Directed Acyclic Graphs

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Atelier Inserm
Best practices and recent advances in causal analyses
Practical phase

October 13-16, 2025 - Poitiers

Outline of the DAG session

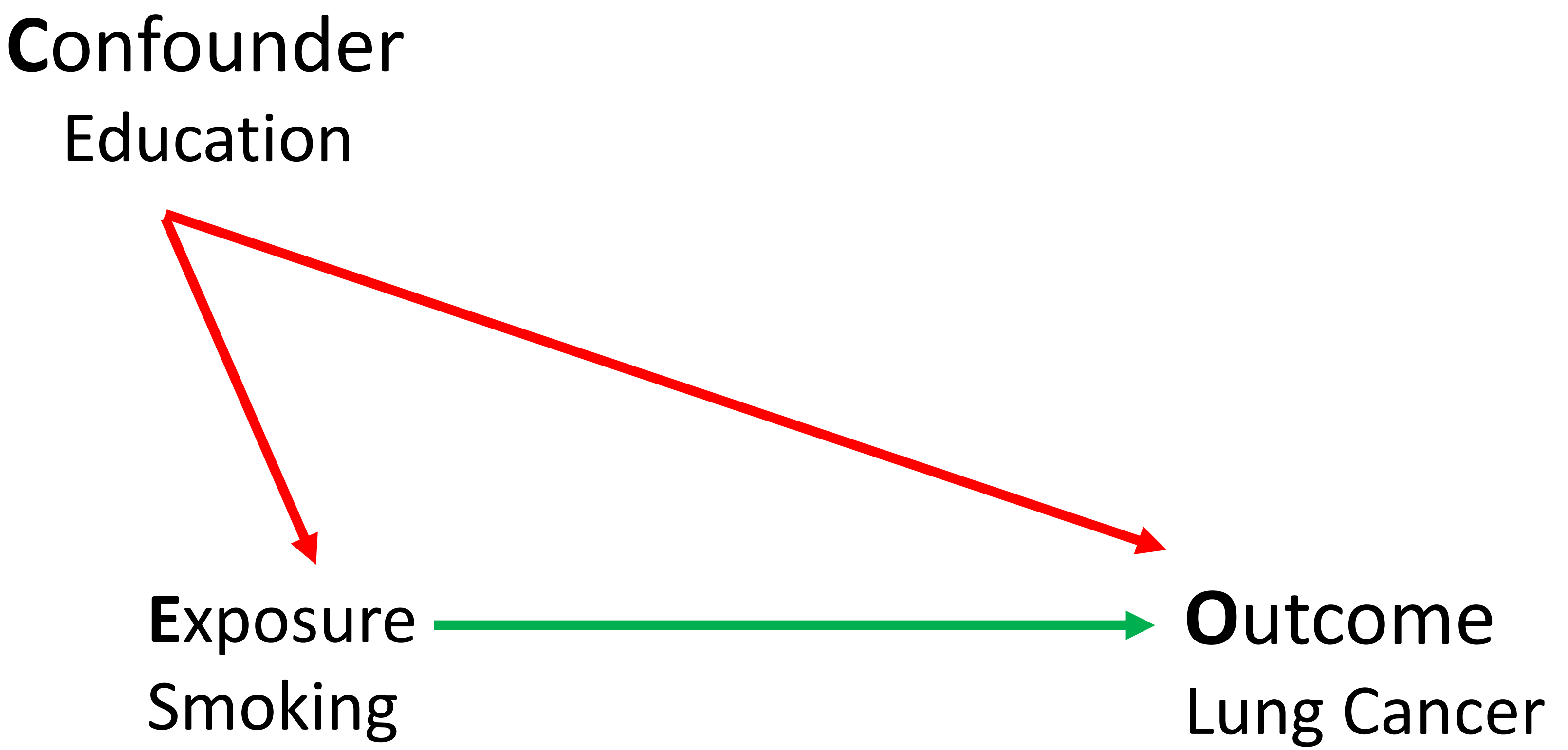
- Recall of principles
- Use of DAGitty
- Working groups
  - 3 groups working on 3 research questions
    - Julien Asselineau (CHU Brest)
    - Nathalie Costet (Irset Rennes)
    - Lisa Le Gall (Inserm BPH Bordeaux)
  - 3 facilitators
    - Joe de Kaiser (Inserm Scale-Epi, CHU Poitiers)
    - Lisa Durocher (CHU Poitiers)
    - Karen Leffondré (Inserm BPH Bordeaux)

DAGs in epidemiology

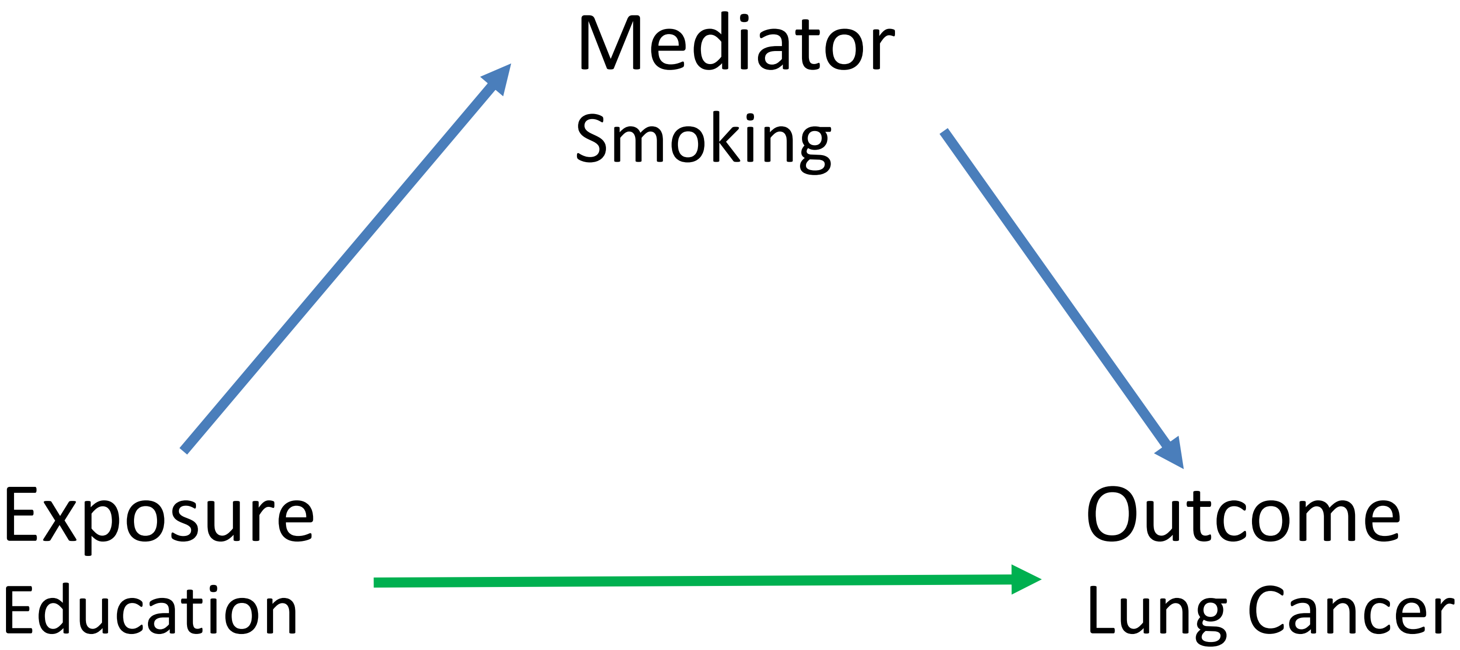
- DAGs are used in epidemiology to represent hypothetical causal relationships among variables of interest
  - At the time of developing the study design
    - To identify potential selection and confounding bias
  - Before etiological analysis
    - To identify the set of covariates for adjustment

- Pearl. Causal diagrams for empirical research. *Biometrika* 1995
- Greenland, Pearl, Robins. Causal diagrams for epidemiological research. *Epidemiol* 1999
- Glymour, Greenland. Causal diagrams. In: Rothman, Greenland, Lash. *Modern Epidemiology* 2008
- Digitale, Martin, Glymour. Tutorial on DAG. *J Clin Epidemiol* 2022

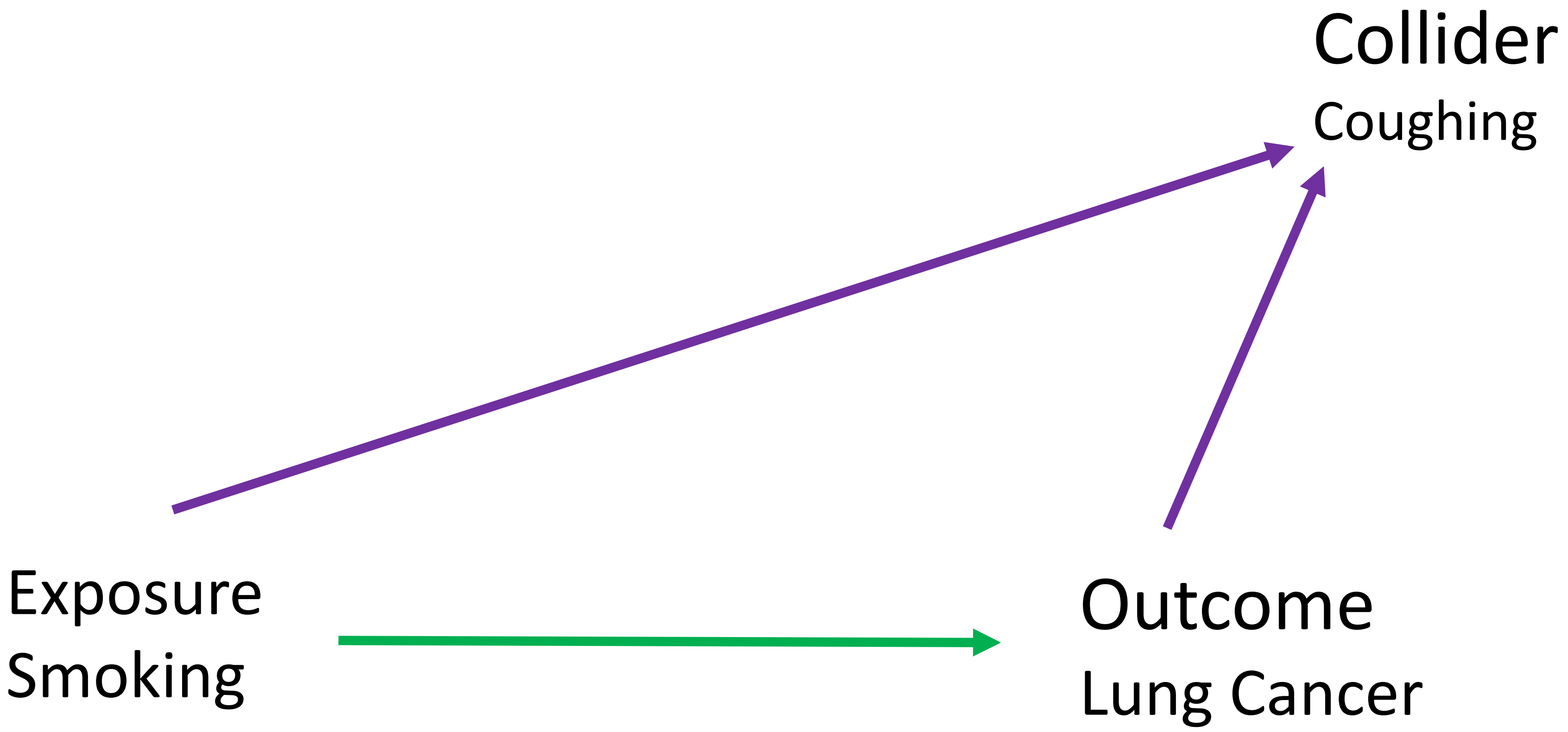
Confounder


Confounder
Education
Exposure
Smoking
Outcome
Lung Cancer

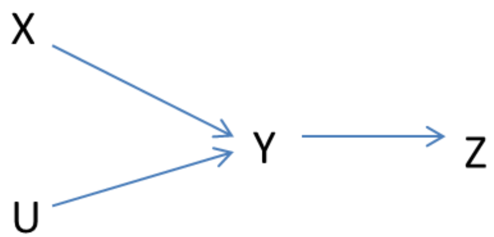
Mediator



Collider



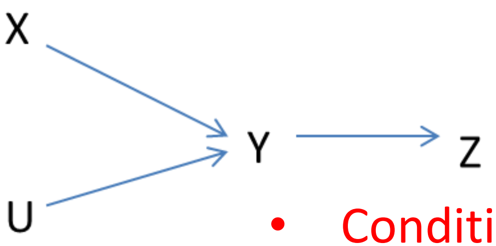
Marginal associations in a DAG



- A path is said to be open (unblocked, active) if there is no collider on the path
  - Path X → Y → Z
  - Path U → Y → Z
- A path is said to be closed (blocked, inactive) if there is a collider on the path
  - Path U → Y ← X
  - Path X → Y ← U
- If there is no open path between U and X, they are marginally independent
  - $\Pr(X = x) = \Pr(X = x \mid U = u)$

Glymour, Greenland. Causal diagrams. In: Rothman, Greenland, Lash. *Modern Epidemiology* 2008

Conditional associations in a DAG



- Conditioning on a noncollider closes the path
  - Conditioning on Y close the path $X \rightarrow Y \rightarrow Z$
    - X and Z are marginally associated

      but after conditioning on Y, they become independent

      $Pr(Z = z \mid Y = y) = Pr(Z = z \mid Y= y, X = x)$

      ➢ X and Z are **independent conditionally** on Y (Y separates Z from X)

- Conditioning on a collider opens the path
  - Conditioning on Y open the path $X \rightarrow Y \leftarrow U$
    - X and U are marginally independent

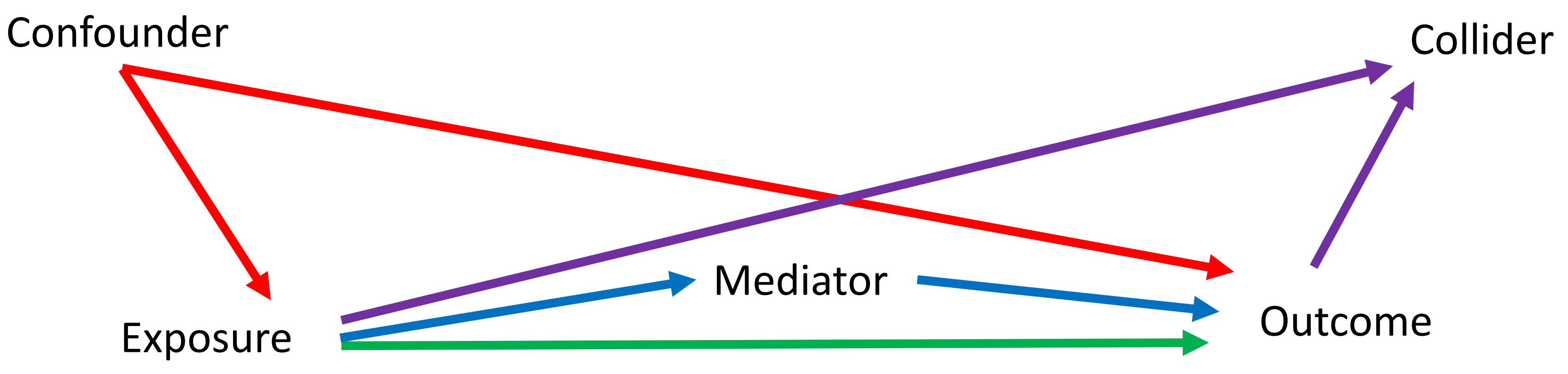
      $Pr(X = x) = Pr(X = x \mid U = u)$

      but after conditioning on Y, they become associated

      ➢ X and U are **associated conditionally** on Y

Glymour, Greenland. Causal diagrams. In: Rothman, Greenland, Lash. *Modern Epidemiology* 2008

