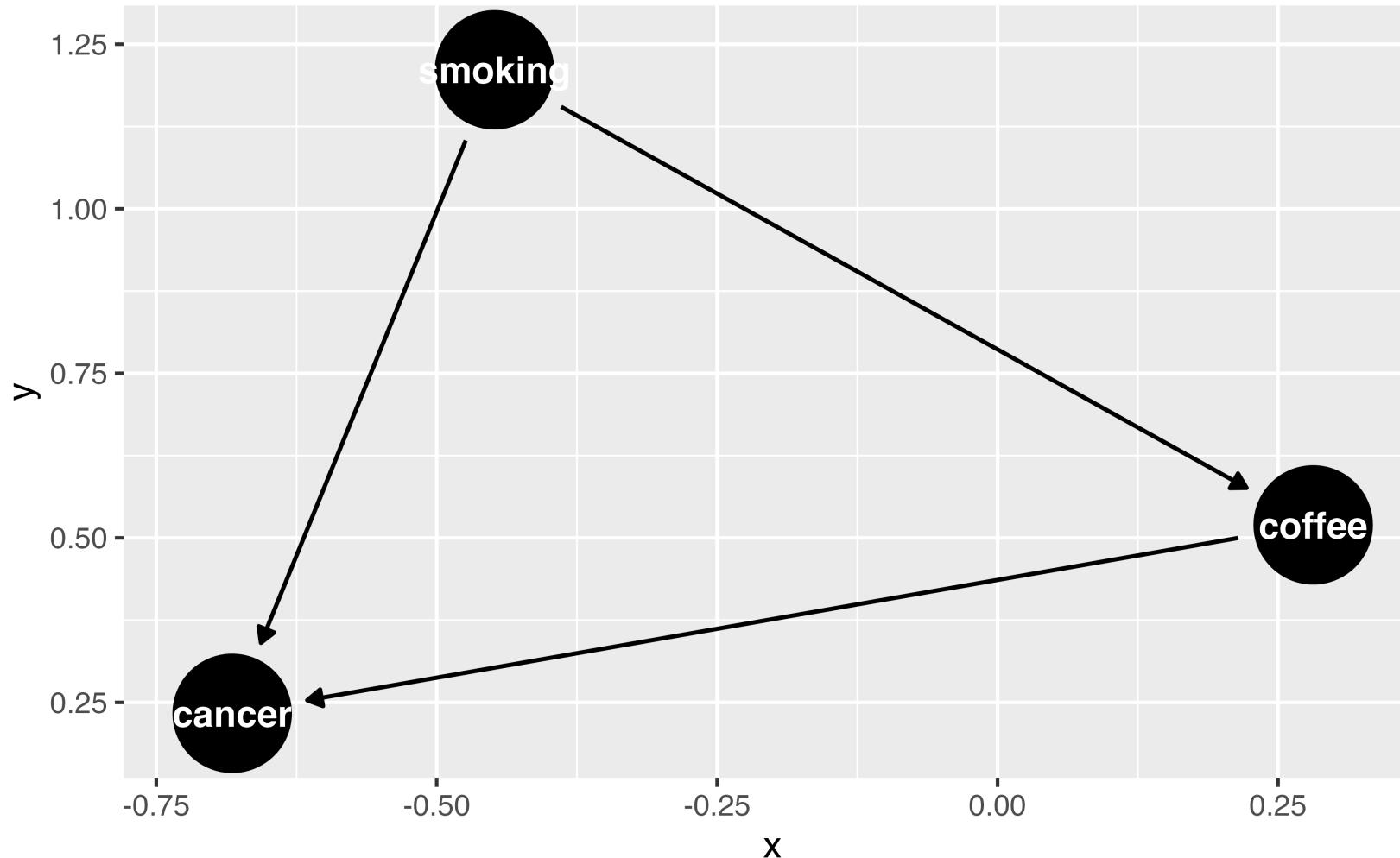
# Step 1: Specify your DAG



# 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.

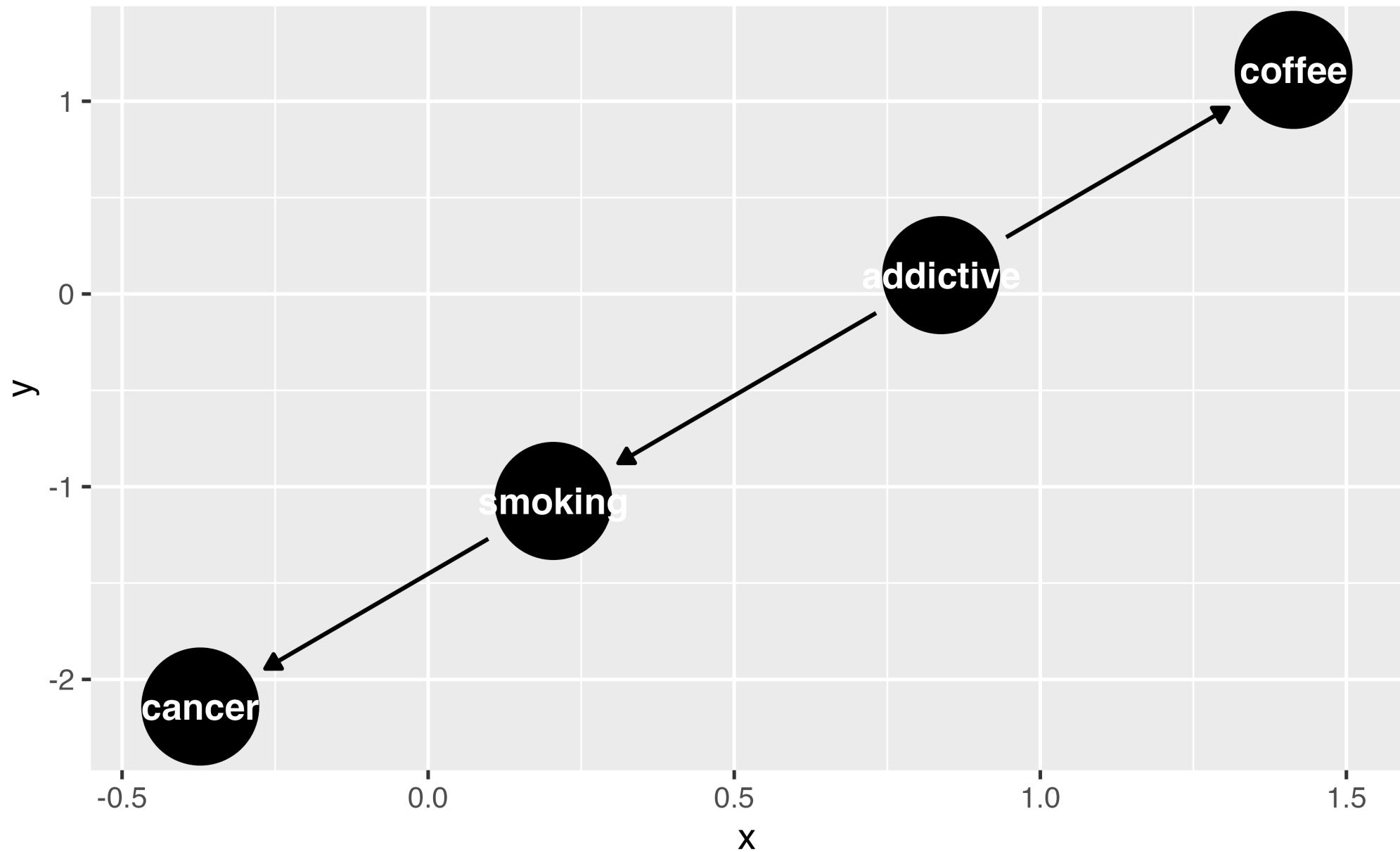
Specify "coffee" as the exposure and "cancer" as the outcome (both in quotations marks).

