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)

ggdag

dagitty

ggplot2
ggraph

dagitty

ggplot2
ggraph

powerful,
robust
algorithms

dagitty

ggplot2
ggraph

powerful,
robust
algorithms

unlimited
flexibility

beautiful
plots

dagitty

ggplot2
ggraph

Data structure: tidy DAGs

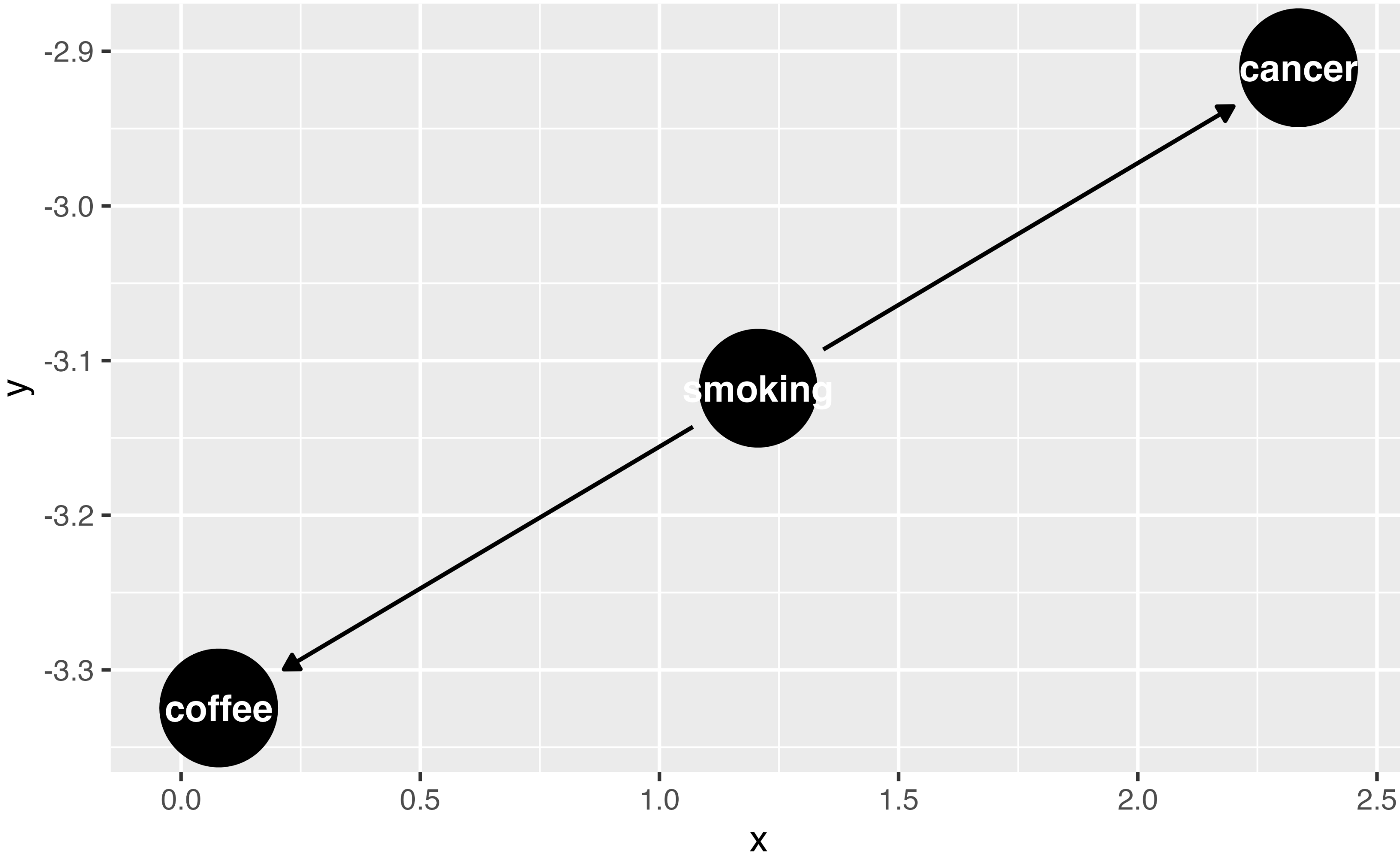
Step 1: Specify your DAG

```r
dagify(
  cancer ~ smoking,
  coffee ~ smoking
)
```