Identification of the set of covariates for adjustment

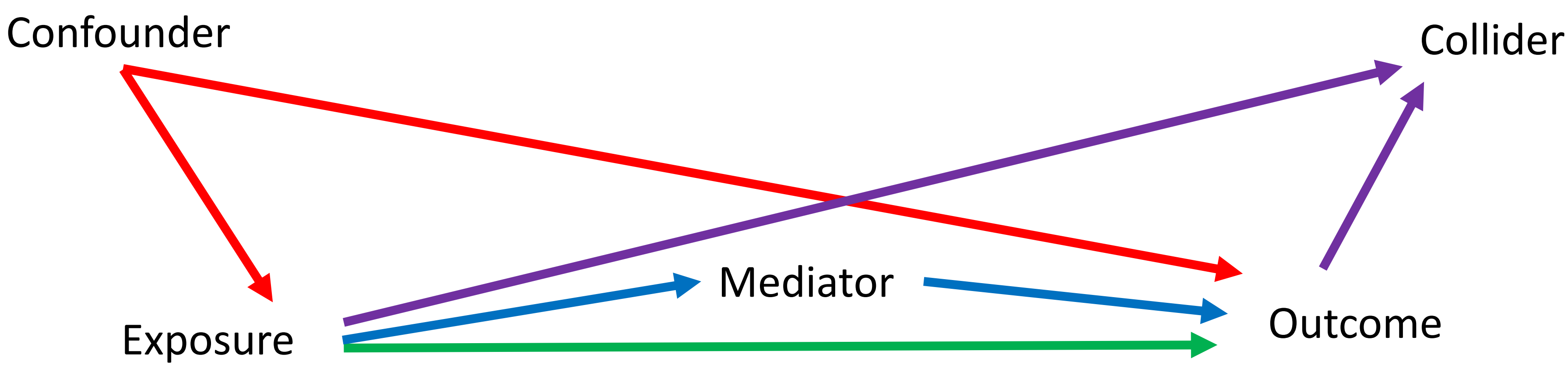


- Identify all paths from the exposure to the outcome
  - Causal paths (all paths where all arrows go from the exposure to the outcome)
  - Not causal paths (all other paths: confounding paths, paths with a collider)

- Causal paths
  - Naturally open, we don't want to close them

- Confounding paths (backdoor paths)
  - Naturally open, we want to close them
    (because association flows along all open paths)

Identification of the set of covariates for adjustment



- Paths with a collider
  - Naturally closed, we don't want to open them
    (because association cannot flow along closed path)

- Total effect
  - Effect of the exposure on the outcome through all causal paths

- Sufficient set of covariates for adjustment
  - After adjustment, all causal paths are open and all non-causal paths are closed

Softwares

- The daggle app
  - Hanly et al. The daggle app - a tool to support learning and teaching the graphical rules of selecting adjustment variables using DAGs. *Int J Epidemiol* 2023

- DAGitty
  - Textor, Hardt, Knüppel. DAGitty: A graphical tool for analyzing causal diagrams. *Epidemiol* 2011.
  - Textor et al. Robust causal inference using DAGs: the R package ‘dagitty’. *Int J Epidemiol* 2016

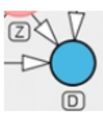
➢ « **Just** » have to put your DAG, and it gives you the set of covariates for adjustment

DAGitty website

https://www.dagitty.net 70 %

DAGitty — draw and analyze causal diagrams

DAGitty is a browser-based environment for creating, editing, and analyzing causal diagrams (also known as directed acyclic graphs or causal Bayesian networks). The focus is on the use of causal diagrams for minimizing bias in empirical studies in epidemiology and other disciplines. For background information, see the "learn" page.

Launch	Download	Learn	Code
 Launch DAGitty online in your browser.	Download DAGitty's source for offline use.	Learn more about DAGs and DAGitty.	The R package "dagitty" is available on CRAN or github.

DAGitty is developed and maintained by Johannes Textor (Institute for Computing and Information Sciences, Radboud University, and Medical BioSciences department, Radboudumc, Nijmegen, The Netherlands).

Many algorithms implemented in DAGitty were developed in close collaboration with Maciej Liśkiewicz and Benito van der Zander, University of Lübeck, Germany (see literature references below).

DAGitty development happens on github. You can download all source code from there and also get involved.

How can I get help?

Johannes Textor
@johannes_textor@mastodo...

After 12 years, I am moving the #dagitty website to a new server. There will be interruptions and issues in the coming days. I hope everything will be up again smoothly soon. Thanks for your patience!

08 oct. 2023, 11:20 · · Web

0 boost · **5** favoris

Changelog

2023-10-07

Moved to a new webserver after 12 years.

2023-07-11

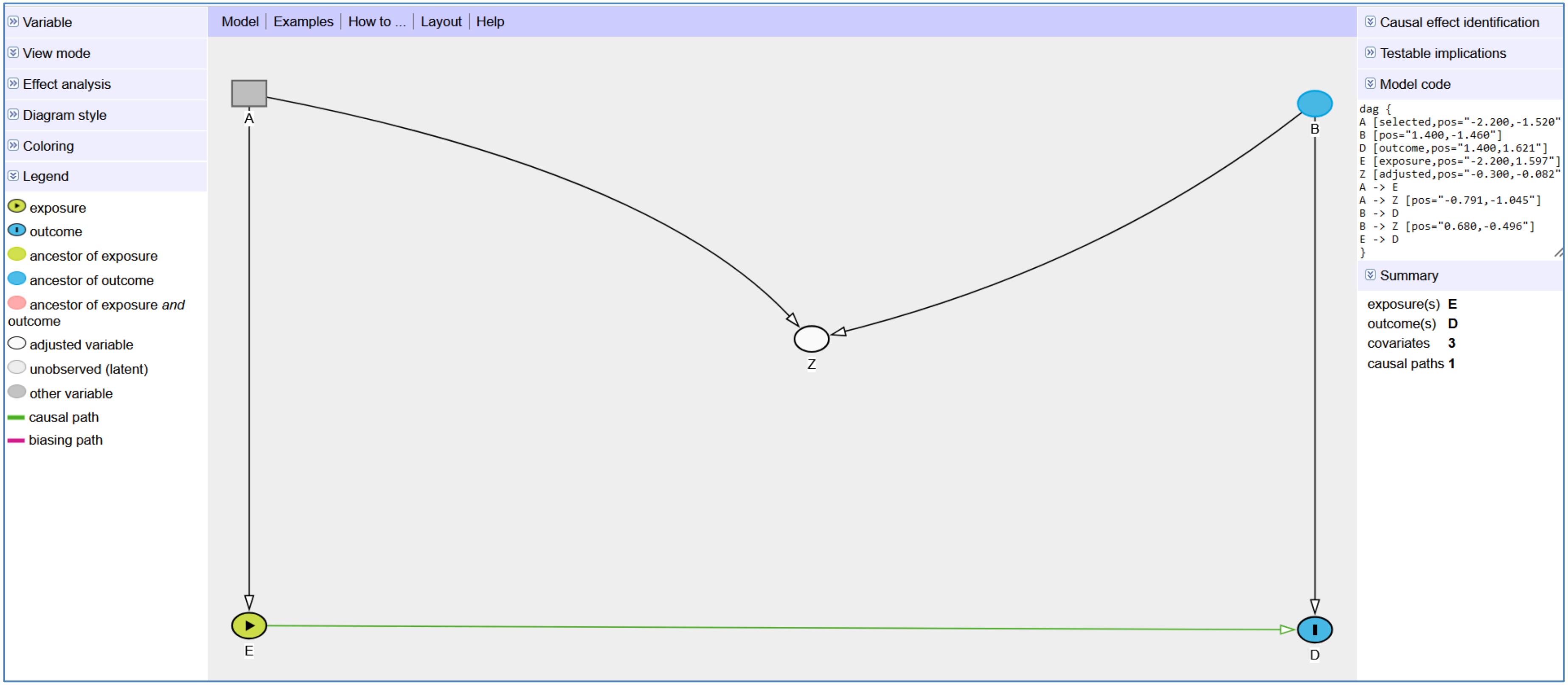
Version 3.1 is out, featuring selection variables.

2020-01-09

Version 3.0 has been released! Complete reimplementation of the interface, should work with mobile/touch now.

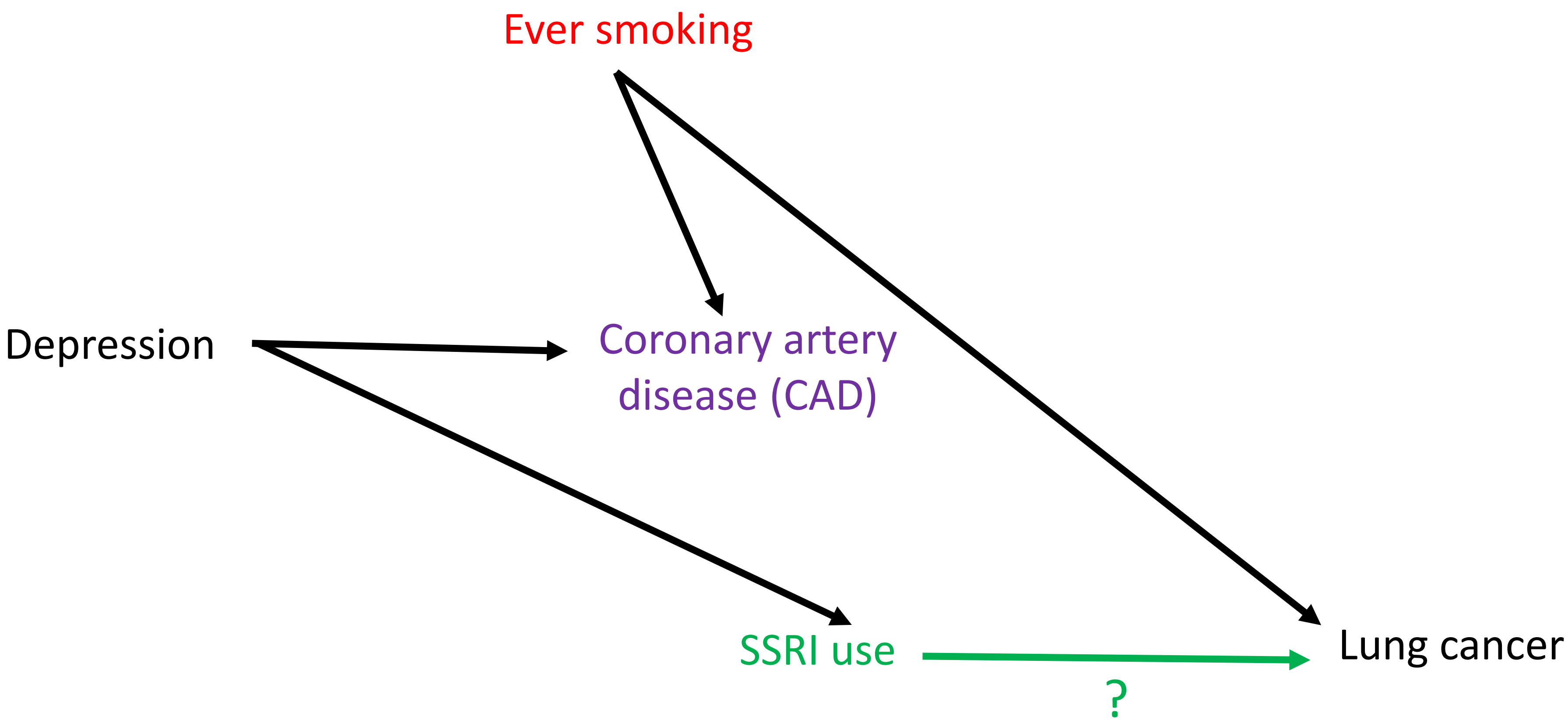
2018-04-04

DAGitty online
https://www.dagitty.net/dags.html#



Example 1

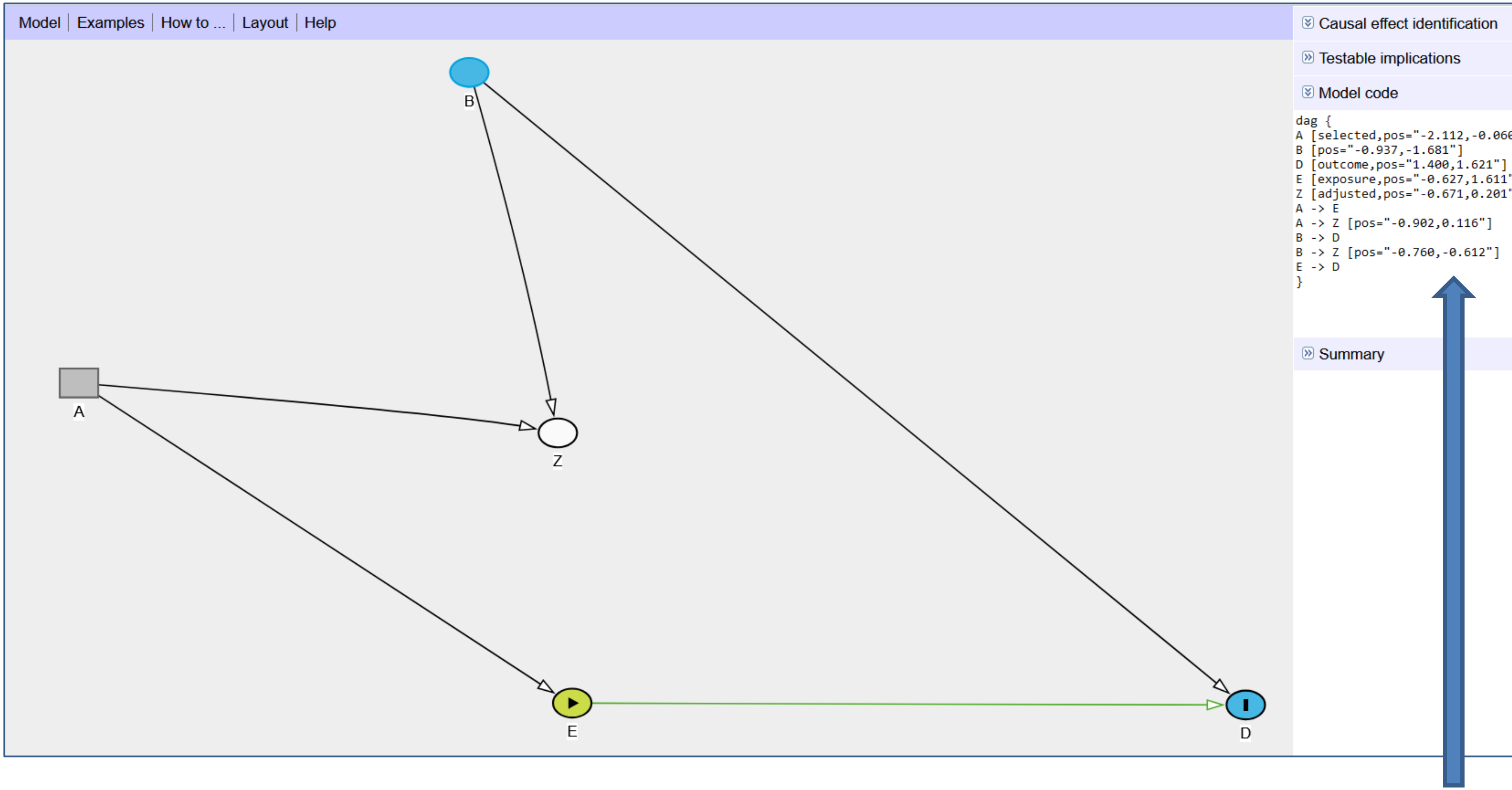
Use of selective serotonin reuptake inhibitors (SSRIs) and lung cancer



Liu et al. Implication of M Biais in epidemiological studies: A simulation study. *Am J Epidemiol* 2012