Plot the DAG using `ggdag()`

# 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?

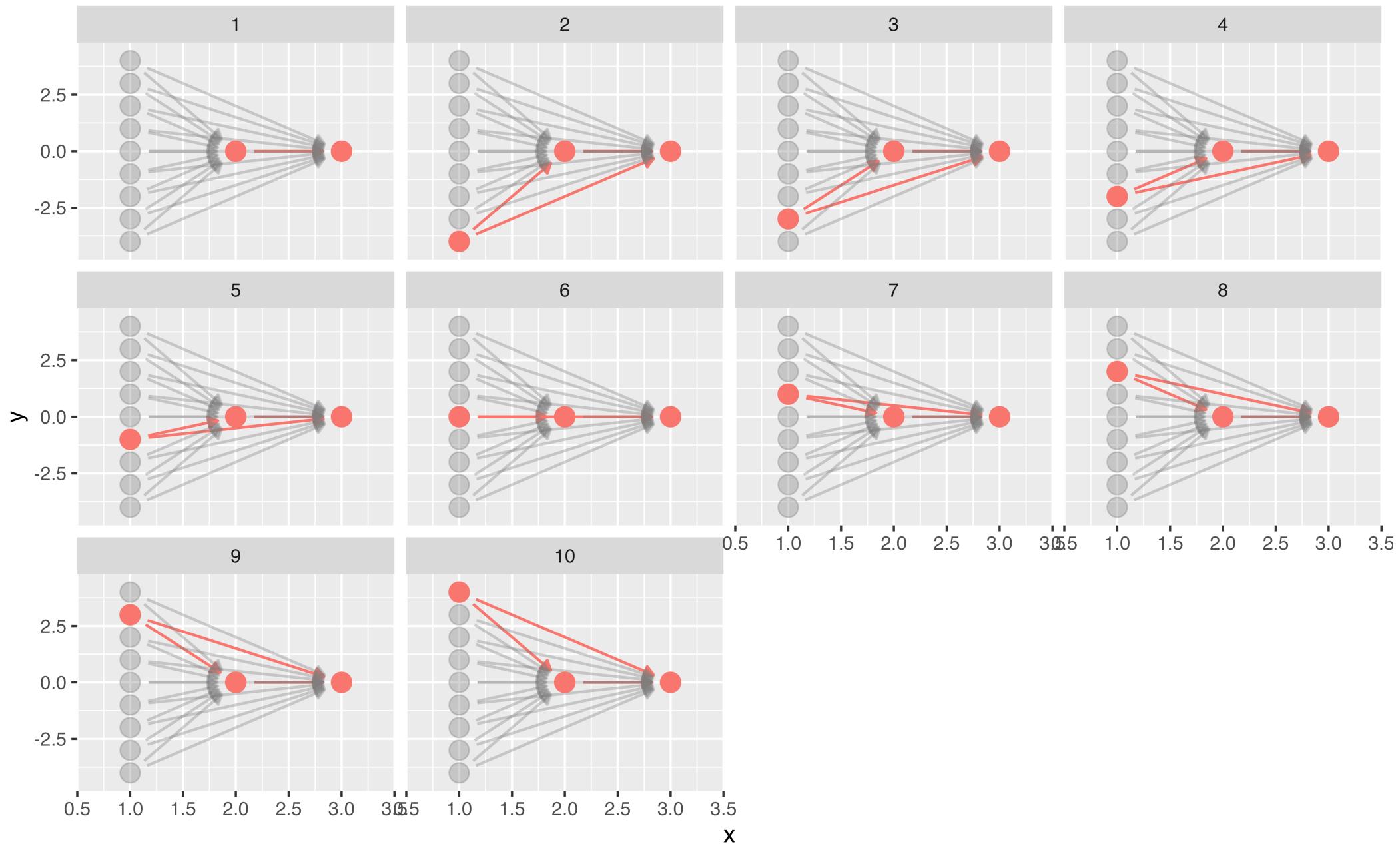
We want to know if  $x \rightarrow y$ ...

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?

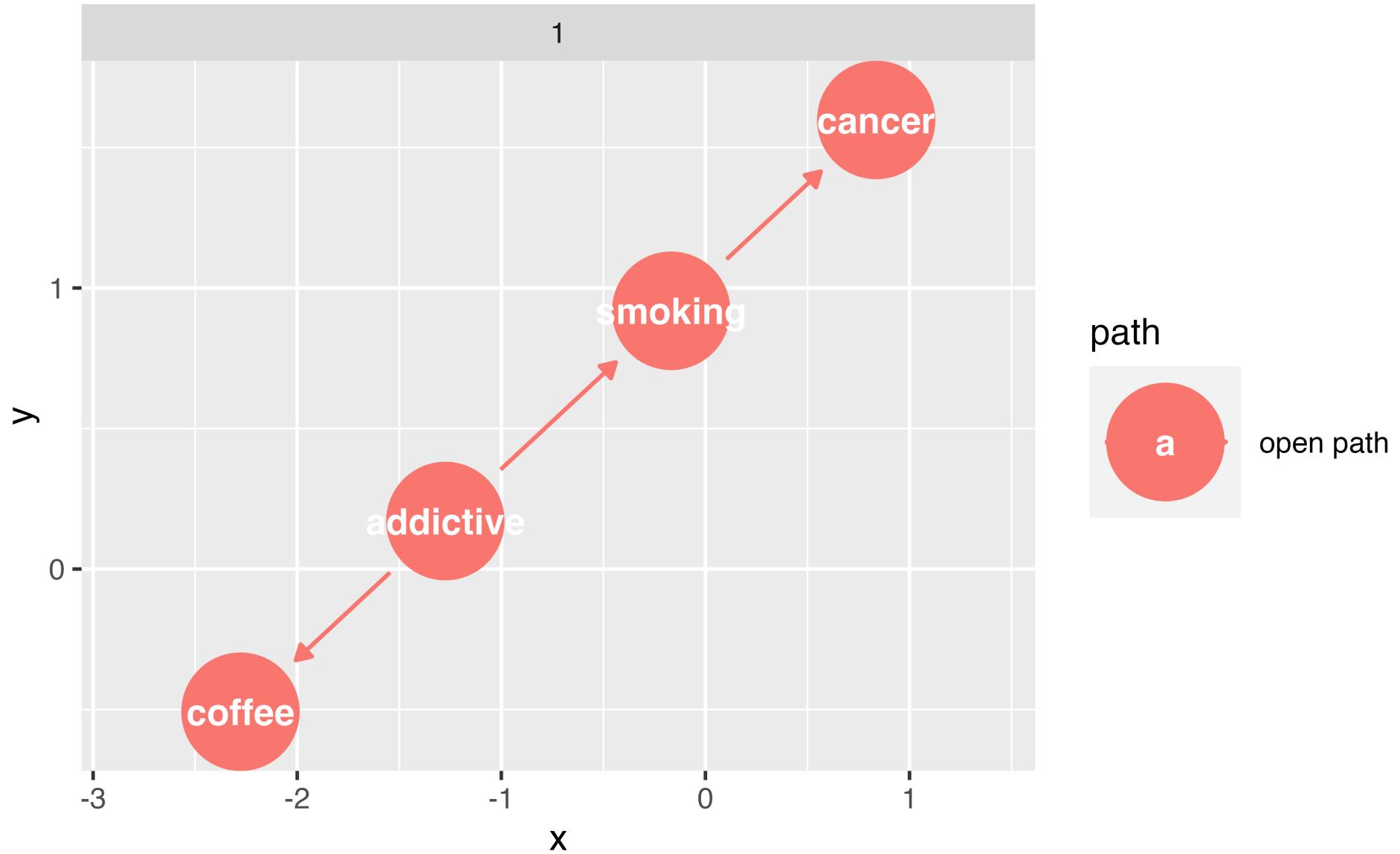
Plot the open paths with `ggdag_paths()`. (Just give it `coffee_cancer_dag` rather than using `dag_paths()`; the quick plot function will do that for you.) Remember, since we assume there is *no* causal path from coffee to lung cancer, any open paths must be confounding pathways.