Step 1: Specify your DAG

```
dagify(
  cancer ~ smoking,
  coffee ~ smoking
) |> ggdag()
```

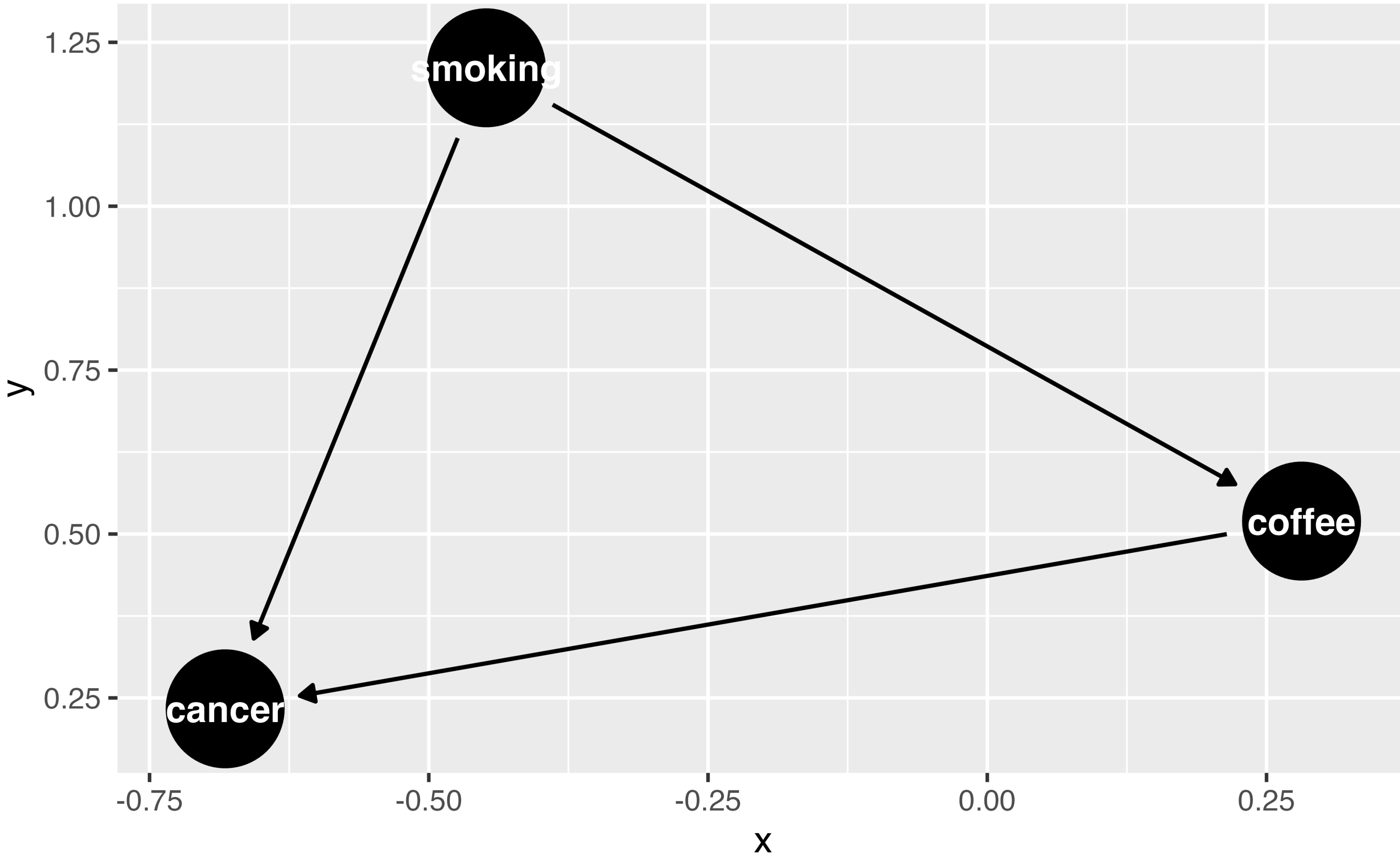
Step 1: Specify your DAG



Step 1: Specify your DAG

```r
dagify(
  cancer ~ smoking + coffee,
  coffee ~ smoking
) |> 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).

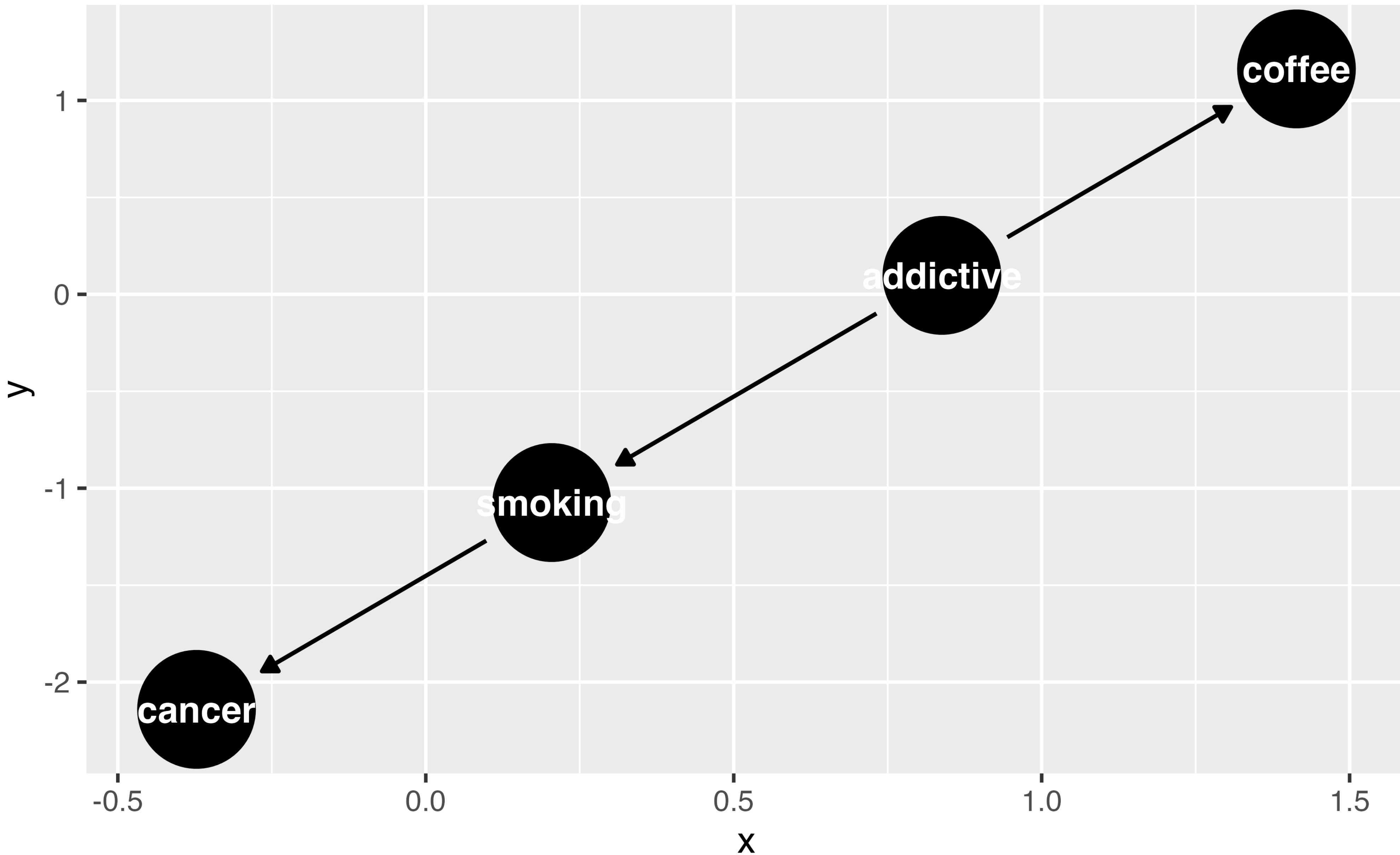
Plot the DAG using `ggdag()`

05:00

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

```r
coffee_cancer_dag <- dagify(
  cancer ~ smoking,
  smoking ~ addictive,
  coffee ~ addictive,
  exposure = "coffee",
  outcome = "cancer",
  labels = c(
    "coffee" = "Coffee",
    "cancer" = "Lung Cancer",
    "smoking" = "Smoking",
    "addictive" = "Addictive \nBehavior"
  )
)
```