Implement Exemple 1 in DAGitty

Move variables so that all arcs flows in the same direction

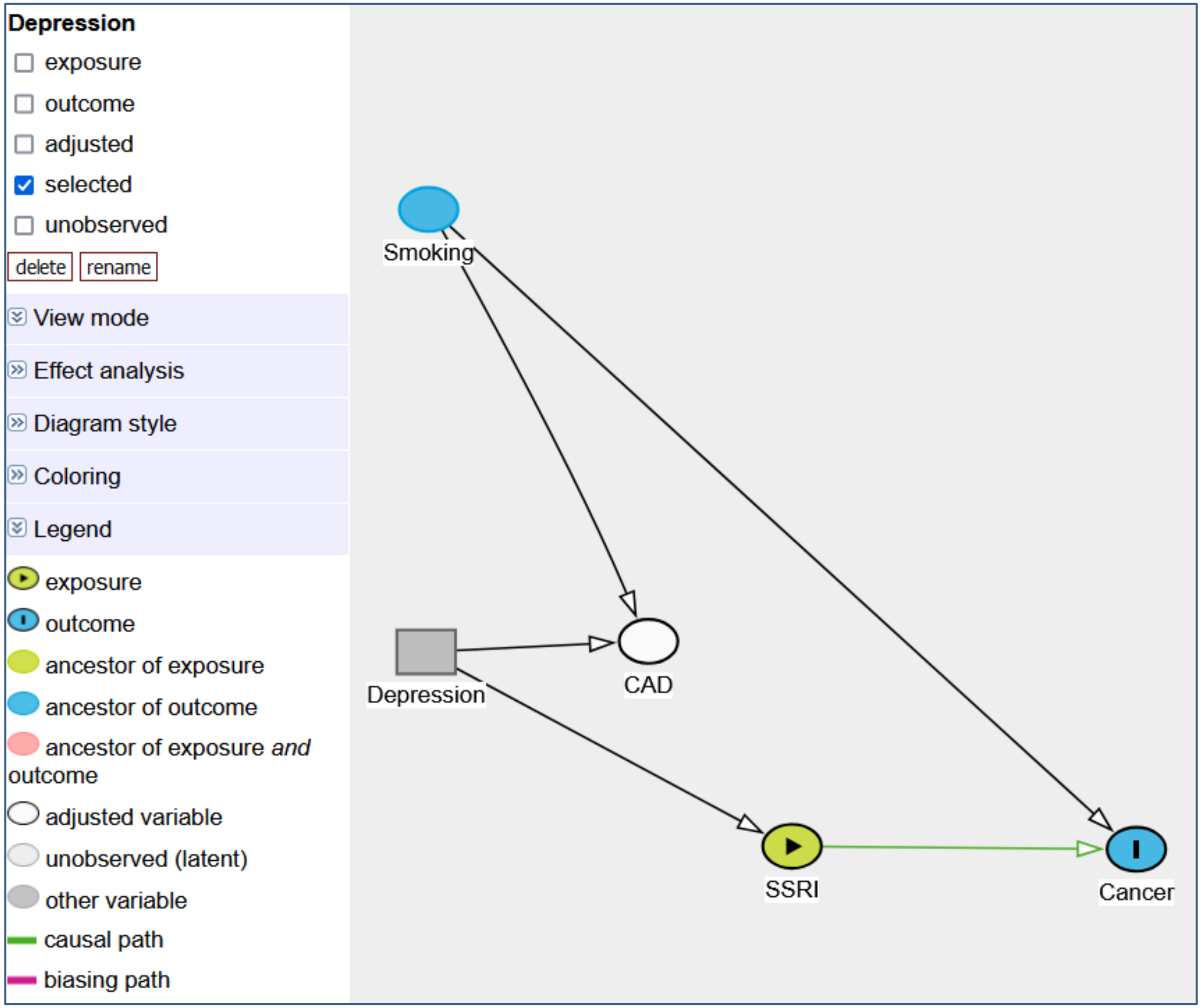


Save model code in a doc!

Model code

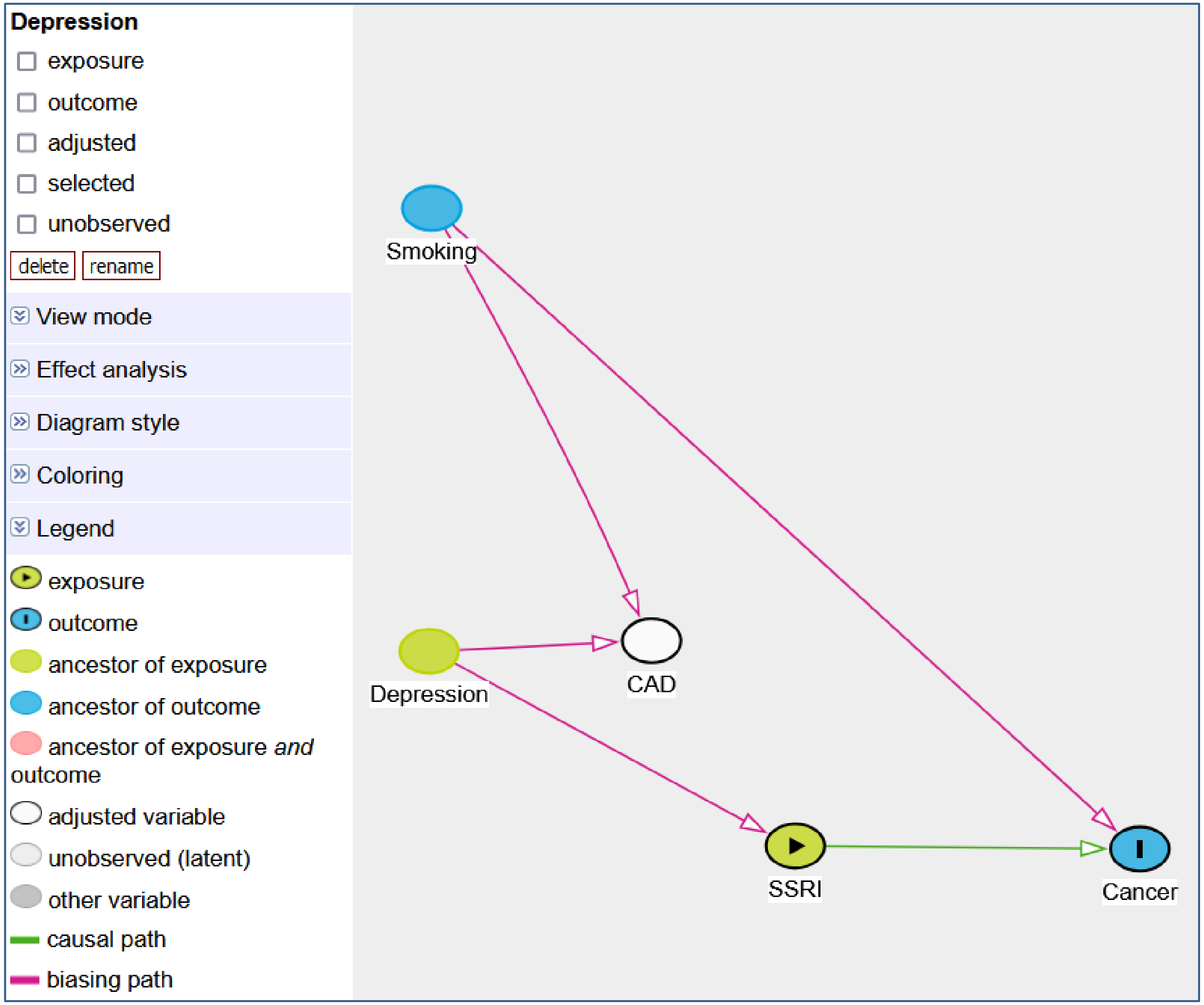
```
dag {
A [selected,   pos="-1.967,0.301"]
B [pos="-1.093,-1.621"]
D [outcome,  pos="1.400,1.621"]
E [exposure,  pos="-0.286,1.576"]
Z [adjusted,   pos="-0.202,0.437"]
A -> E
A -> Z [pos="-0.734,0.377"]
B -> D
B -> Z [pos="-0.497,-0.321"]
E -> D
}
```

Rename variables



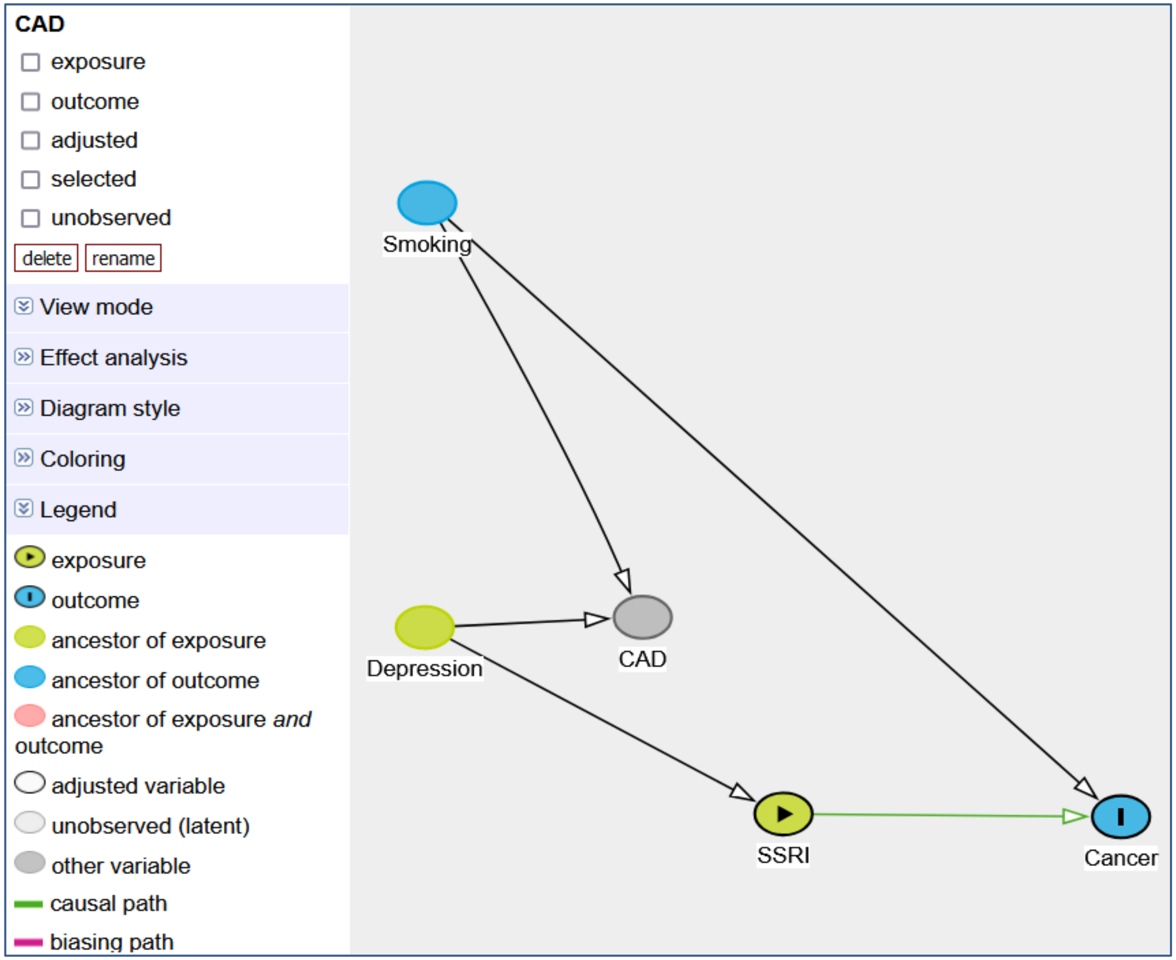

```
dag {
CAD [adjusted,pos="-0.995,-0.291"]
Cancer [outcome,pos="0.172,0.352"]
Depression [selected,pos="-1.811,-0.446"]
SSRI [exposure,pos="-0.714,0.352"]
Smoking [pos="-1.817,-1.656"]
Depression -> CAD [pos="-1.177,-0.341"]
Depression -> SSRI
SSRI -> Cancer
Smoking -> CAD [pos="-1.154,-0.612"]
Smoking -> Cancer}
```

Unselect Depression



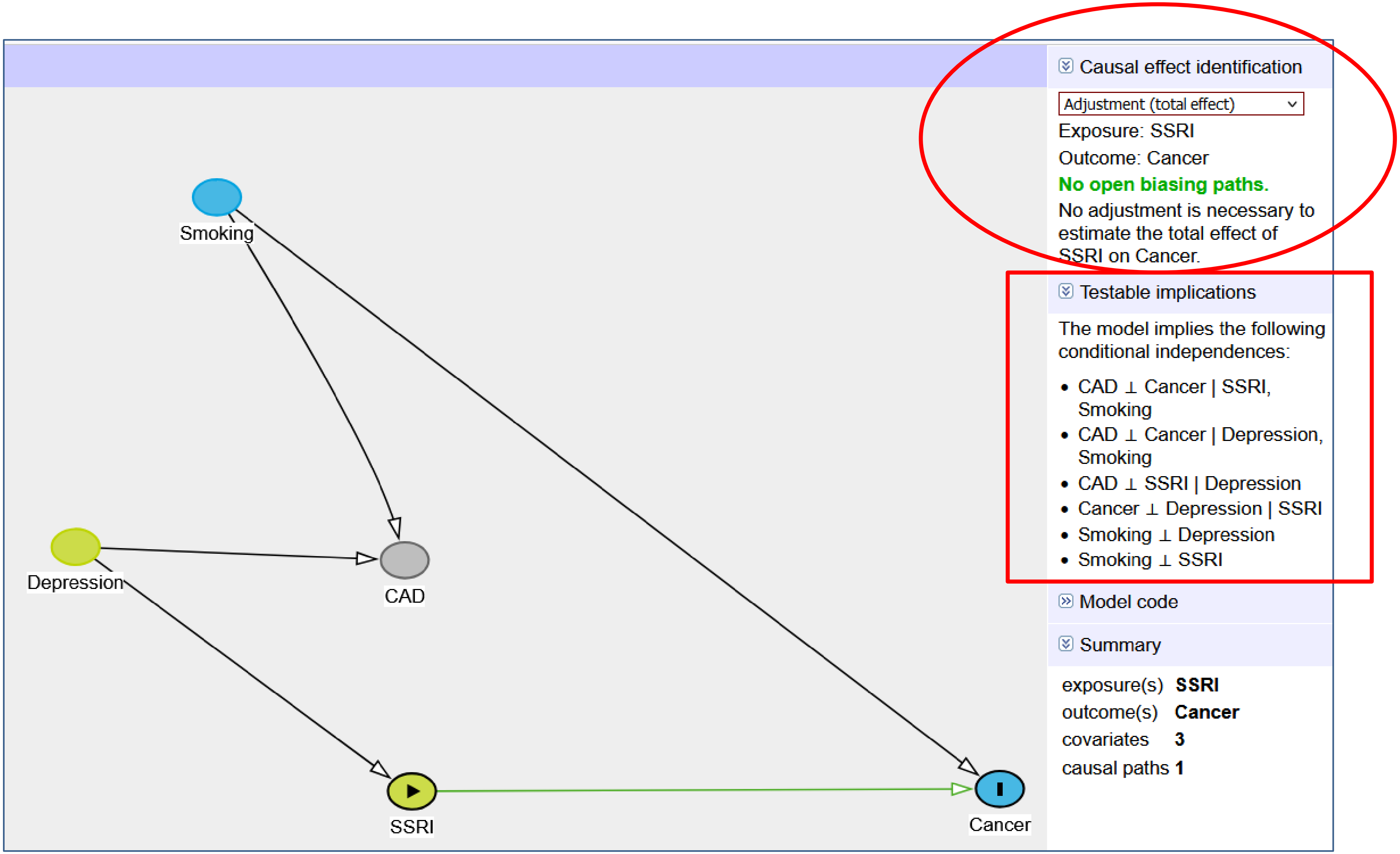

```
dag {
CAD [adjusted,pos="-0.995,-0.291"]
Cancer [outcome,pos="0.172,0.352"]
Depression [pos="-1.811,-0.446"]
SSRI [exposure,pos="-0.714,0.352"]
Smoking [pos="-1.817,-1.656"]
Depression -> CAD [pos="-1.177,-0.341"]
Depression -> SSRI
SSRI -> Cancer
Smoking -> CAD [pos="-1.154,-0.612"]
Smoking -> Cancer}
```