# Your Turn 2

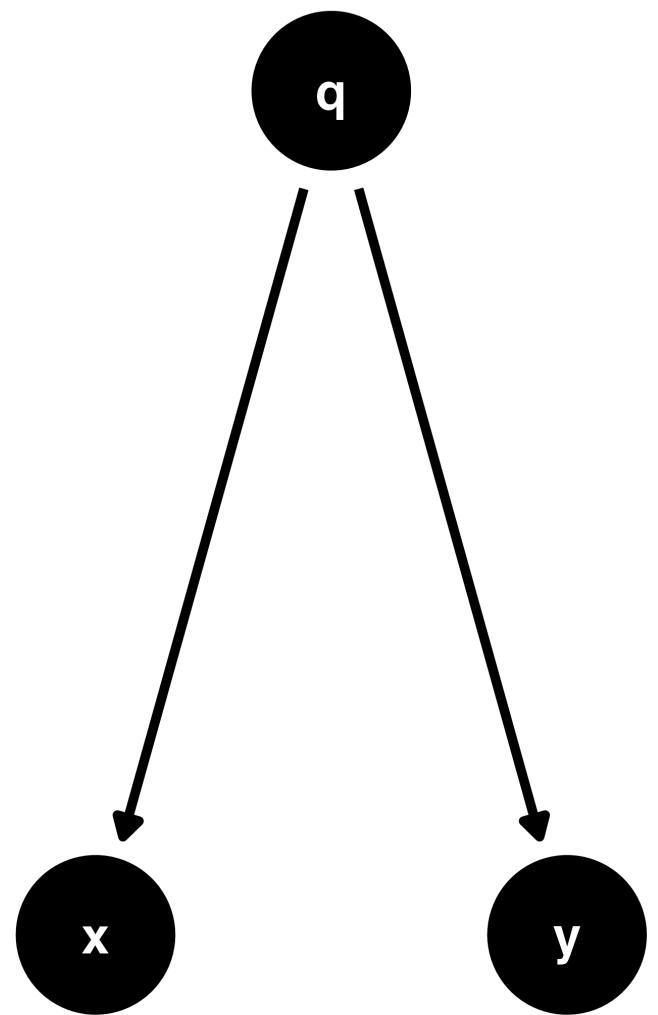
```
1 coffee_cancer_dag |>
2   tidy_dagitty() |>
3   dag_paths()

# 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  0.616 -1.27  ->    coff...  0.185 -0.127
2 1     addictive  0.616 -1.27  ->    smok...  1.09   -2.52 
3 1     cancer     1.52   -3.66  <NA>     <NA>     NA     NA  
4 1     coffee     0.185 -0.127 <NA>     <NA>     NA     NA  
5 1     smoking    1.09   -2.52  ->    canc...  1.52   -3.66 
" . "  .     .     .     .     .     .     .     .     .
```

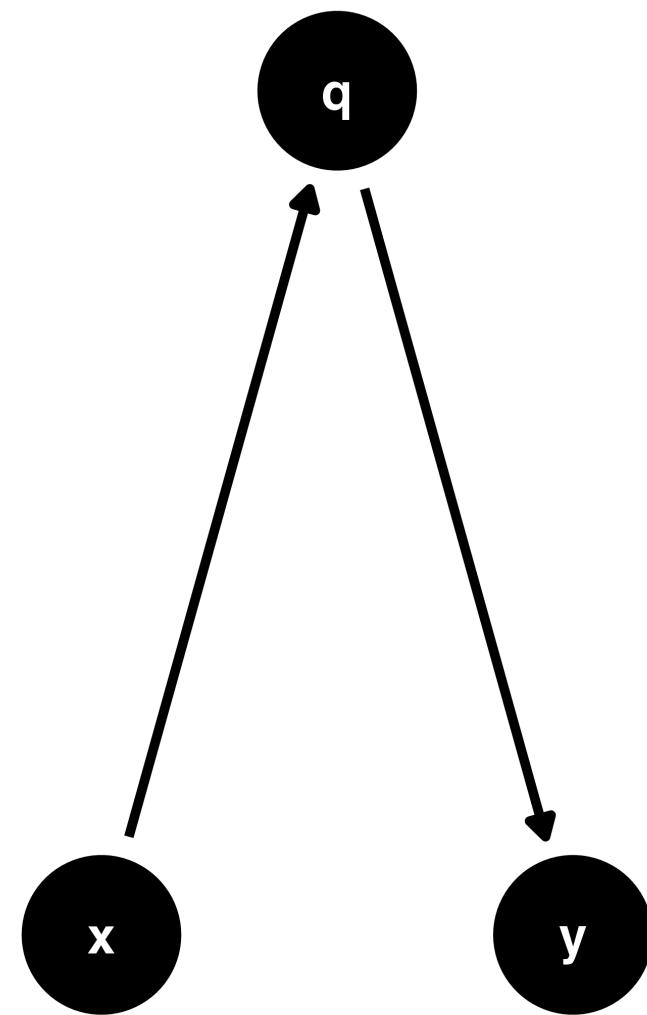
```
1 coffee_cancer_dag |>  
2 ggdag_paths()
```