```r
ggdag(coffee_cancer_dag)
```



Causal effects and backdoor paths

Ok, correlation != causation. But why not?

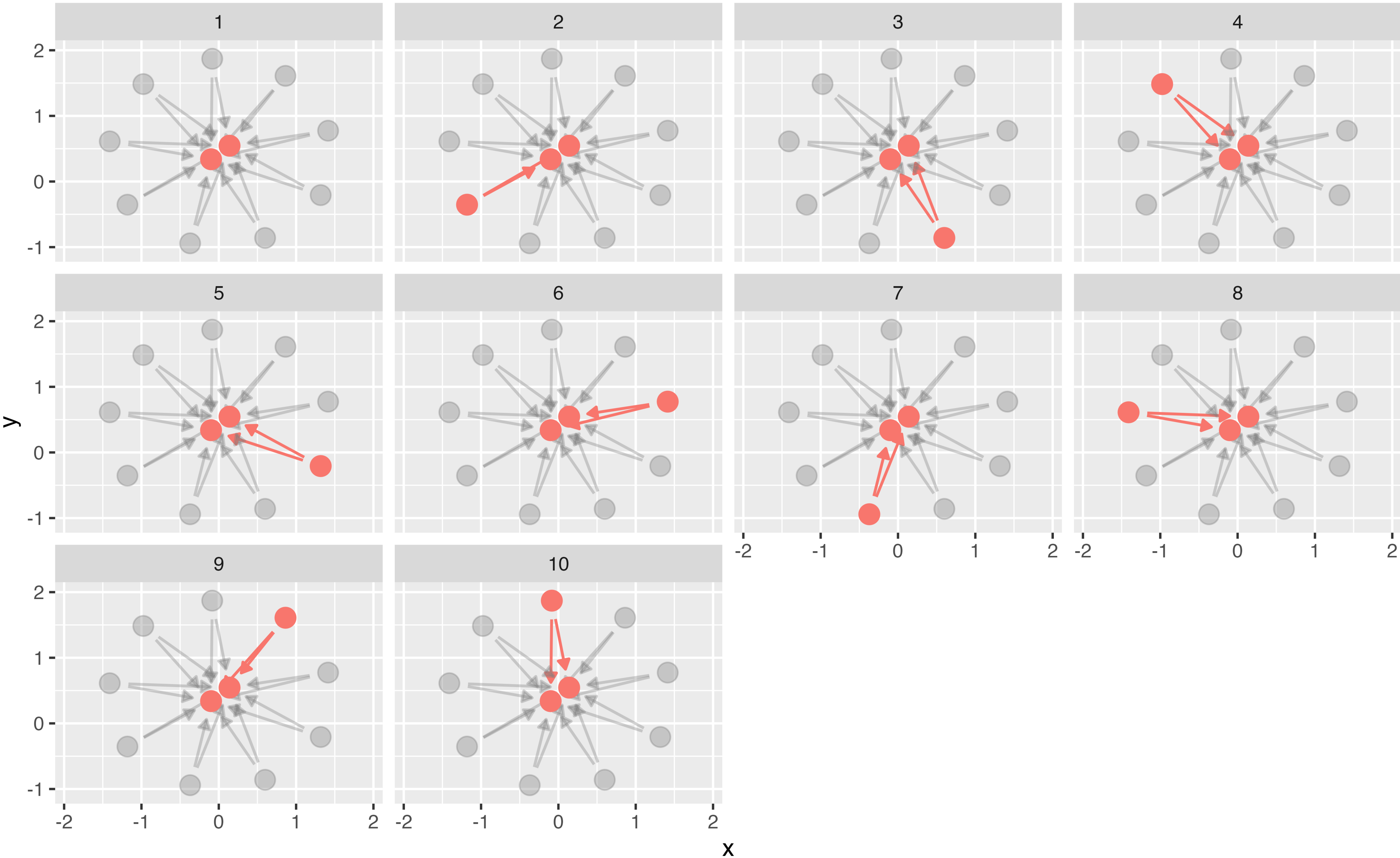
We want to know if `x -> y`…

But other paths also cause associations

ggdag_paths()

Identify “backdoor” paths