Unadjust for CAD

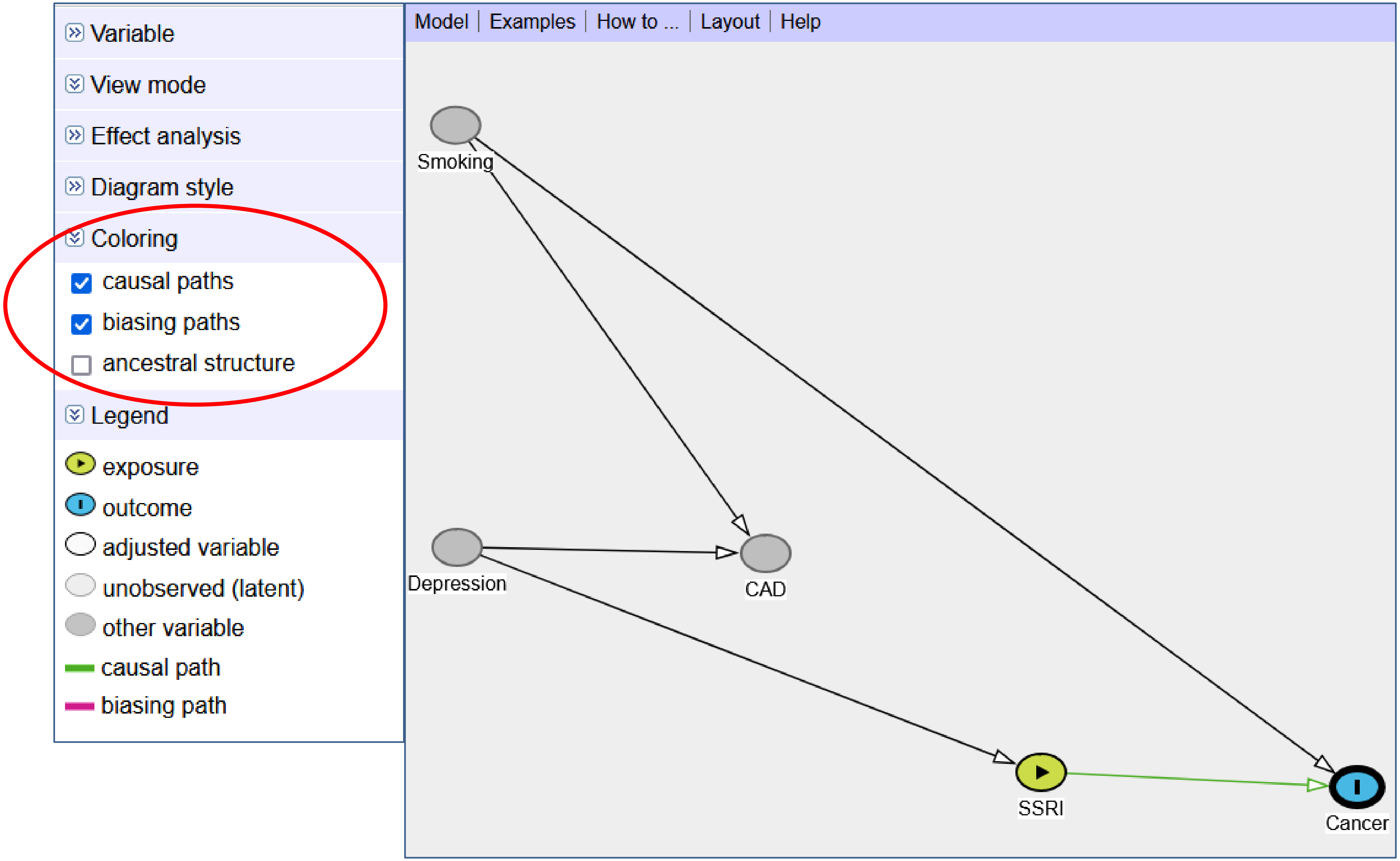



```
dag {
CAD [pos="-0.995,-0.291"]
Cancer [outcome,pos="0.172,0.352"]
Depression [pos="-1.811,-0.446"]
SSRI [exposure,pos="-0.714,0.352"]
Smoking [pos="-1.817,-1.656"]
Depression -> CAD
Depression -> SSRI
SSRI -> Cancer
Smoking -> CAD [pos="-1.154,-0.612"]
Smoking -> Cancer}
```

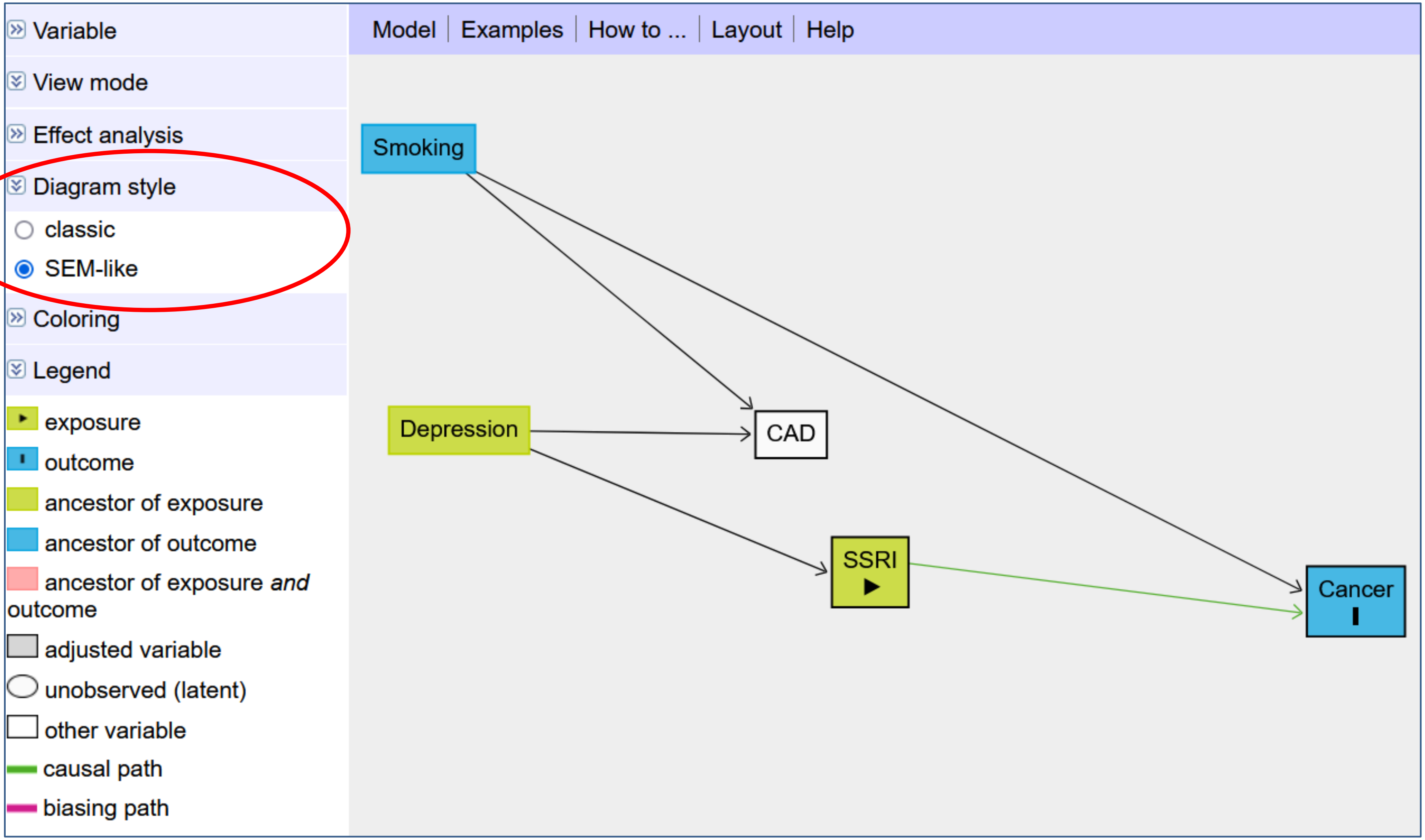
Look at the results



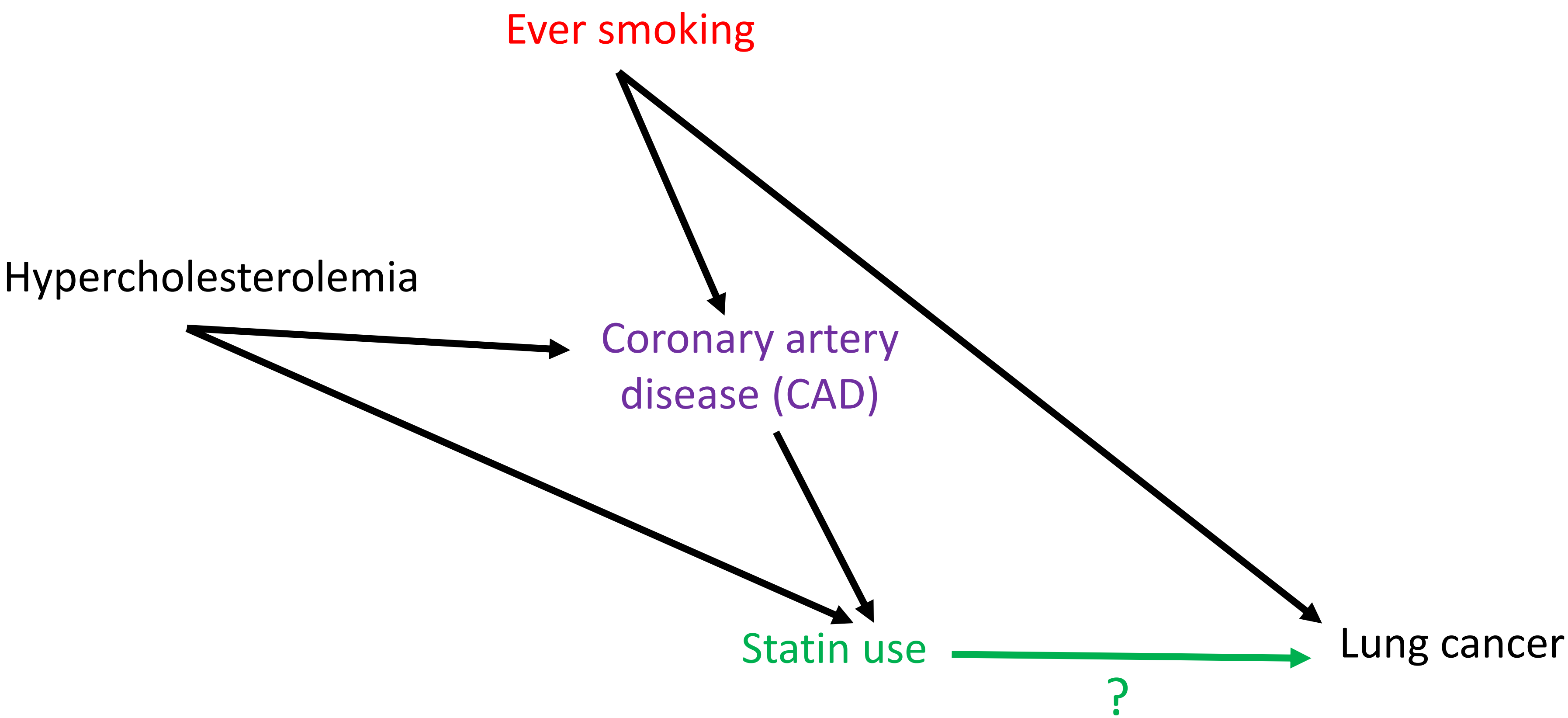
Possibility to not color anscestral structure



Possibility to display the DAG like a SEM



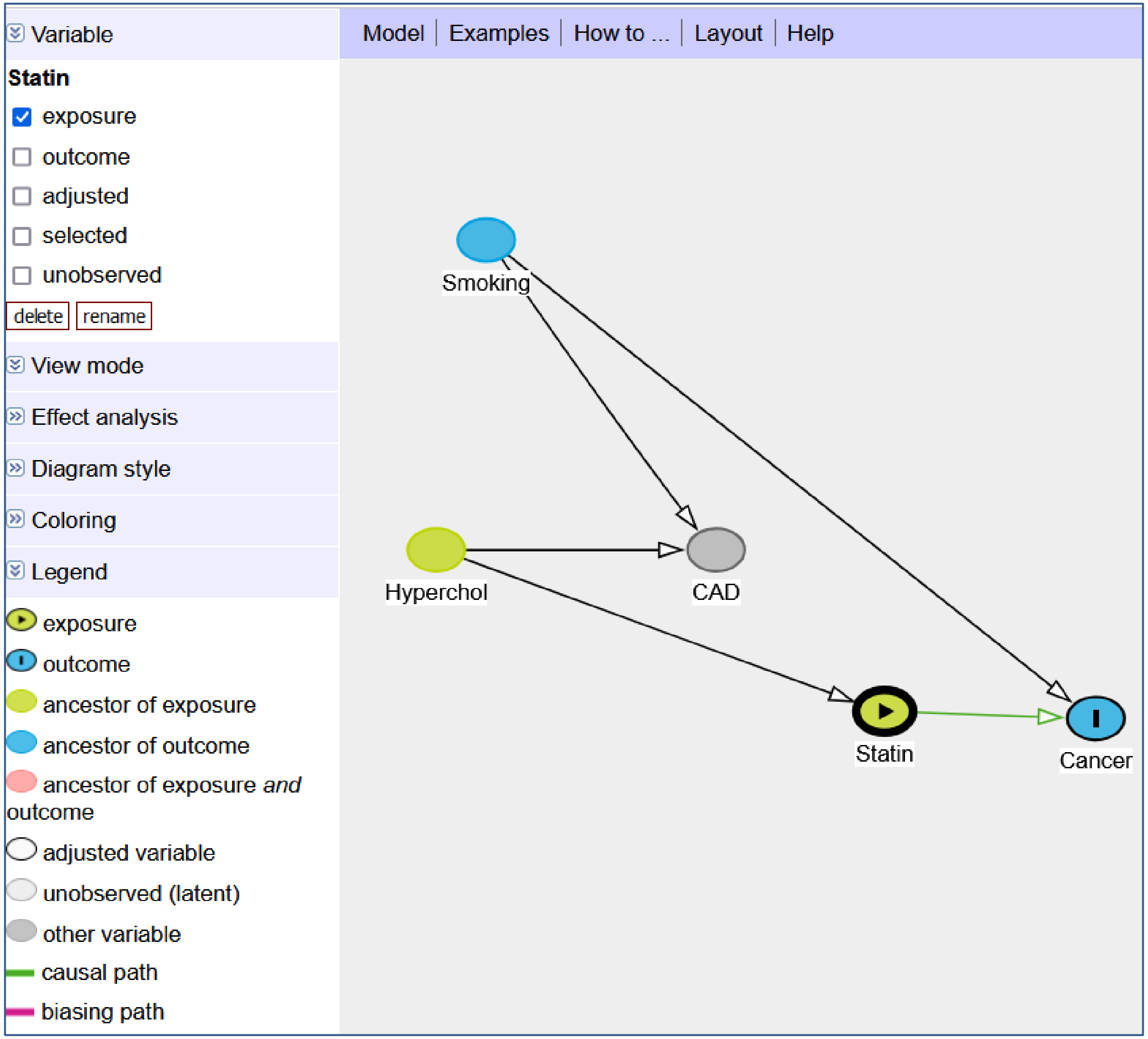
Example 2: Use of statin and lung cancer



Liu et al. Implication of M Biais in epidemiological studies: A simulation study. *Am J Epidemiol* 2012