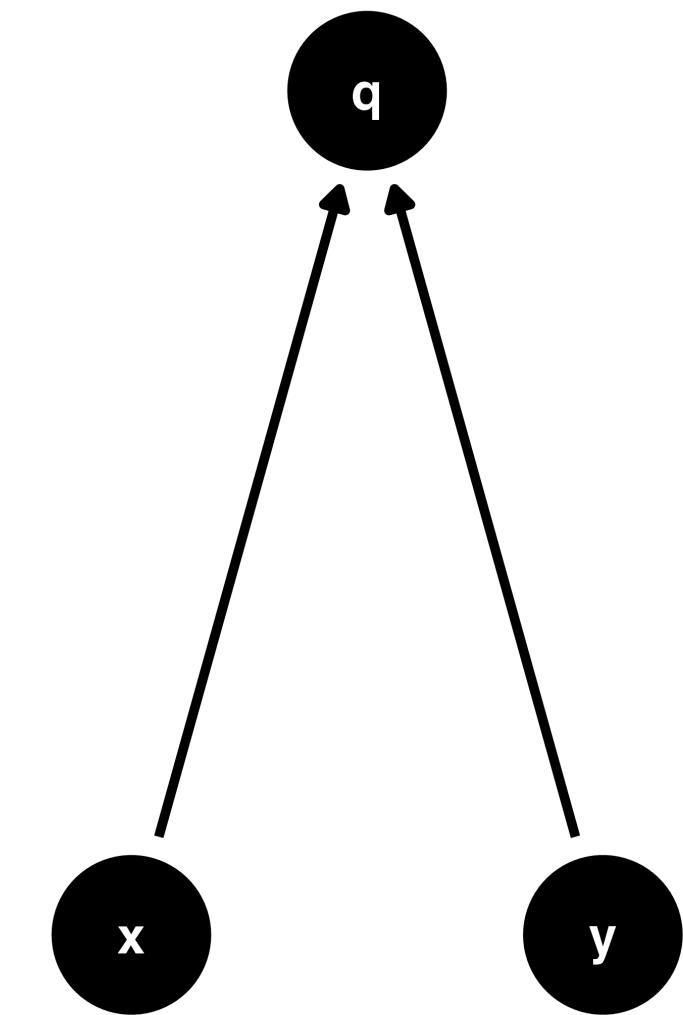
**fork**



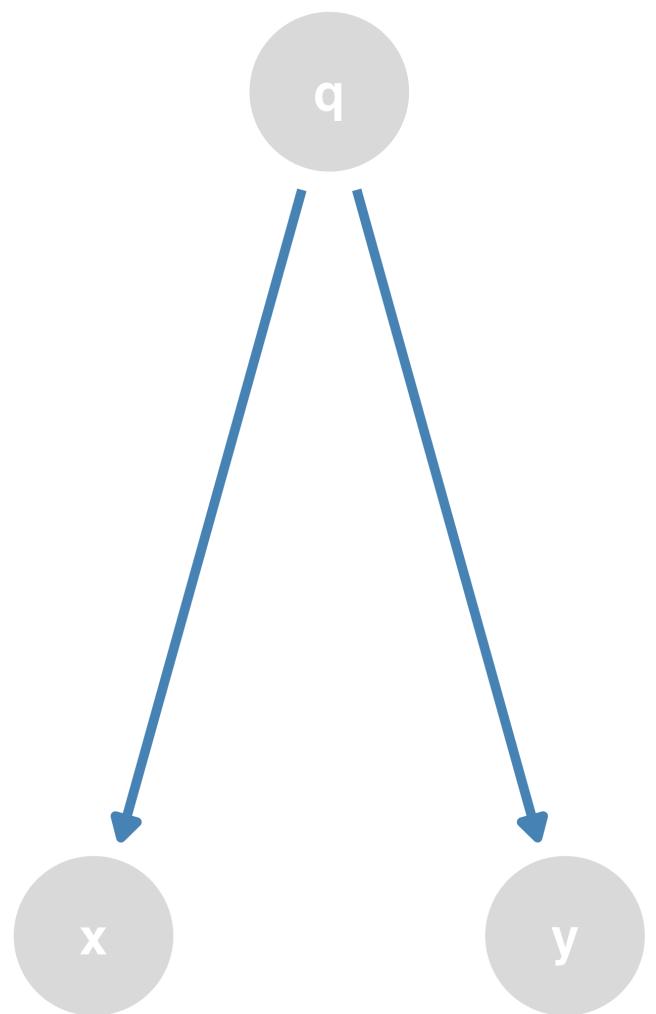
**chain**



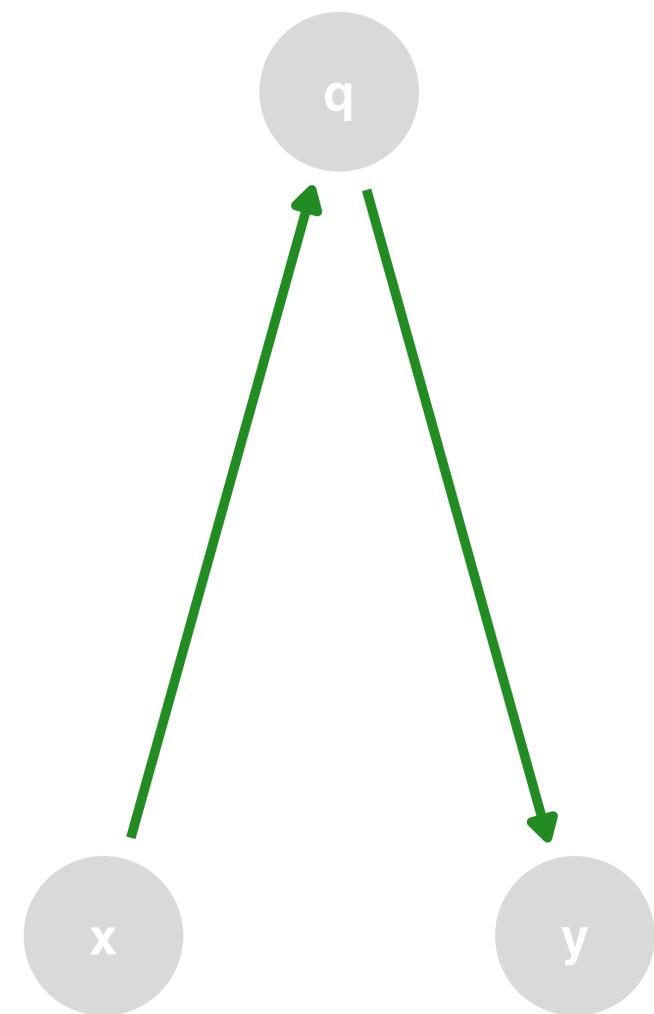
**collider**



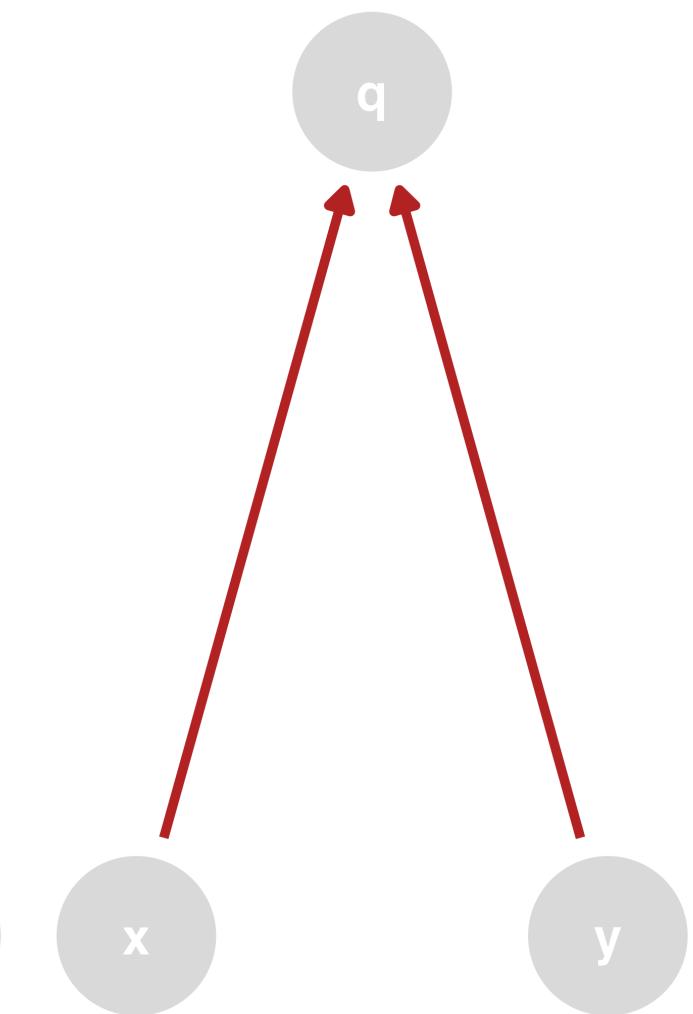
**fork**



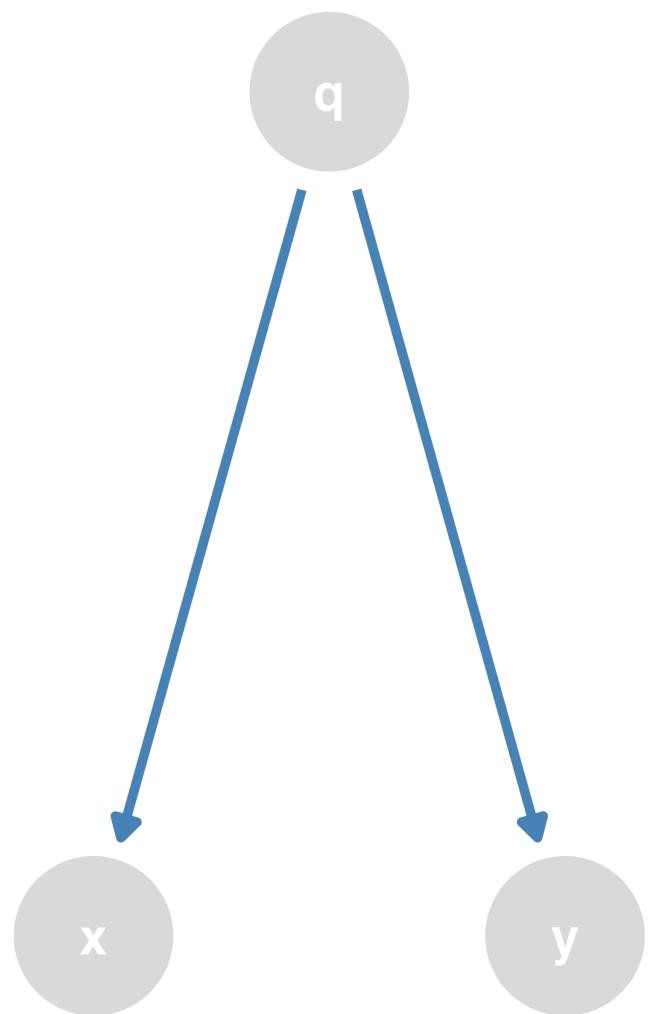