```
ggdag_paths(smk_wt_dag)
```


1
2
3
4
5
6
7
8
9
10
y
x
2
1
0
-1
-2
-1
0
1
2

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.

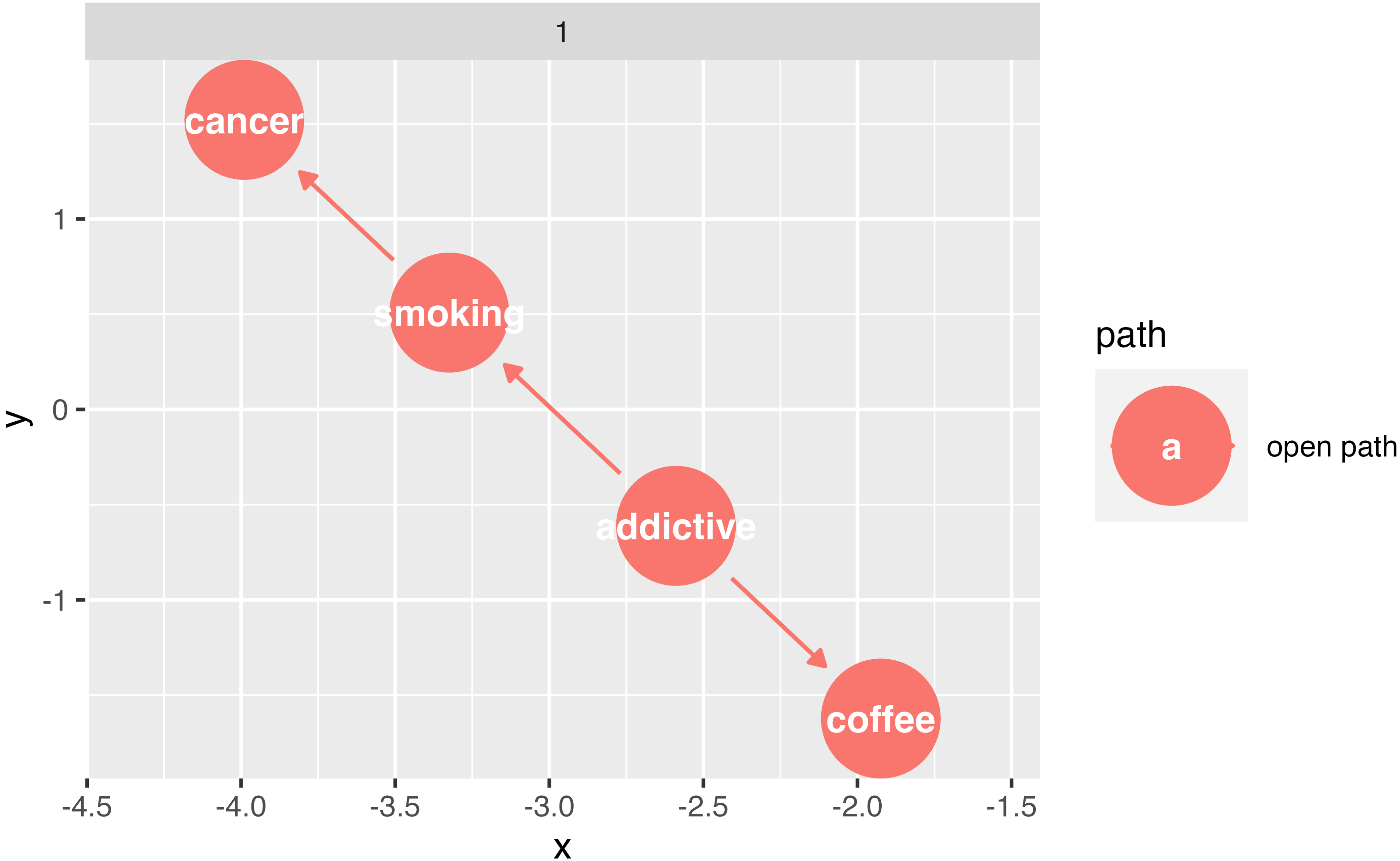
05:00

Your Turn 2

```r
coffee_cancer_dag |>
  tidy_dagitty() |>
  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   0.494 2.00  ->        coff… -0.423  2.81
2 1     addictive   0.494 2.00  ->        smok…  1.50   1.11
3 1     cancer      2.41  0.310 <NA>      <NA>  NA     NA
4 1     coffee     -0.423 2.81  <NA>      <NA>  NA     NA
5 1     smoking     1.50  1.11  ->        canc…  2.41   0.310
```