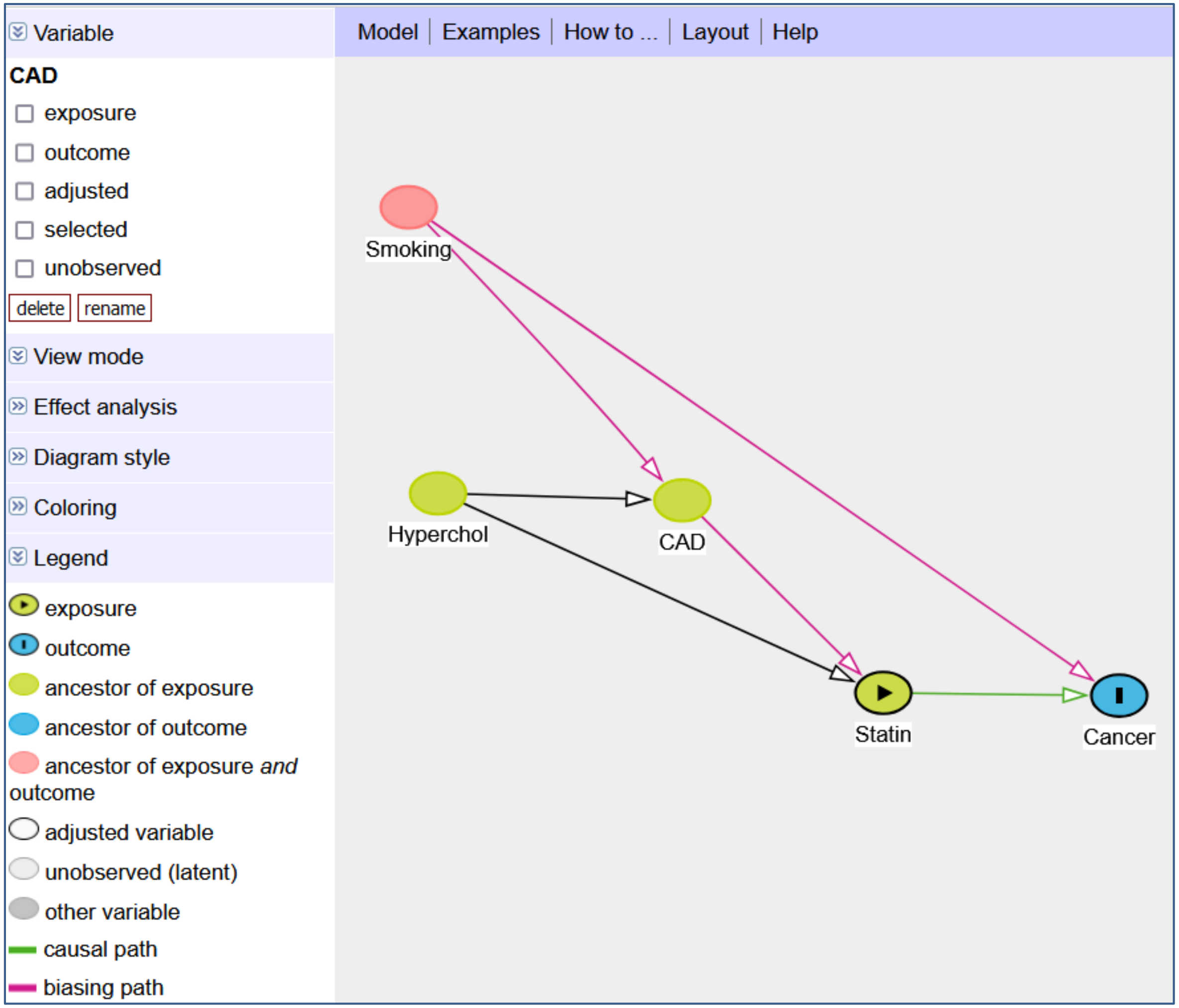
Take the code for the DAG of Example 1

Rename « Depression » as « Hyperchol » and « SSRI » as « Statin »



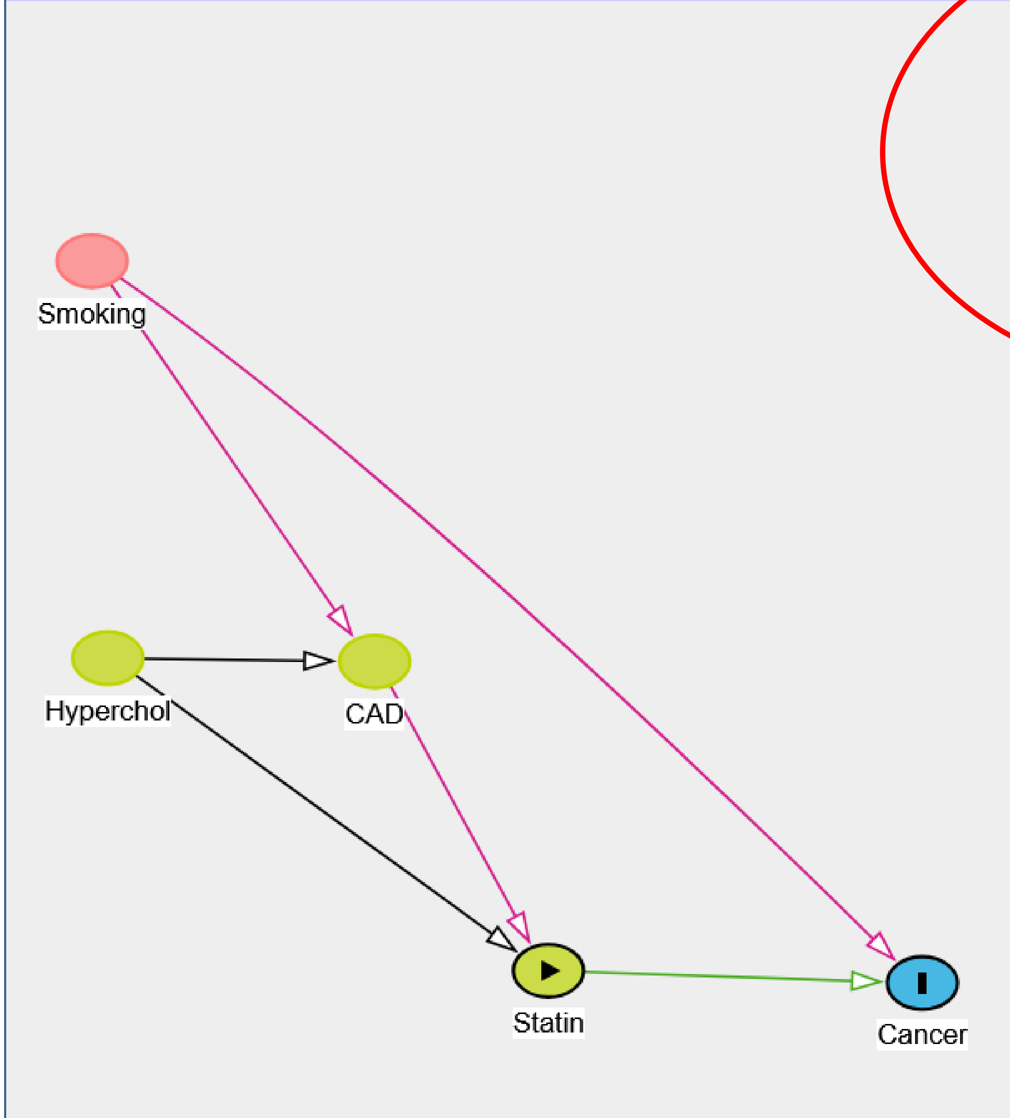

```
dag {
CAD [pos="-1.568,-0.469"]
Cancer [outcome,pos="-1.036,-0.014"]
Hyperchol [pos="-1.811,-0.446"]
Smoking [pos="-1.808,-1.416"]
Statin [exposure,pos="-1.412,-0.020"]
Hyperchol -> CAD
Hyperchol -> Statin
Smoking -> CAD [pos="-1.642,-0.822"]
Smoking -> Cancer
Statin -> Cancer
}
```

Add an arrow between CAD and statin




```
dag {
CAD [pos="-1.568,-0.469"]
Cancer [outcome,pos="-1.036,-0.014"]
Hyperchol [pos="-1.811,-0.446"]
Smoking [pos="-1.808,-1.416"]
Statin [exposure,pos="-1.412,-0.020"]
CAD -> Statin
Hyperchol -> CAD
Hyperchol -> Statin
Smoking -> CAD [pos="-1.642,-0.822"]
Smoking -> Cancer
Statin -> Cancer}
```

Look at the results



Causal effect identification

Adjustment (total effect)

Exposure: Statin

Outcome: Cancer

Biasing paths are open.

Minimal sufficient adjustment sets for estimating the total effect of Statin on Cancer:

- CAD, Hyperchol
- Smoking

Testable implications

The model implies the following conditional independences:

- CAD ⊥ Cancer | Smoking, Statin
- Cancer ⊥ Hyperchol | Smoking, Statin
- Smoking ⊥ Hyperchol
- Smoking ⊥ Statin | CAD, Hyperchol