**chain**



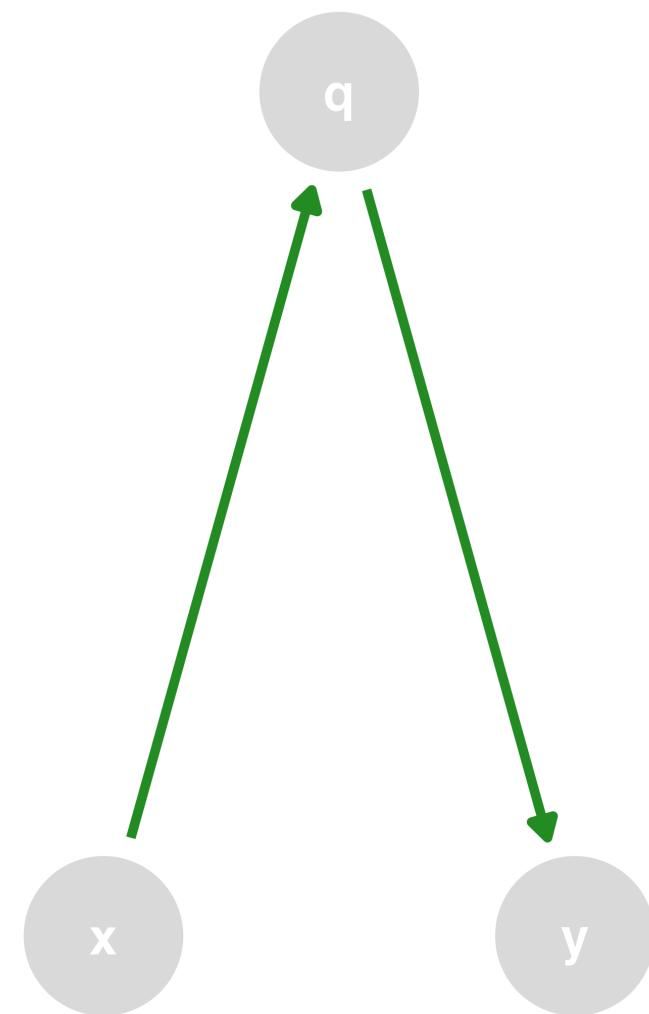
**collider**



**fork**



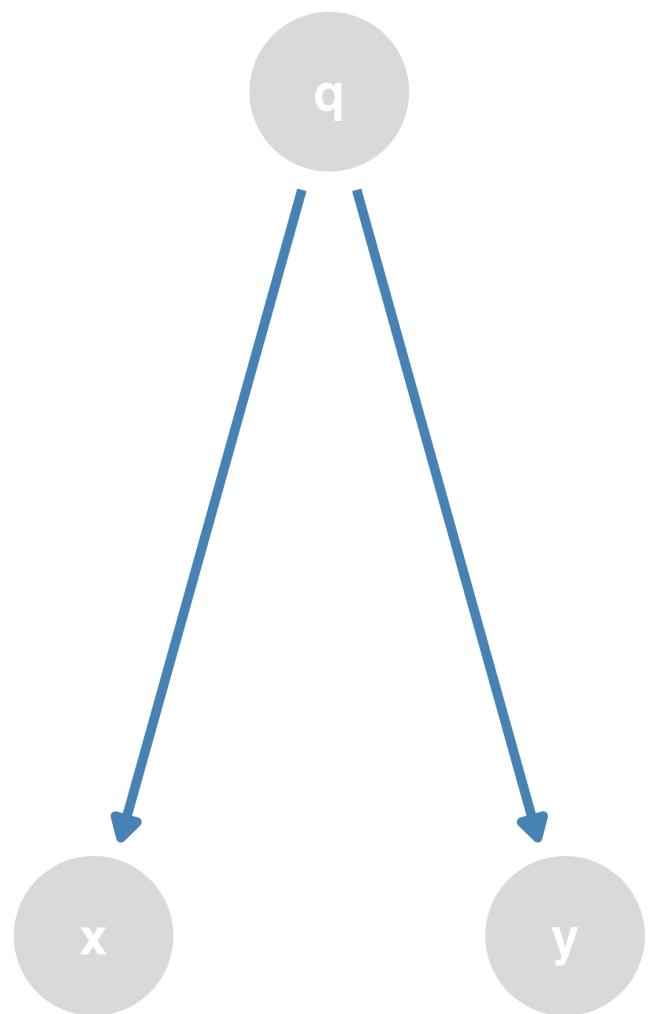
**chain**



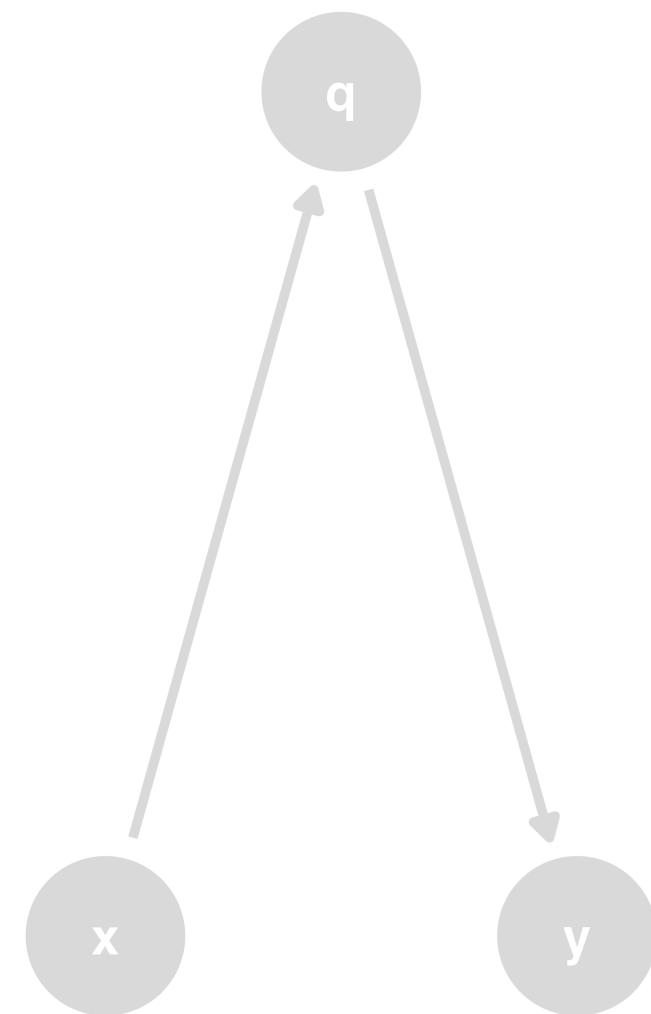
**collider**



**fork**



**chain**



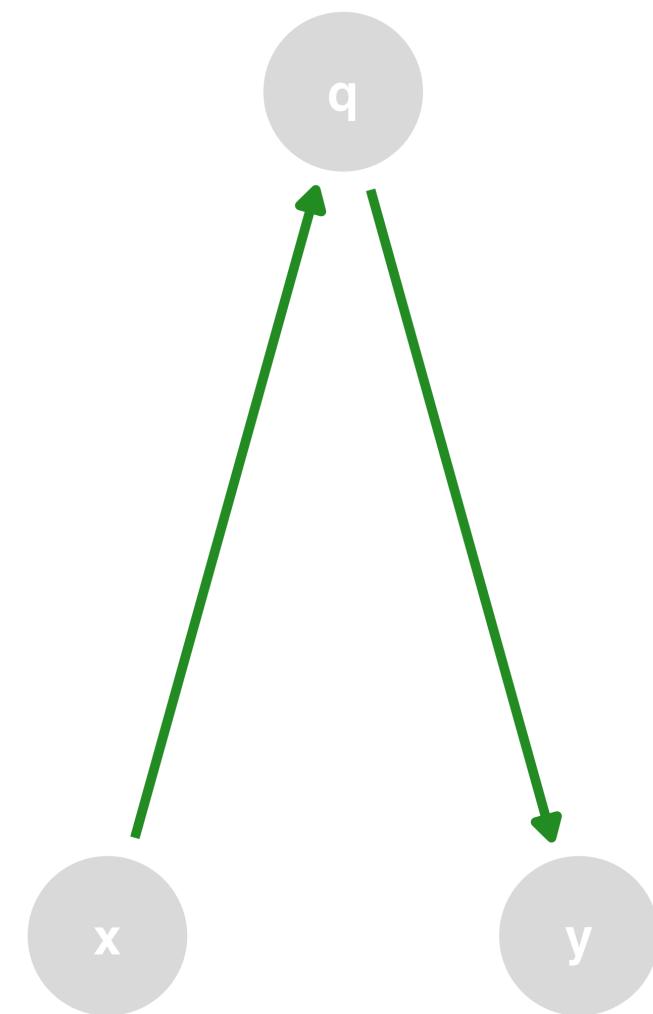
**collider**



**fork**



**chain**



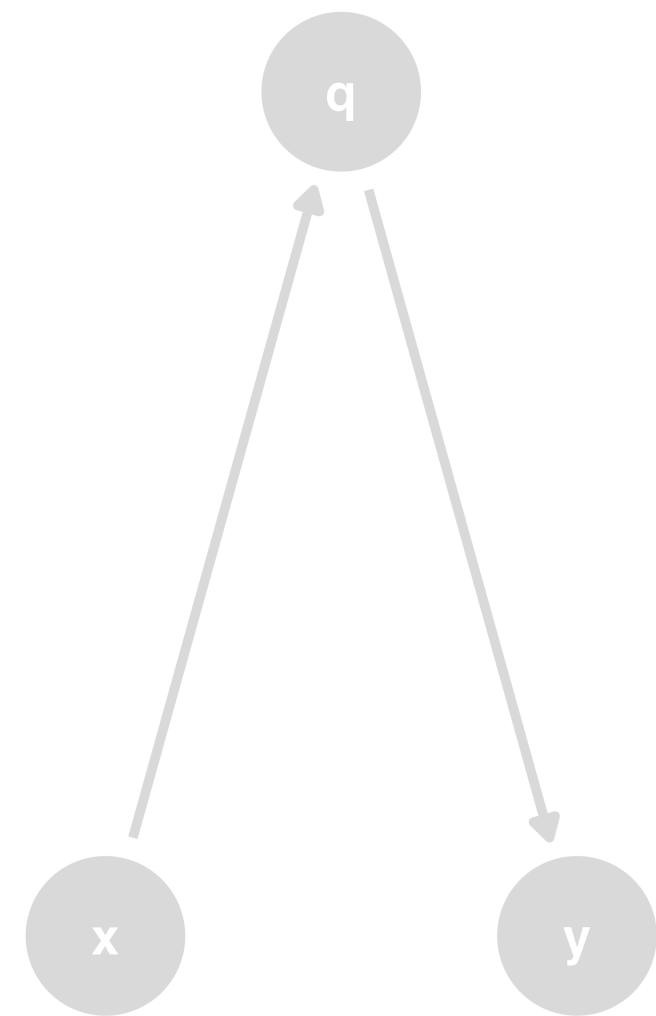