```r
coffee_cancer_dag |>
  ggdag_paths()
```



Closing backdoor paths

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

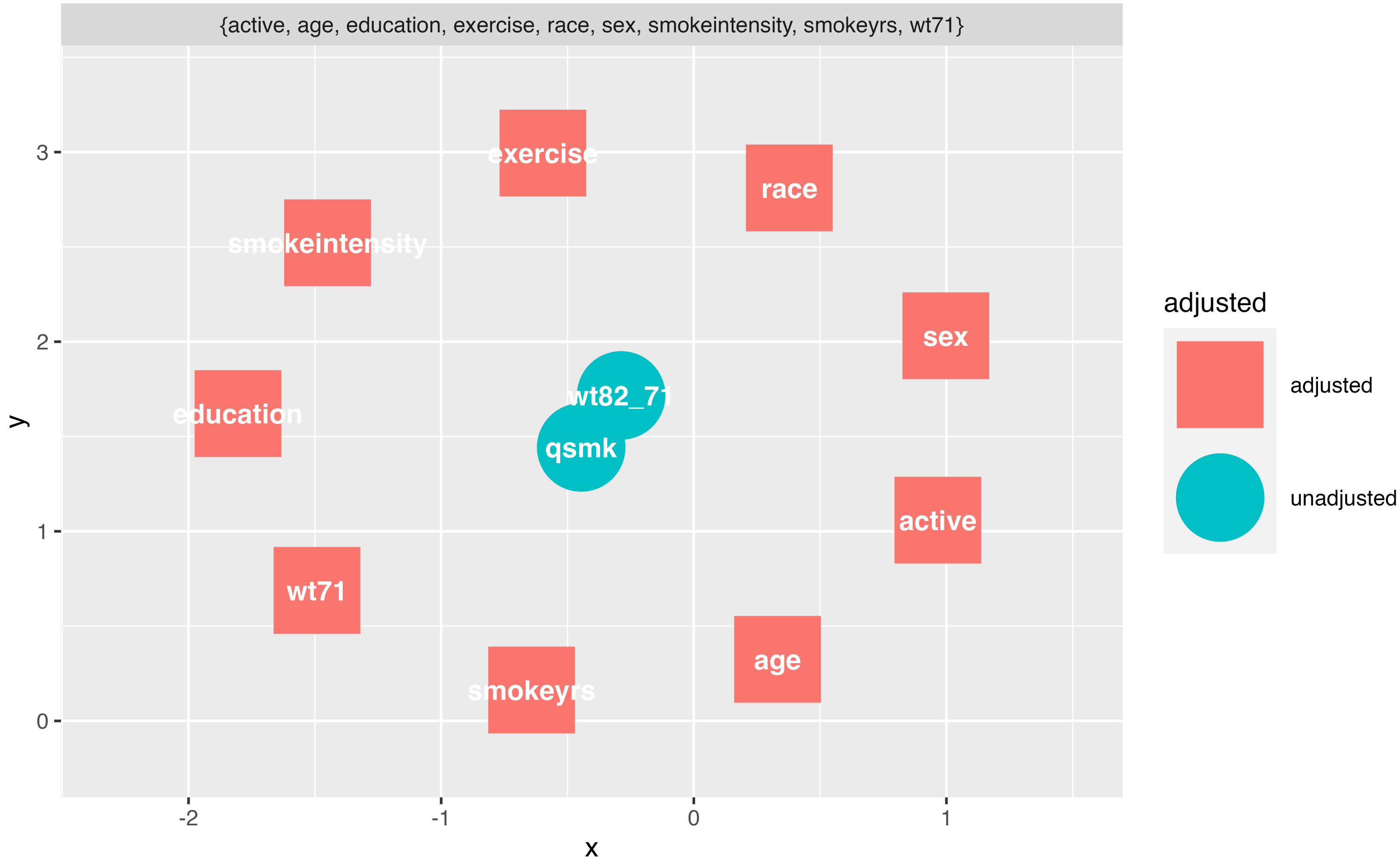
Randomization

Stratification, adjustment, weighting, matching, etc.

Identifying adjustment sets

```
ggdag_adjustment_set(smk_wt_dag)
```

Identifying adjustment sets



Identifying adjustment sets

```r
library(dagitty)
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`.