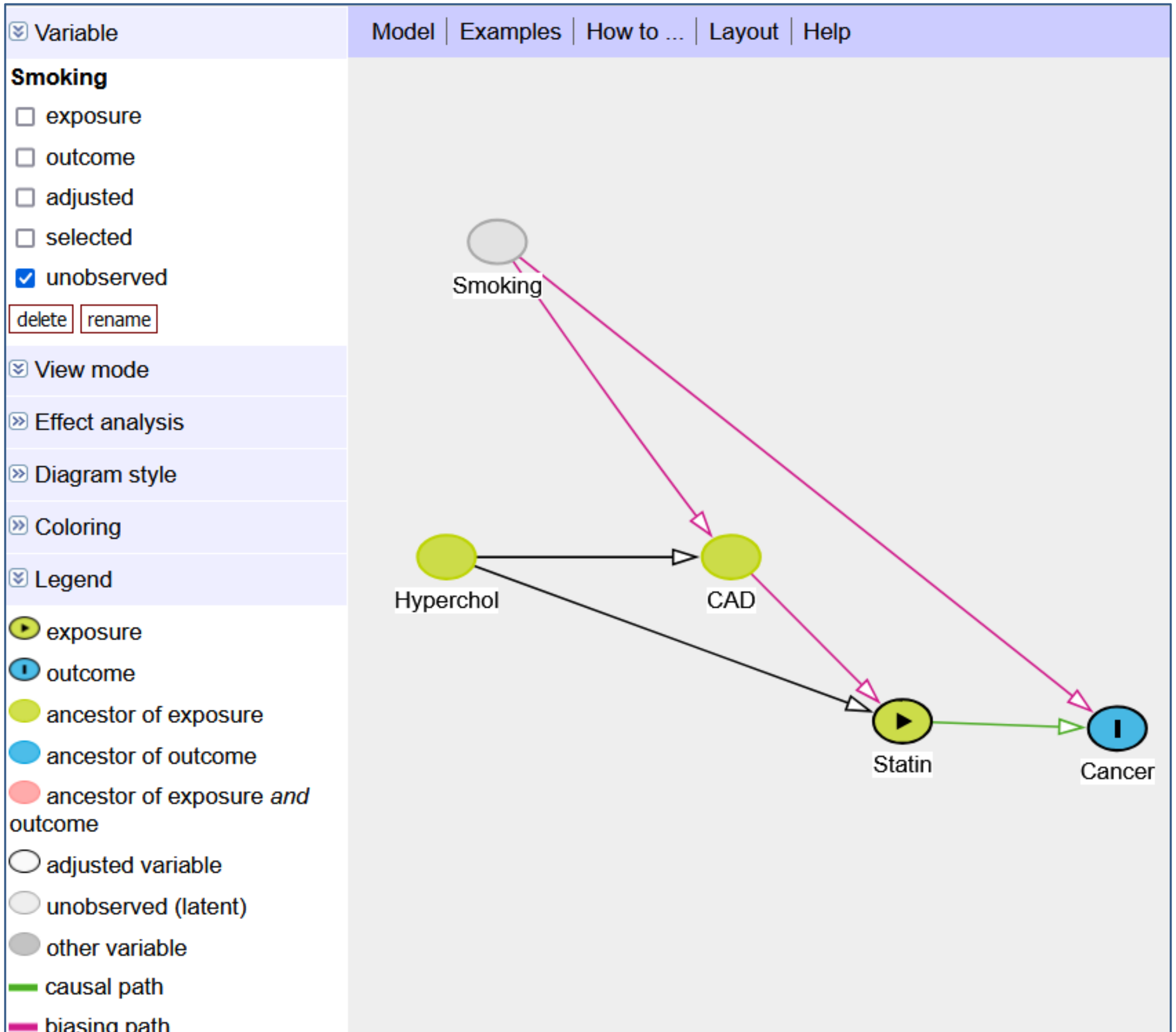
Model code

Summary

exposure(s)	**Statin**
outcome(s)	**Cancer**
covariates	**3**
causal paths	**1**

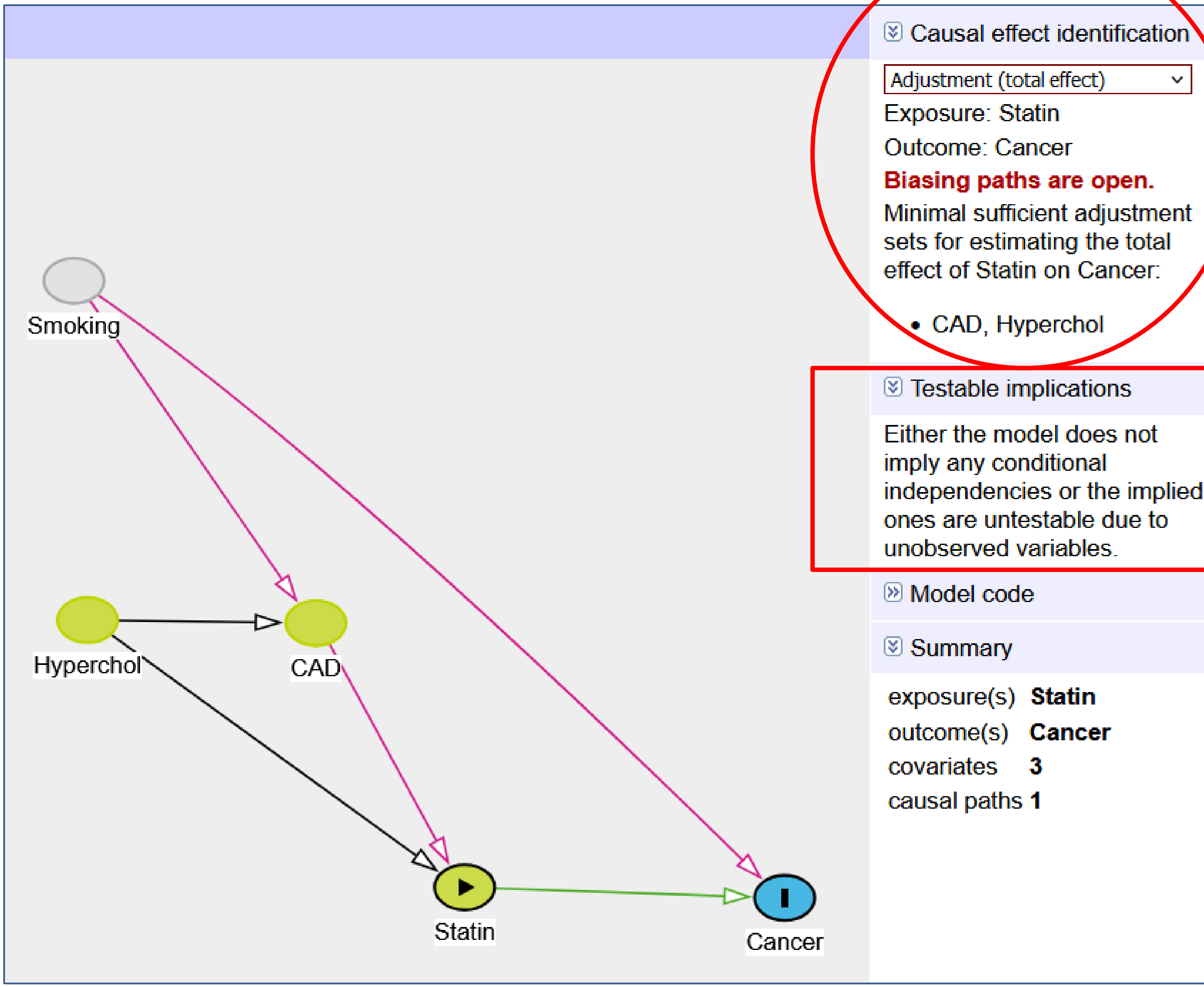
Unobserved (latent) variables

Take Example 2
Indicate that smoking is not observed



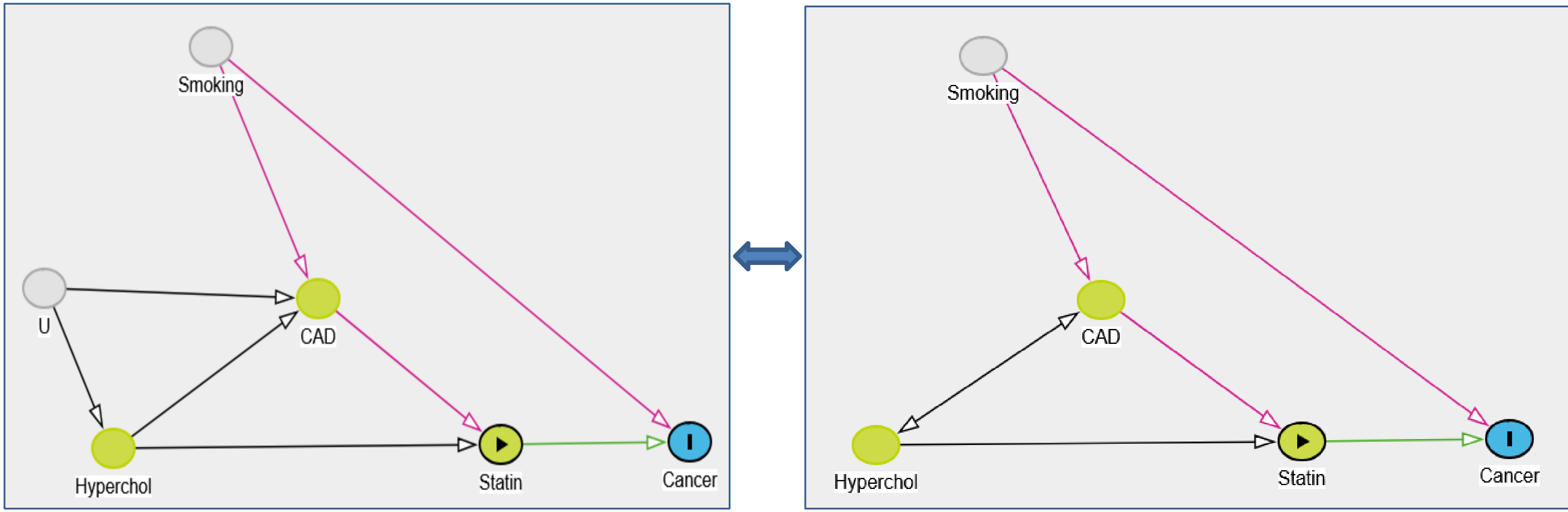

```
dag {
CAD [pos="-1.472,-0.764"]
Cancer [outcome,pos="-1.047,-0.386"]
Hyperchol [pos="-1.786,-0.764"]
Smoking [latent,pos="-1.730,-1.460"]
Statin [exposure,pos="-1.284,-0.402"]
CAD -> Statin
Hyperchol -> CAD
Hyperchol -> Statin
Smoking -> CAD [pos="-1.597,-1.082"]
Smoking -> Cancer
Statin -> Cancer}
```

Look at the results



If several unknown confounders between two variables

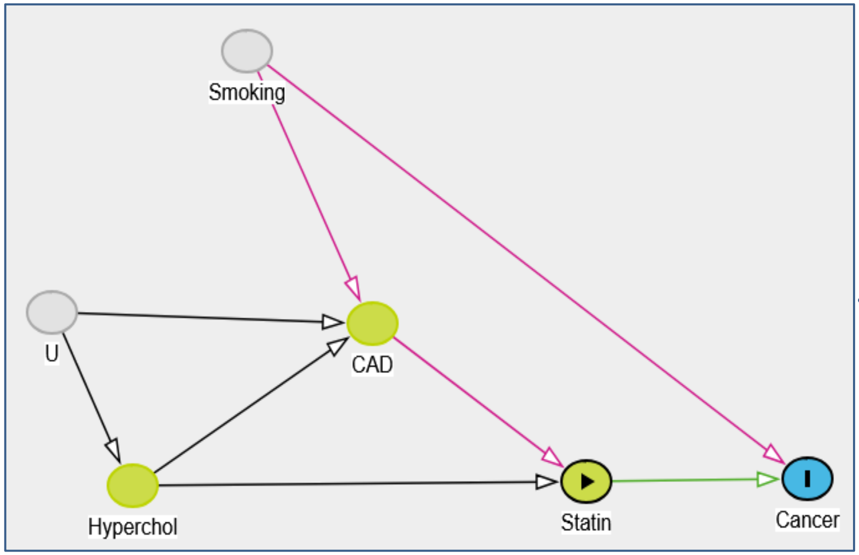
Example: between hyperchol and CAD

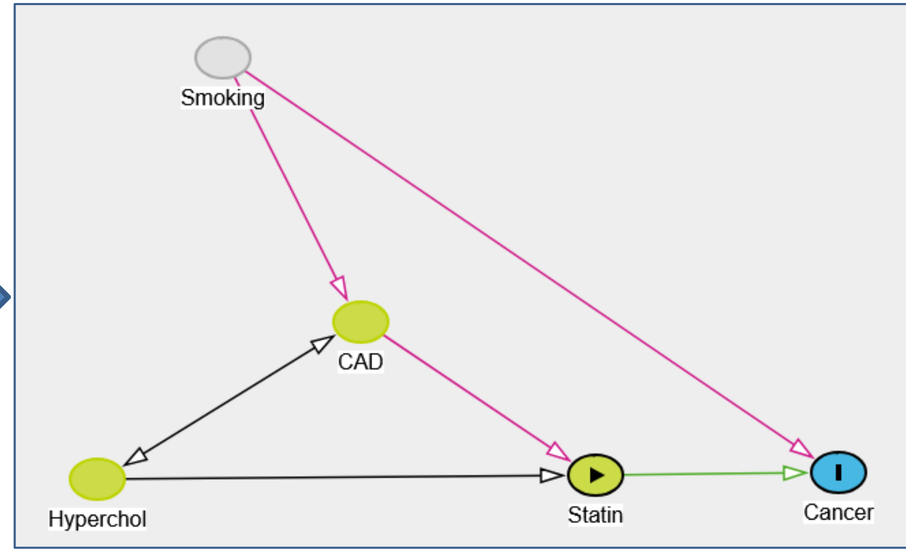



```
dag {
CAD [pos="-1.398,-0.977"]
Cancer [outcome,pos="-1.205,-0.817"]
Hyperchol [pos="-1.504,-0.810"]
Smoking [latent,pos="-1.463,-1.254"]
Statin [exposure,pos="-1.303,-0.814"]
U [latent,pos="-1.479,-0.977"]
CAD -> Statin
Hyperchol -> CAD
Hyperchol -> Statin
Smoking -> CAD
Smoking -> Cancer
Statin -> Cancer
U -> CAD
U -> Hyperchol}
```

```
dag {
CAD [pos="-1.398,-0.977"]
Cancer [outcome,pos="-1.205,-0.817"]
Hyperchol [pos="-1.504,-0.810"]
Smoking [latent,pos="-1.454,-1.258"]
Statin [exposure,pos="-1.303,-0.814"]
CAD -> Statin
CAD <-> Hyperchol
Hyperchol -> Statin
Smoking -> CAD
Smoking -> Cancer
Statin -> Cancer}
```

Look at the results





Causal effect identification

Adjustment (total effect)

Exposure: Statin

Outcome: Cancer

Biasing paths are open.

Minimal sufficient adjustment sets for estimating the total effect of Statin on Cancer:

- CAD, Hyperchol

Testable implications

Either the model does not imply any conditional independencies or the implied ones are untestable due to unobserved variables.

Causal effect identification

Adjustment (total effect)

Exposure: Statin

Outcome: Cancer

Biasing paths are open.

Minimal sufficient adjustment sets for estimating the total effect of Statin on Cancer:

- CAD, Hyperchol

Testable implications

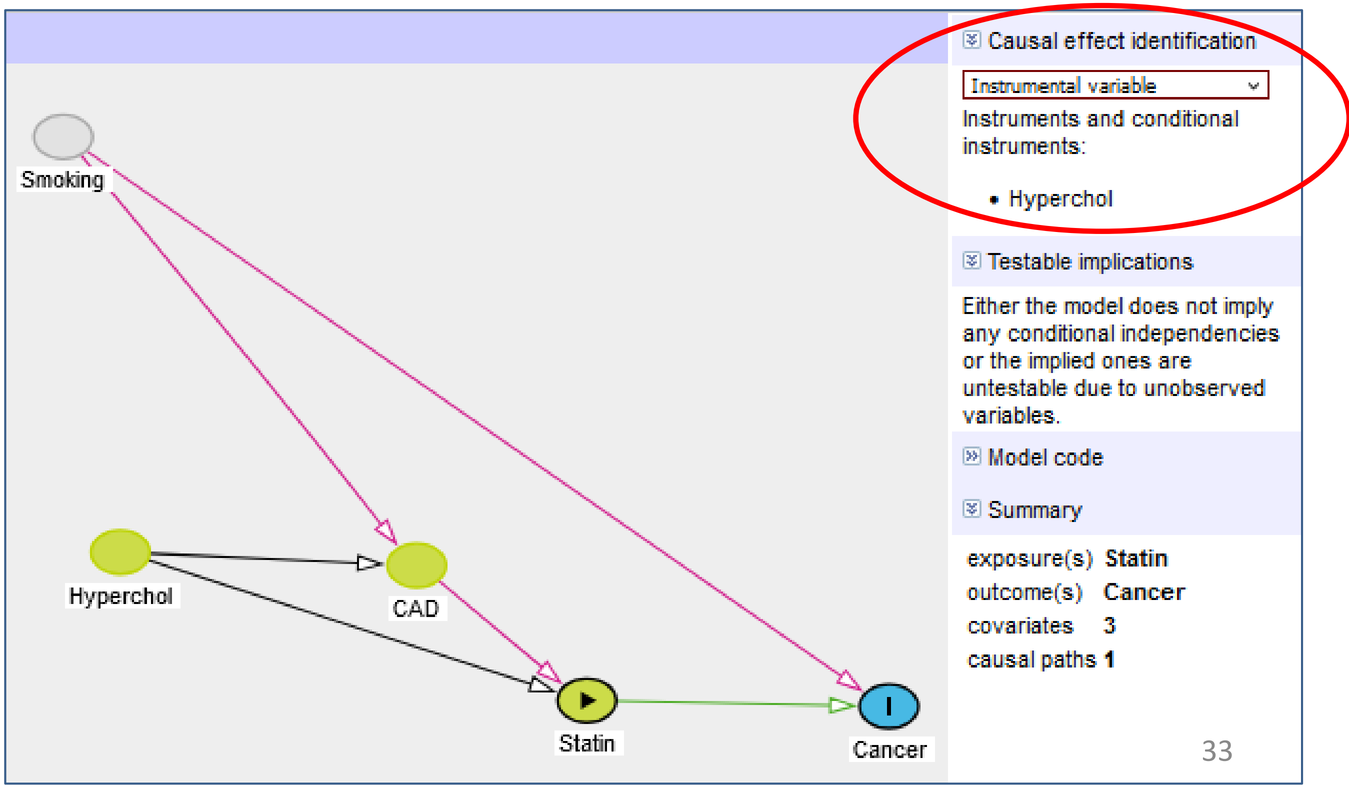
Either the model does not imply any conditional independencies or the implied ones are untestable due to unobserved variables.

Instrumental variables

Ask to display instrumental variables

Take Example 2: Smoking still unobserved

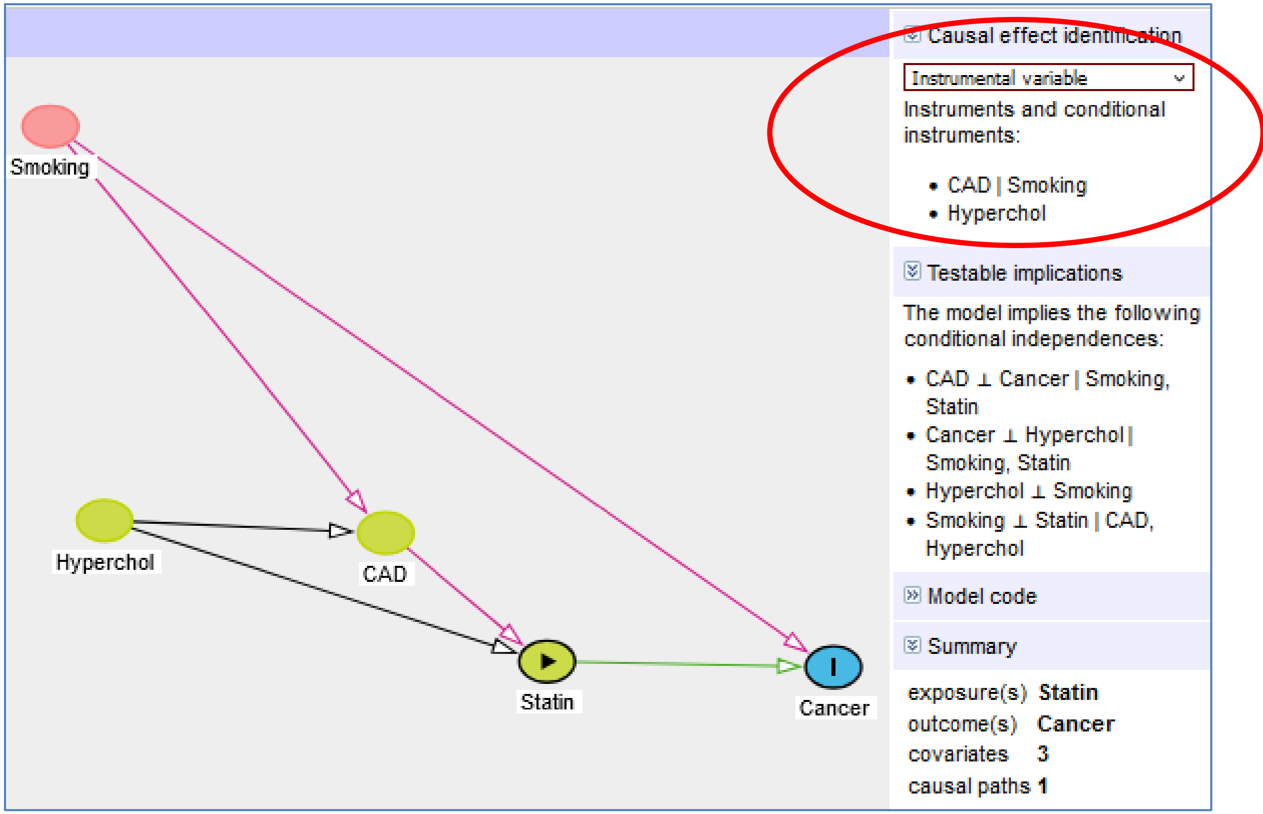
- Instrumental variable (or instrument I)
    1. There must be an open path between *I* and the exposure *X* (exogeneity); and
    2. All paths between *I* and the outcome *Y* must be closed in a modified graph where all edges out of *X* are removed (exclusion restriction)
- Conditional instrument
    1. There must be a path between *I* and *X* that is opened by **Z**; and
    2. All paths between *I* and *Y* must be closed by **Z** in a modified graph where all edges out of *X* are removed.