**collider**



**fork**



**chain**



**collider**



# Closing backdoor paths

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

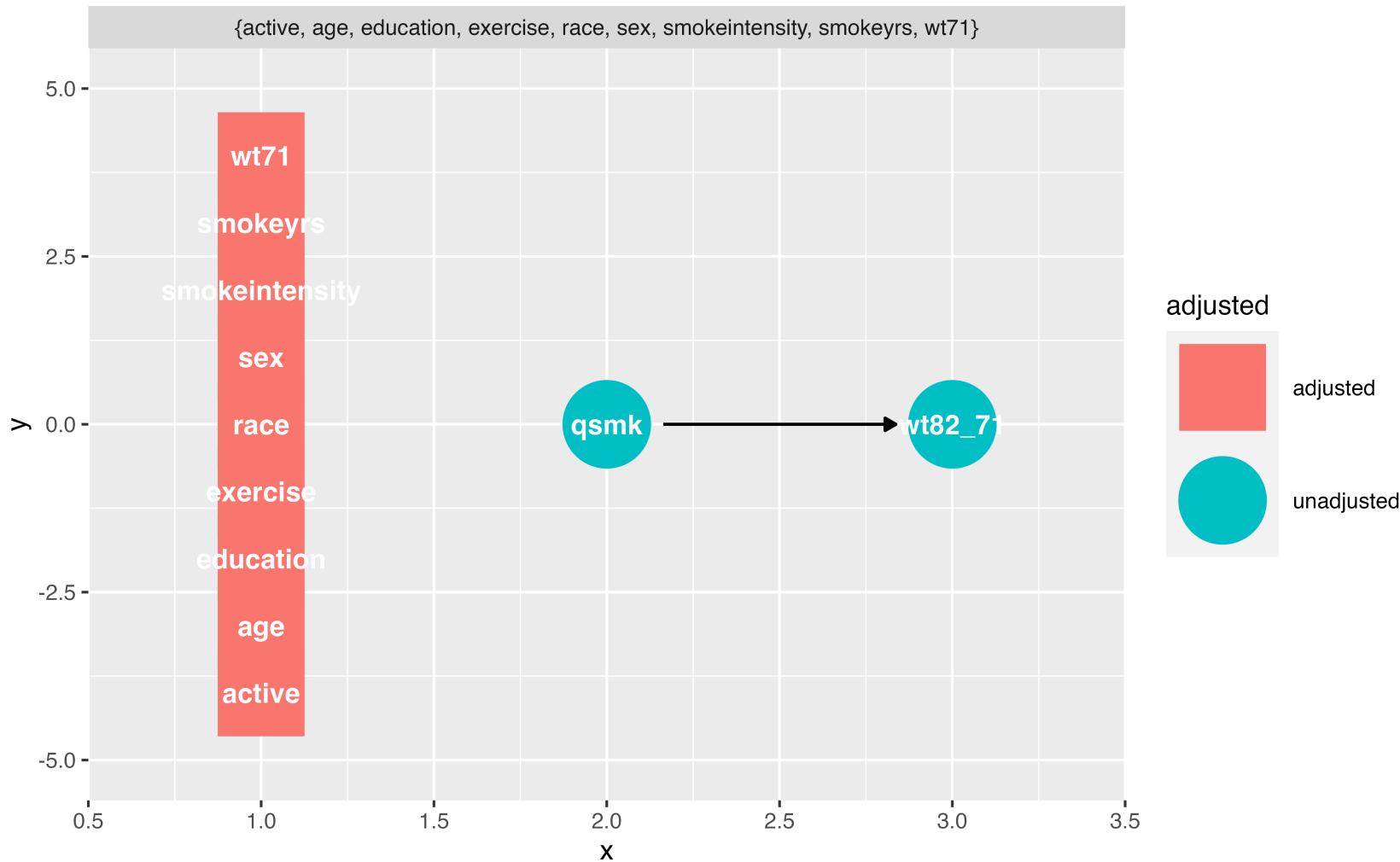
Randomization

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.