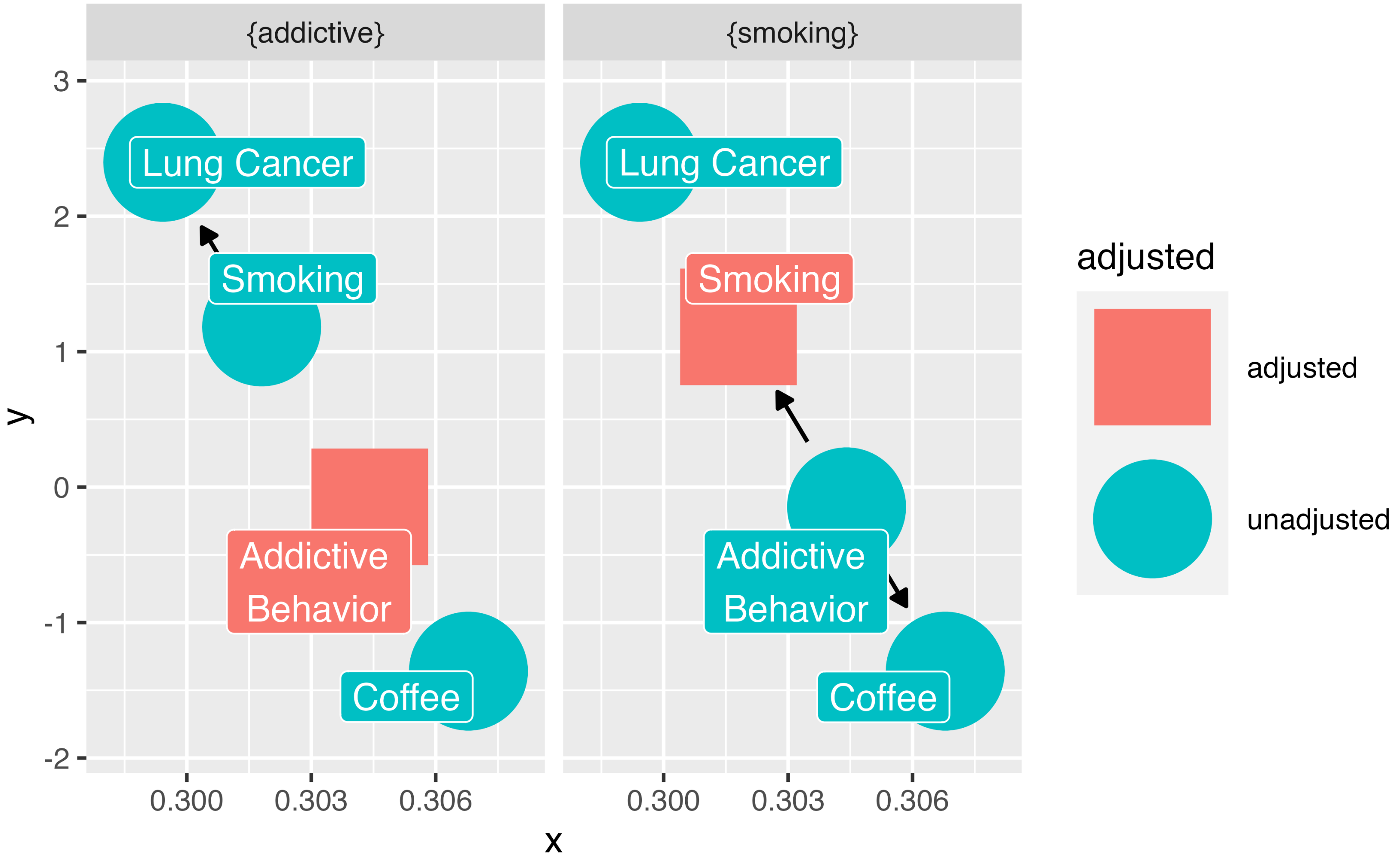
Write an R formula for each adjustment set, as you might if you were fitting a model in `lm()` or `glm()`

05:00

Your Turn 3

```r
ggdag_adjustment_set(
  coffee_cancer_dag,
  use_labels = "label",
  text = FALSE
)
```

Your Turn 3


{addictive}
{smoking}
Lung Cancer
Smoking
Addictive Behavior
Coffee
Lung Cancer
Smoking
Addictive Behavior
Coffee
3
2
1
0
-1
-2
y
0.300
0.303
0.306
0.300
0.303
0.306
x
adjusted
adjusted
unadjusted

Your Turn 3

```
cancer ~ coffee + addictive
cancer ~ coffee + smoking
```

Let's prove it!