Ask to display instrumental variables

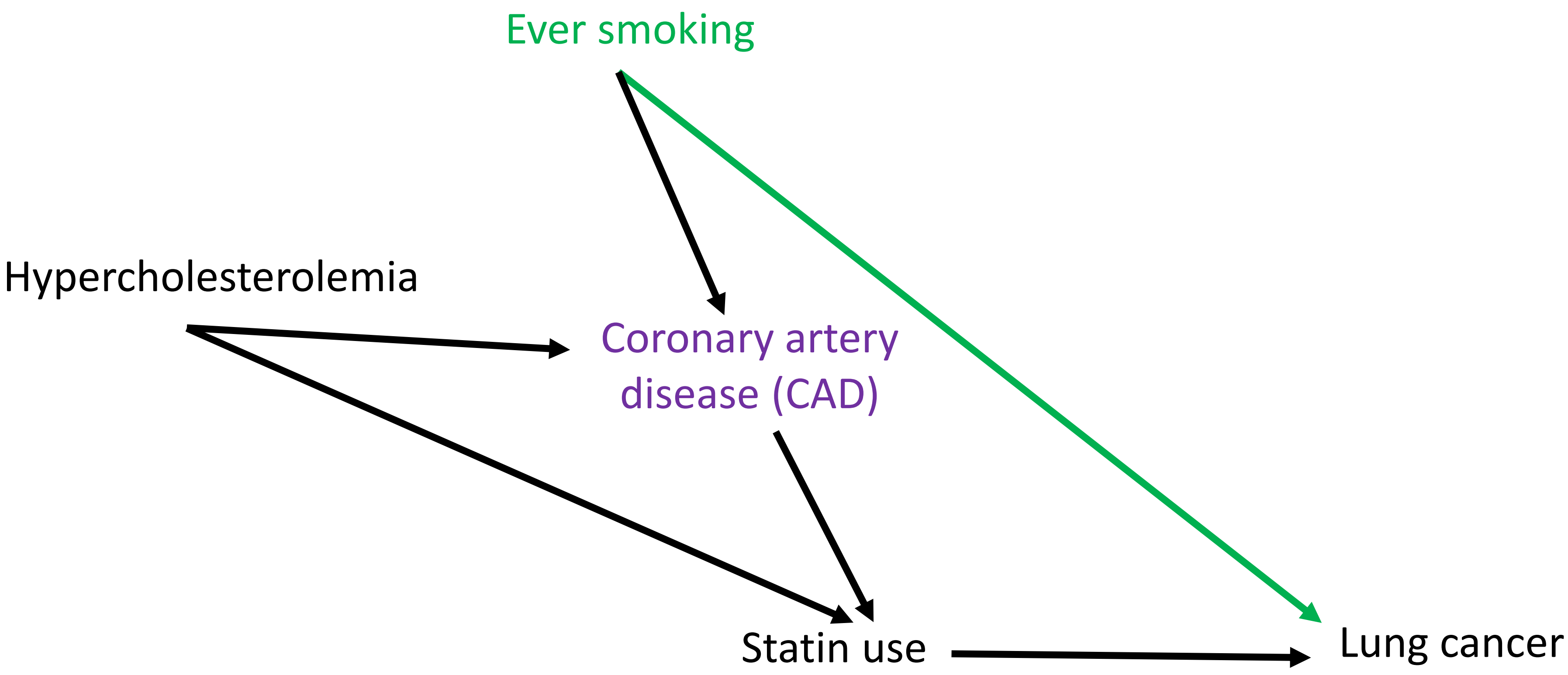
Take Example 2: Smoking observed

- Instrumental variable (or instrument I)
  1. There must be an open path between *I* and the exposure *X* (exogeneity); and
  2. All paths between *I* and the outcome *Y* must be closed in a modified graph where all edges out of *X* are removed (exclusion restriction)
- Conditional instrument
  1. There must be a path between *I* and *X* that is opened by **Z**; and
  2. All paths between *I* and *Y* must be closed by **Z** in a modified graph where all edges out of *X* are removed.



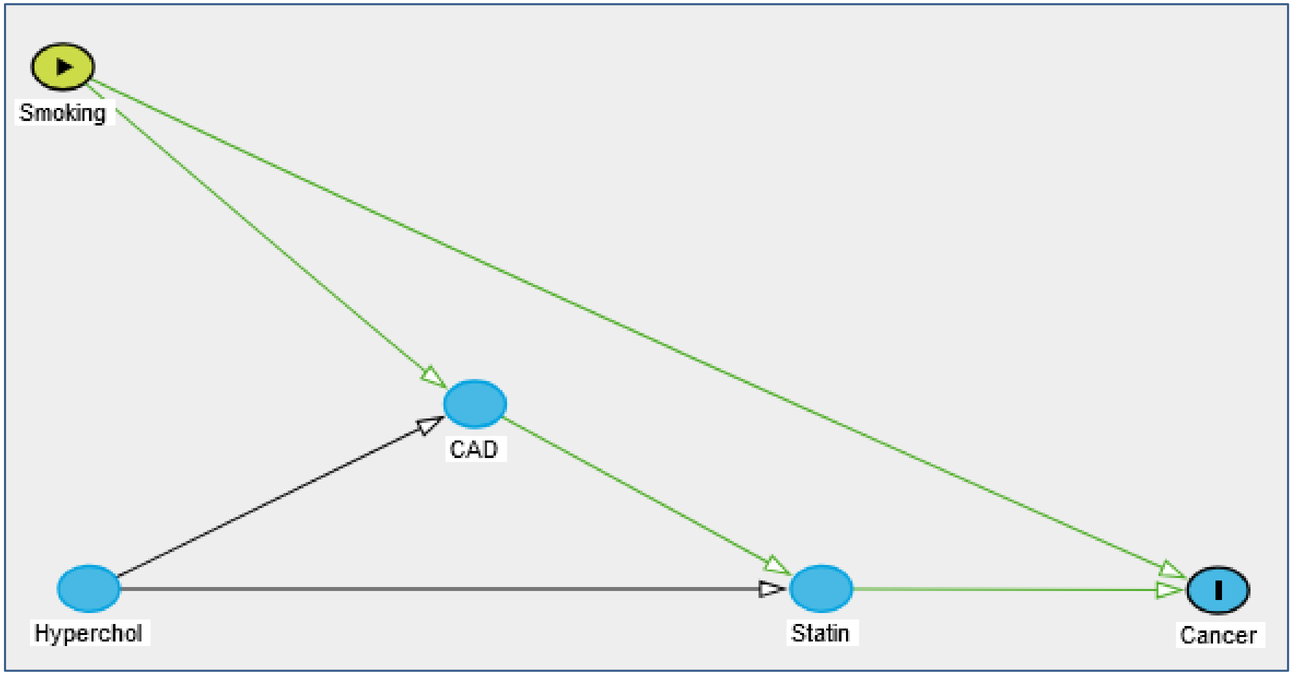
Direct effects

Example 3: Smoking and lung cancer



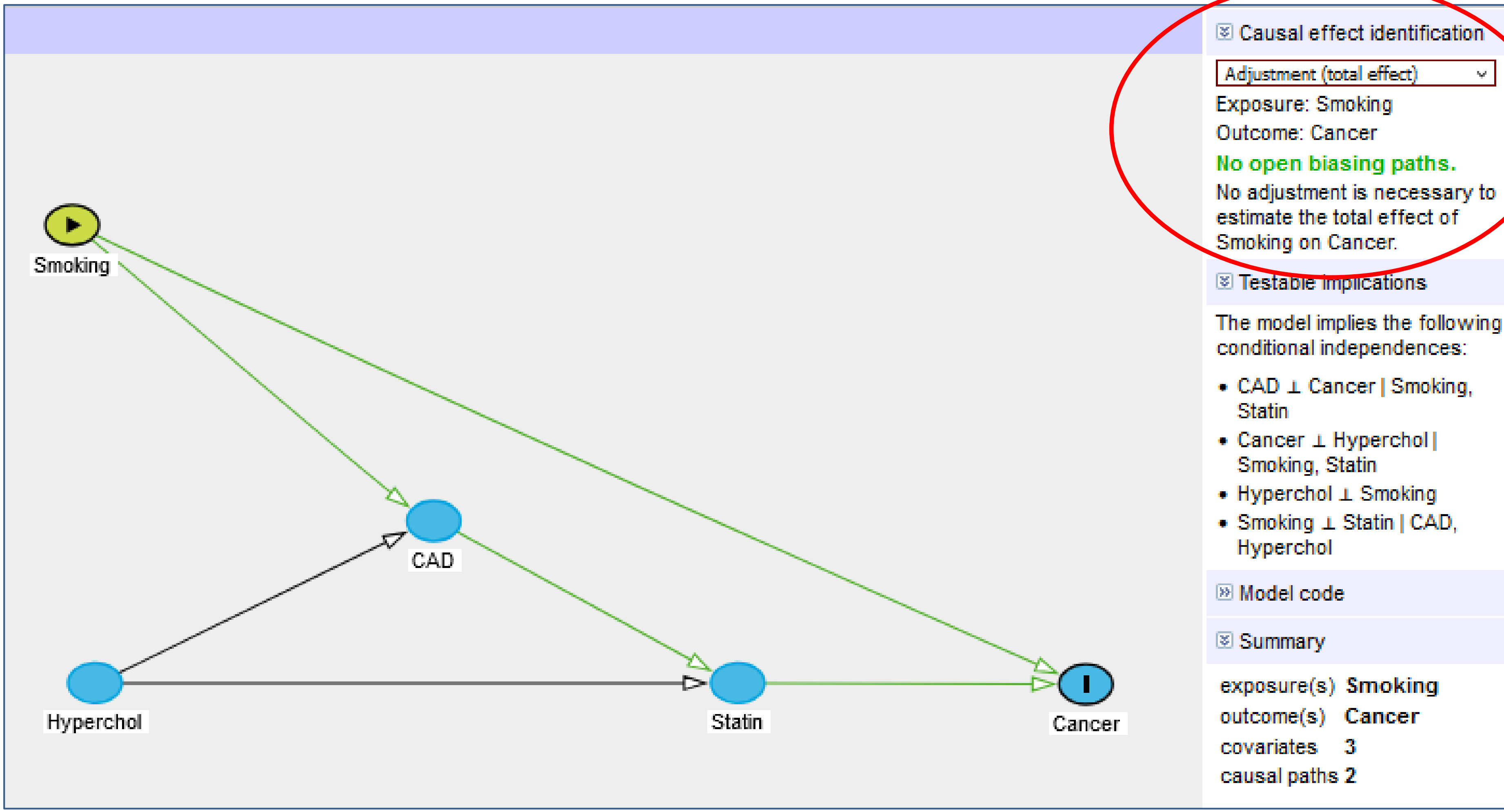
Take the model code for DAG of Example 2

Set Smoking as the observed Exposure

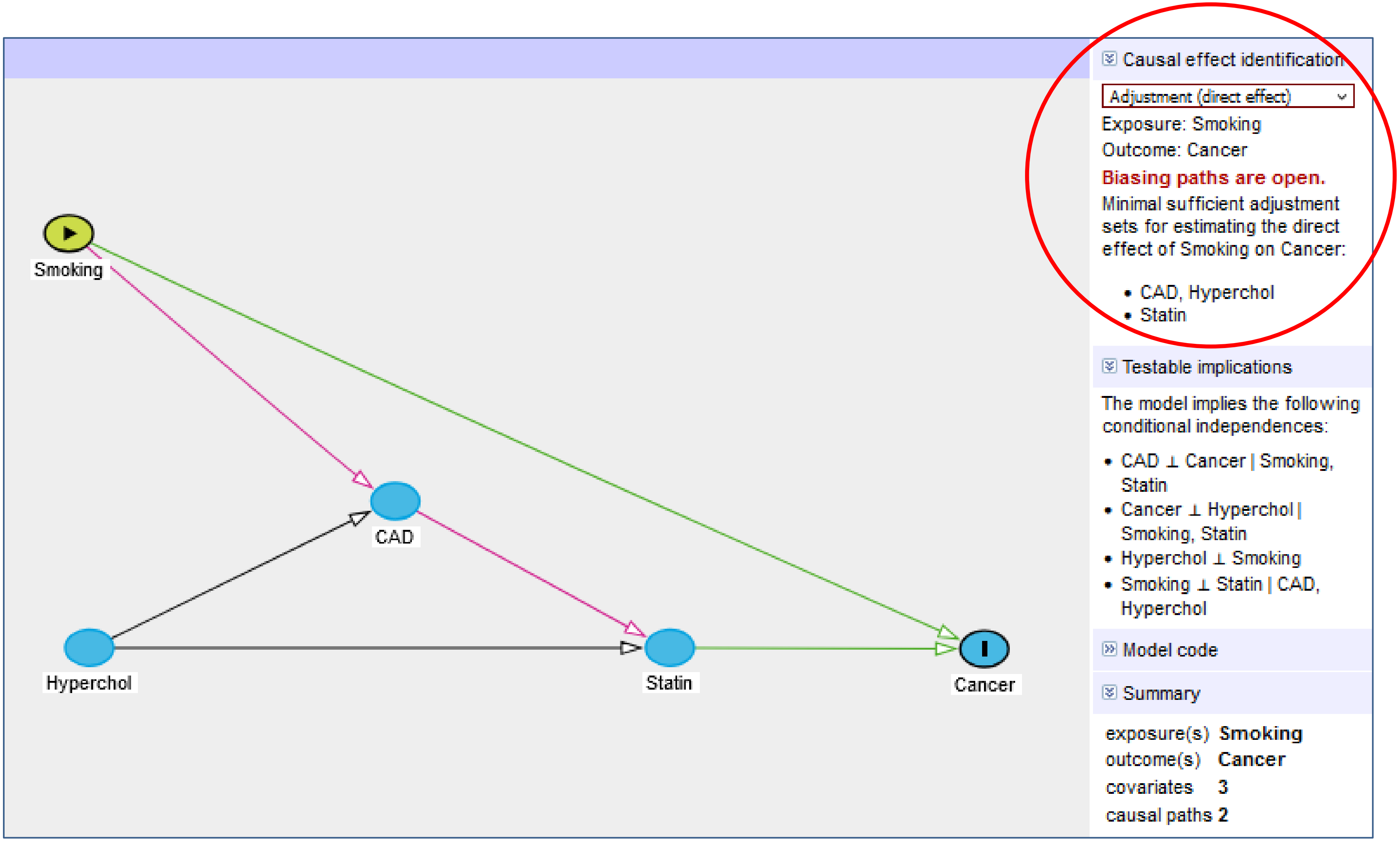



```
dag {
CAD [pos="-1.287,-1.077"]
Cancer [outcome,pos="-1.050,-0.923"]
Hyperchol [pos="-1.391,-0.902"]
Smoking [exposure,pos="-1.394,-1.420"]
Statin [pos="-1.182,-0.930"]
CAD -> Statin
Hyperchol -> CAD
Hyperchol -> Statin
Smoking -> CAD [pos="-1.348,-1.268"]
Smoking -> Cancer [pos="-1.235,-1.204"]
Statin -> Cancer}
```

Look at the results

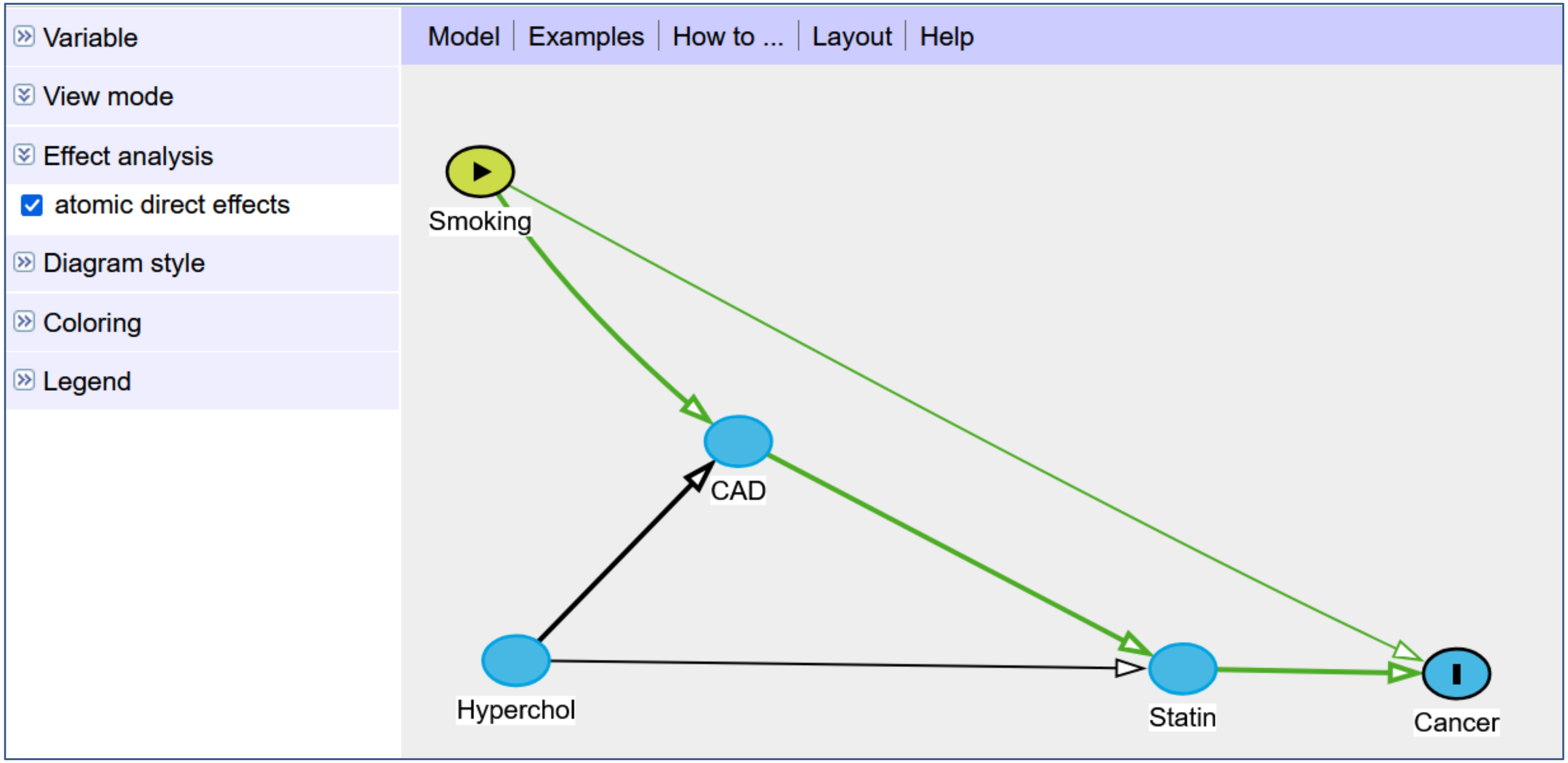


Display adjustment set to estimate the direct effect of smoking



What are atomic direct effects?