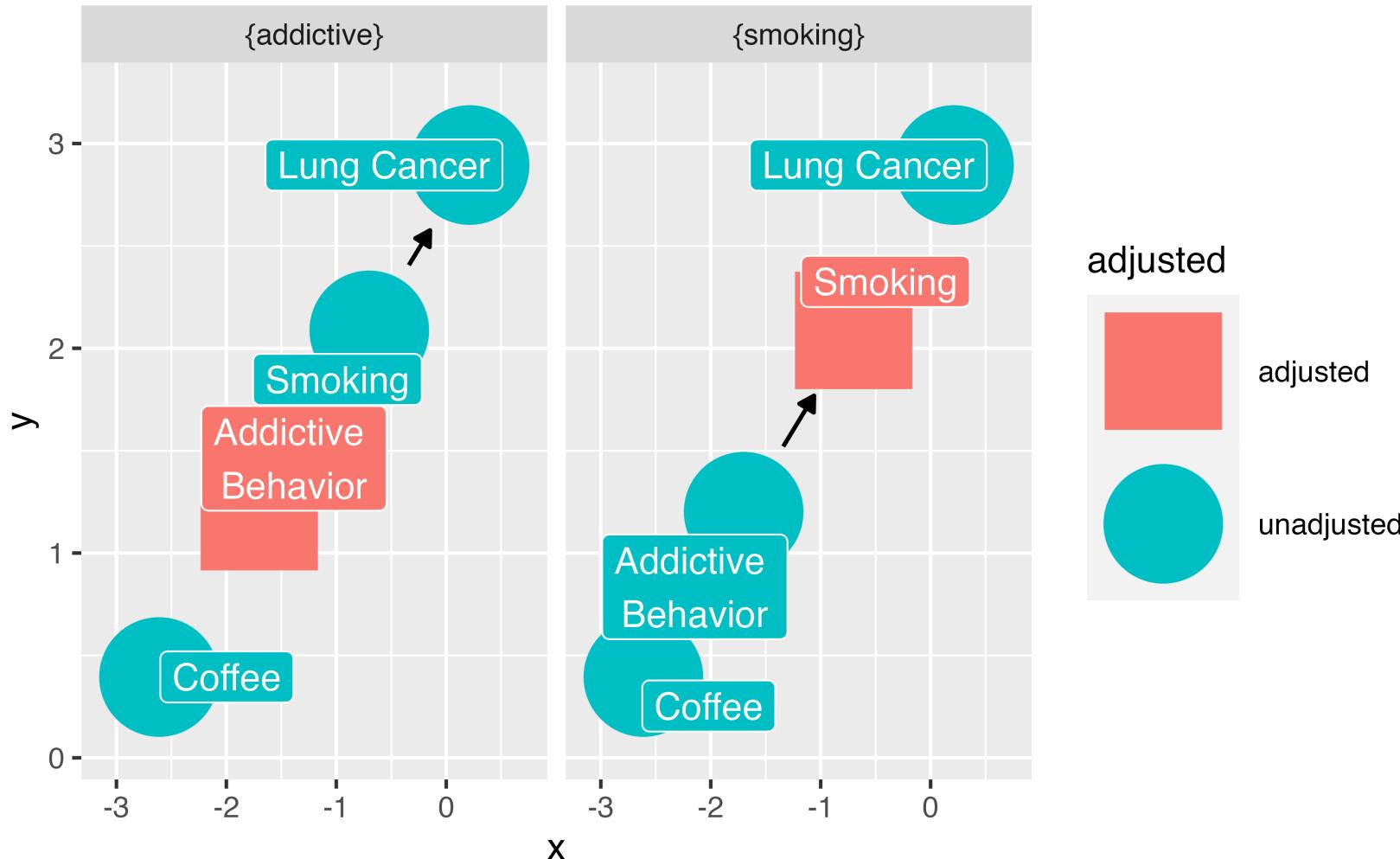
Add the arguments `use_labels = "label"` and `text = FALSE`.

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

## 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!

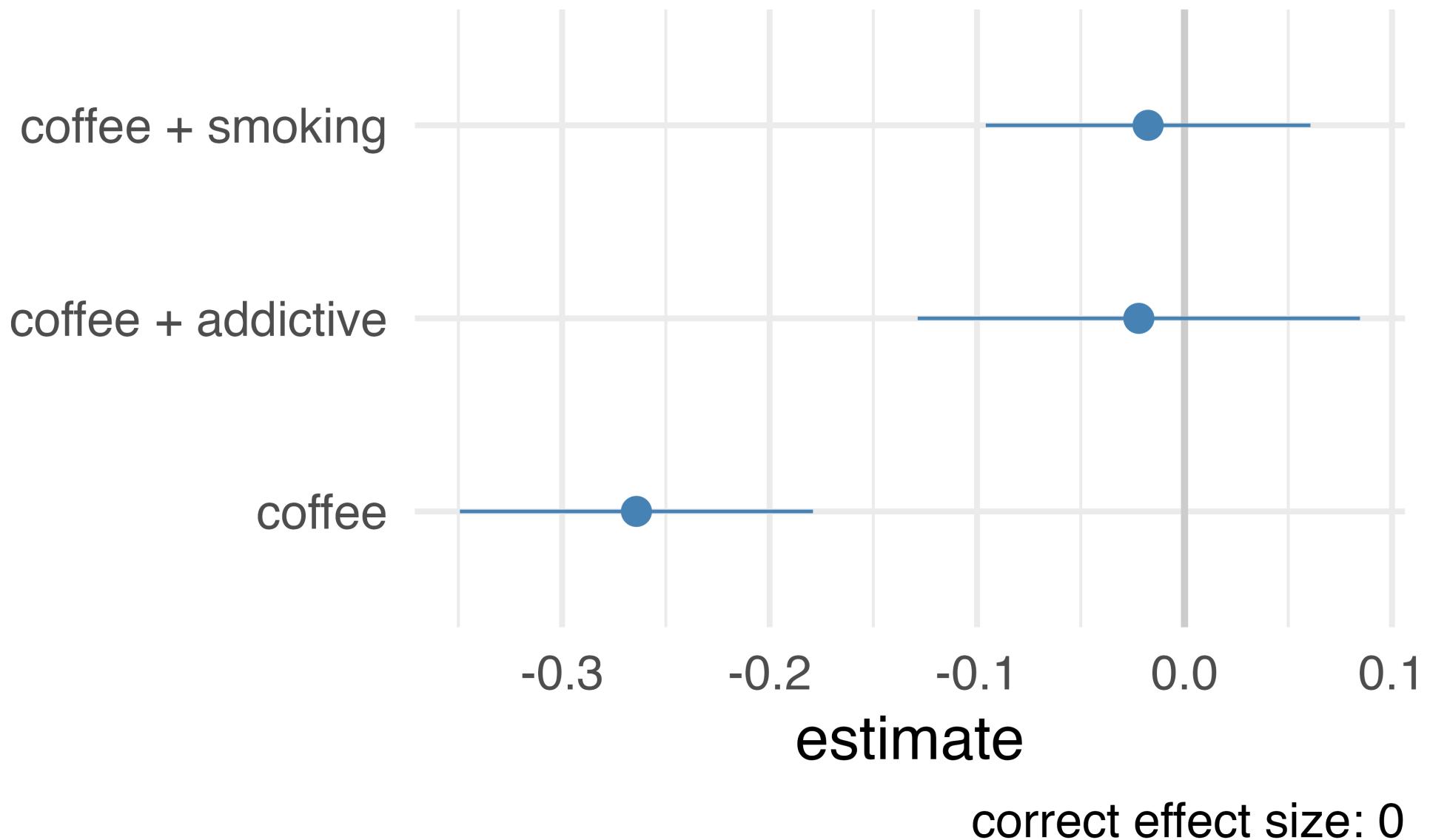
```
1 set.seed(1234)
2 dag_data <- coffee_cancer_dag |>
3   simulate_data(-.6)
```

# Let's prove it!

## 1 dag\_data

	addictive	cancer	coffee	smoking
	<dbl>	<dbl>	<dbl>	<dbl>
1	0.569	3.11	-0.326	-1.29
2	0.411	1.52	0.330	-1.57
3	1.20	1.06	-0.557	-2.40
4	-0.782	-0.504	-0.148	0.376
5	0.0357	-0.709	-0.342	-1.53
6	1.96	1.05	-1.90	-0.823
7	1.13	0.211	-0.581	-0.534
8	0.697	0.892	-1.36	-0.267
9	-0.779	0.748	0.455	0.302
10	-1.13	0.930	0.568	0.742
"	1.00	0.00	0.00	0.00