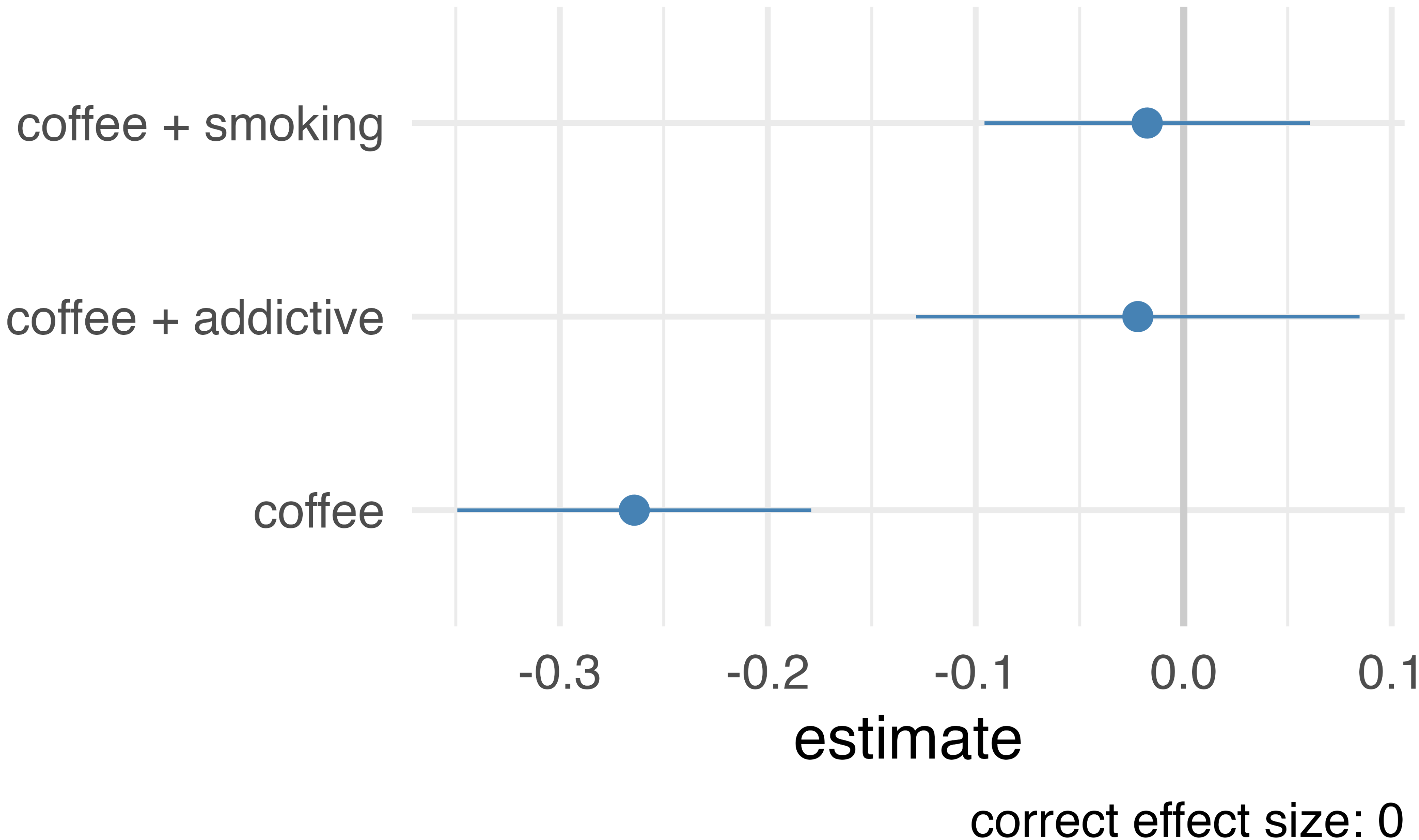
```r
set.seed(1234)
dag_data <- coffee_cancer_dag |>
  simulate_data(-.6)
```

Let’s prove it!

```r
dag_data
```

```
# A tibble: 500 × 4
   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
```

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

Selection bias and colliders (more later!)

Resources: ggdag vignettes

An Introduction to ggdag

An Introduction to Directed Acyclic Graphs

Common Structures of Bias