# Let's prove it!



# 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

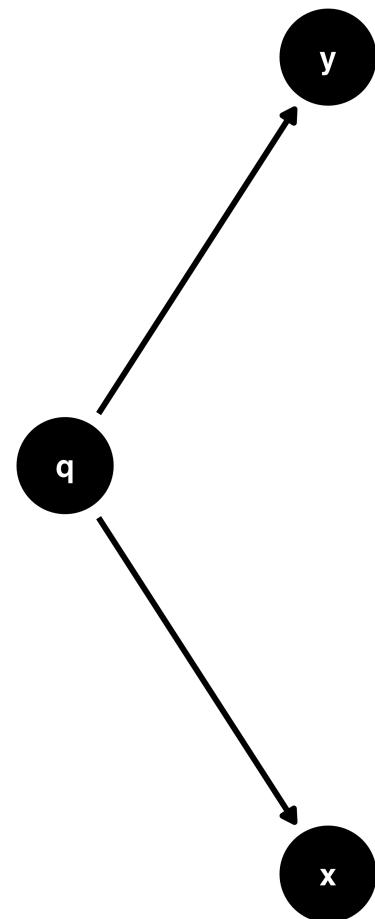
Forgetting to consider time-ordering (something has to happen before something else to cause it!)

Selection bias and colliders (more later!)

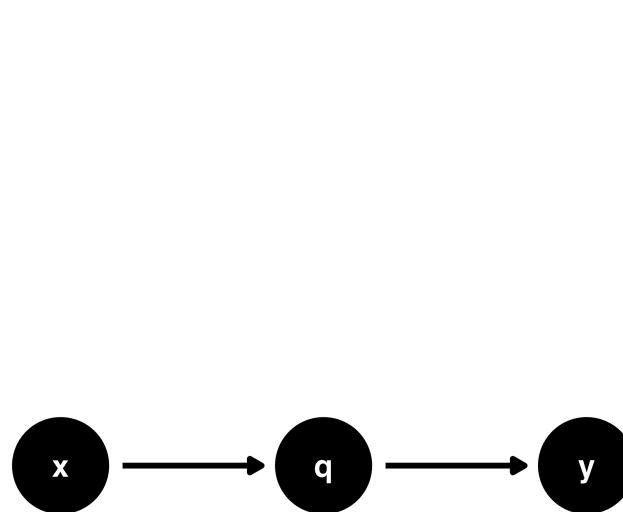
Incorrect functional form for confounders (e.g. BMI often non-linear)

# Time-ordering

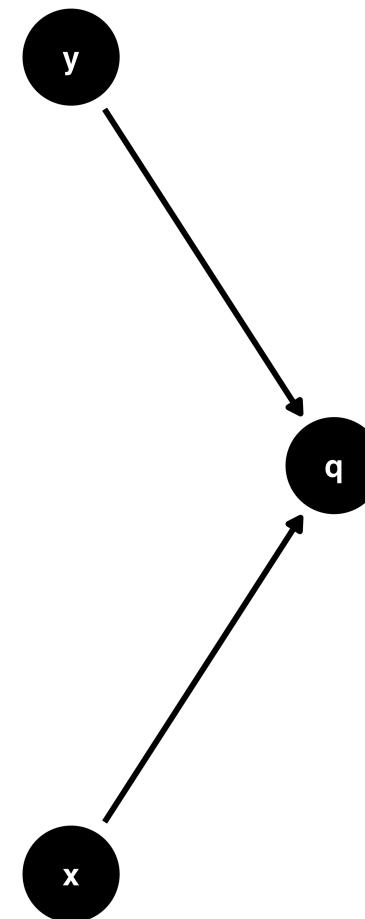
fork



chain



collider



**don't adjust for the future!**

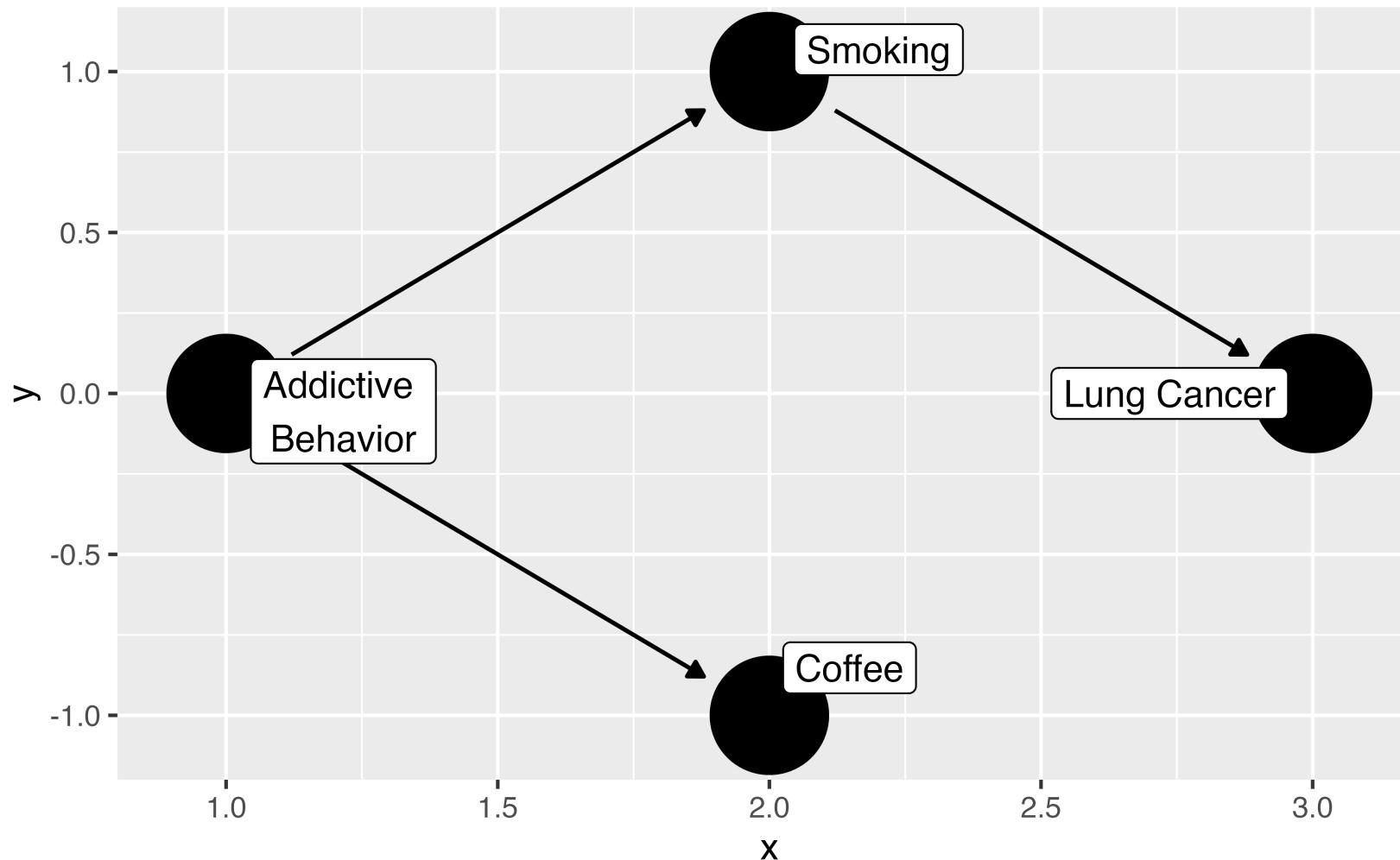
## Your Turn 4

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 #TODO: UPDATE LABELS ARGS
```

## Your Turn 4



# Resources: ggdag vignettes

[An Introduction to ggdag](#)

[An Introduction to Directed Acyclic Graphs](#)

[Common Structures of Bias](#)