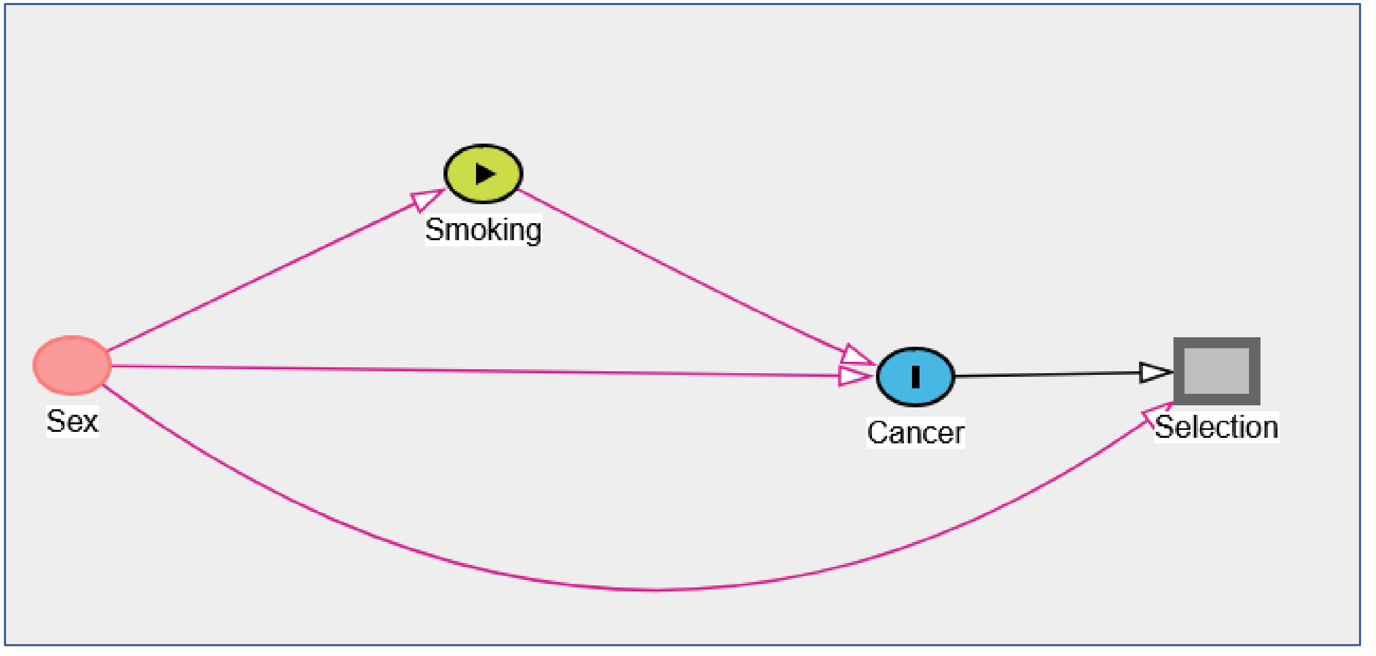
- Arrows (in bold) for which there is no corresponding indirect path
- Removing one of these arrows from the diagram means that there will no longer be any causal effect between the corresponding variables.



Selection bias

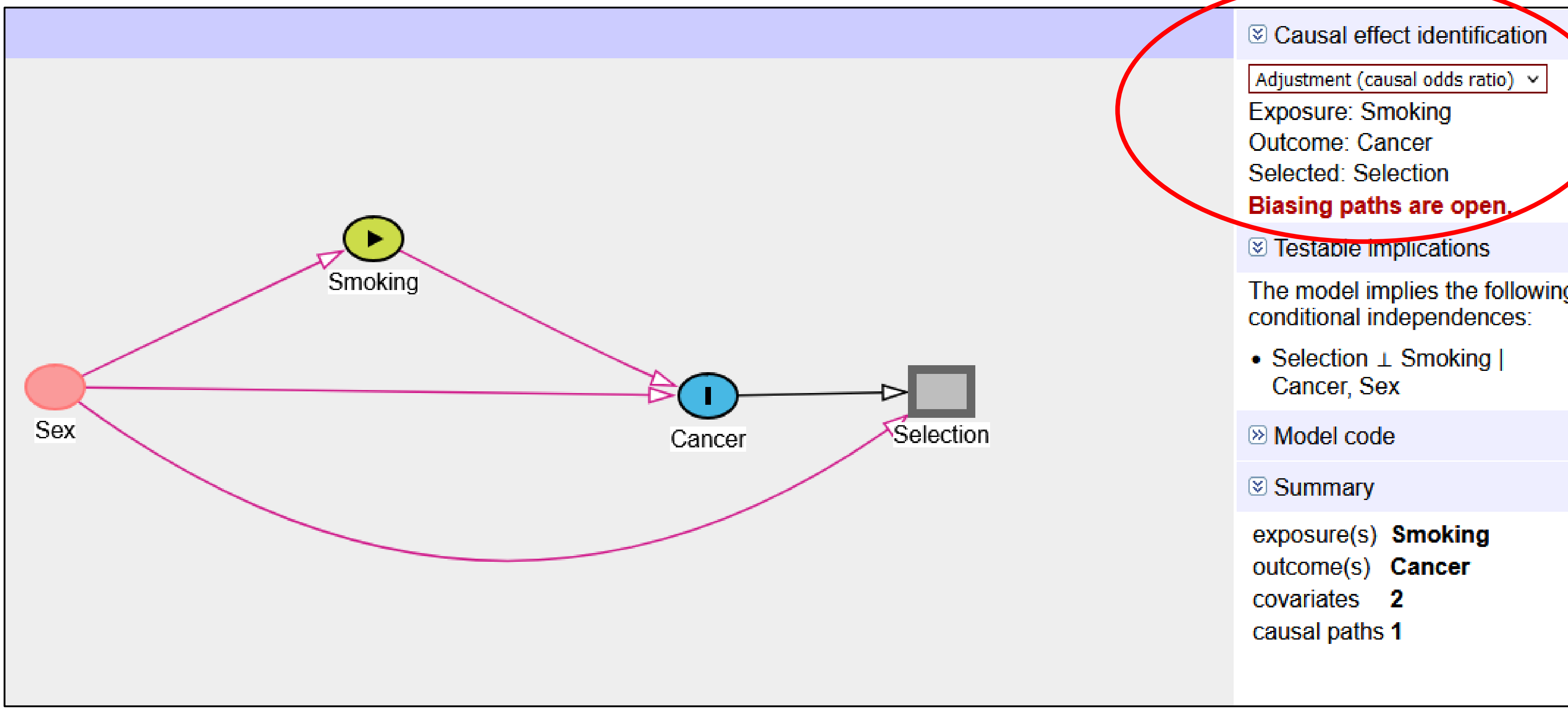
Exemple 4

A case-control study on smoking and lung cancer, matched on sex, with sex a true confounder

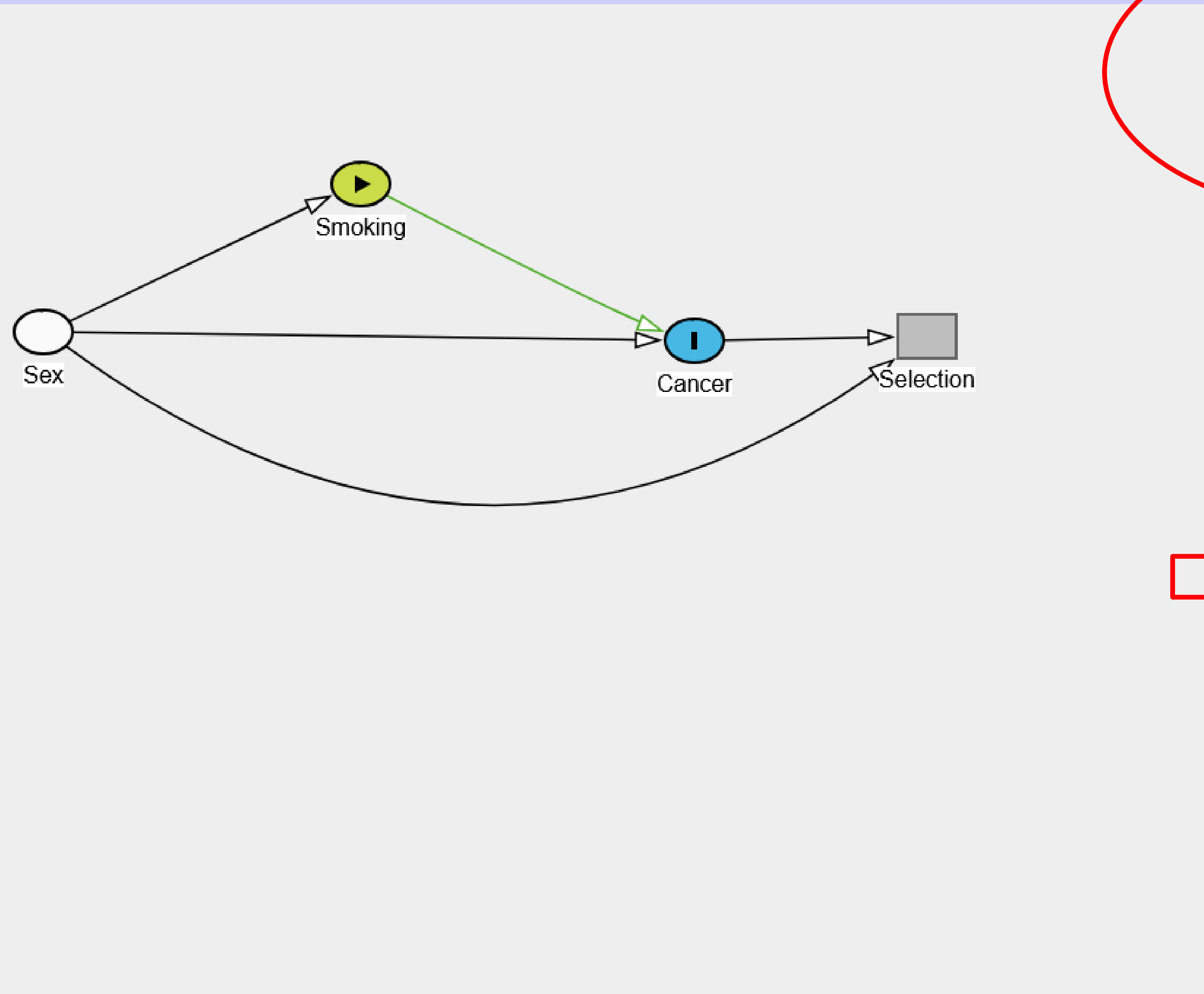



```
dag {
Cancer [outcome,pos="-1.081,-1.335"]
Selection [selected,pos="-1.073,-1.335"]
Sex [pos="-1.105,-1.335"]
Smoking [exposure,pos="-1.093,-1.347"]
Cancer -> Selection
Sex -> Cancer
Sex -> Selection [pos="-1.089,-1.309"]
Sex -> Smoking
Smoking -> Cancer [pos="-1.085,-1.337"]}
```

Look at the results: adjustment for causal odds ratio



Need to adjust for the matching factor (sex)



Causal effect identification

Adjustment (causal odds ratio)

Exposure: Smoking
Outcome: Cancer
Selected: Selection
Adjusted: Sex
Correctly adjusted.

Testable implications

The model implies the following conditional independences:

- Selection ⊥ Smoking | Cancer, Sex

Model code

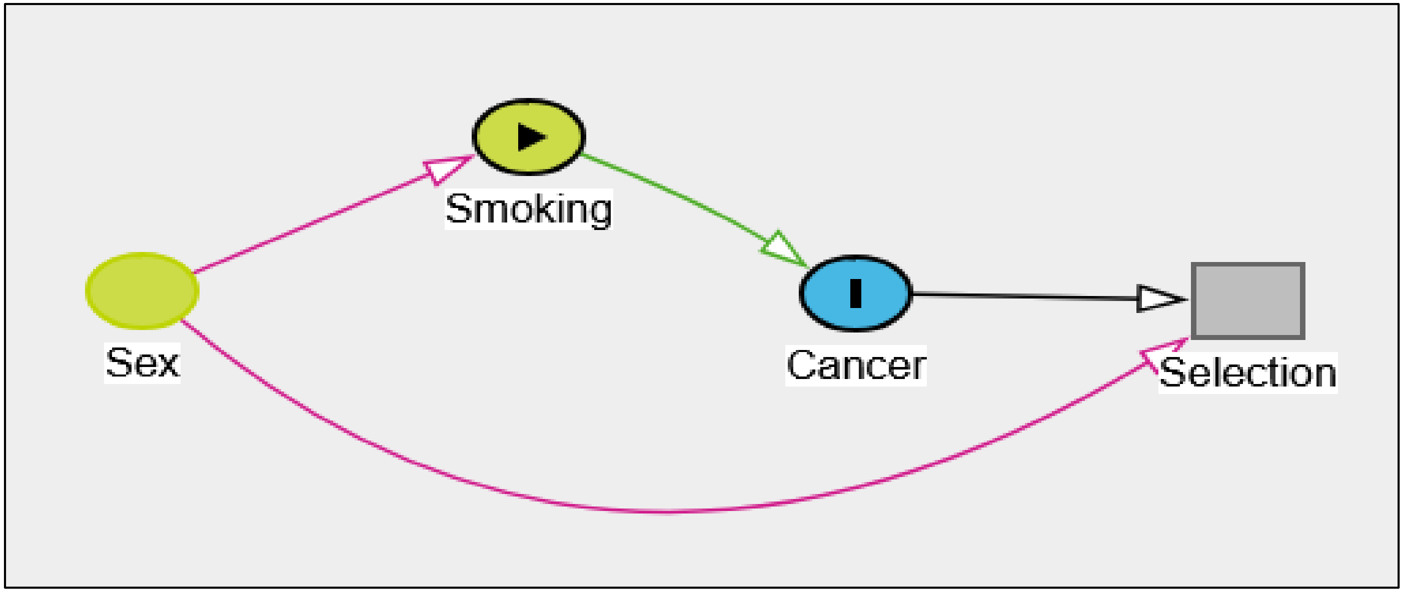
```
dag {
Cancer
[outcome,pos="-1.081,-1.335"]
Selection
[selected,pos="-1.073,-1.335"]
Sex
[adjusted,pos="-1.105,-1.335"]
Smoking
[exposure,pos="-1.093,-1.347"]
Cancer -> Selection
Sex -> Cancer
Sex -> Selection
[pos="-1.089,-1.309"]
Sex -> Smoking
Smoking -> Cancer
[pos="-1.085,-1.337"]
}
```

Summary

exposure(s)	**Smoking**
outcome(s)	**Cancer**
covariates	**2**
causal paths	**1**

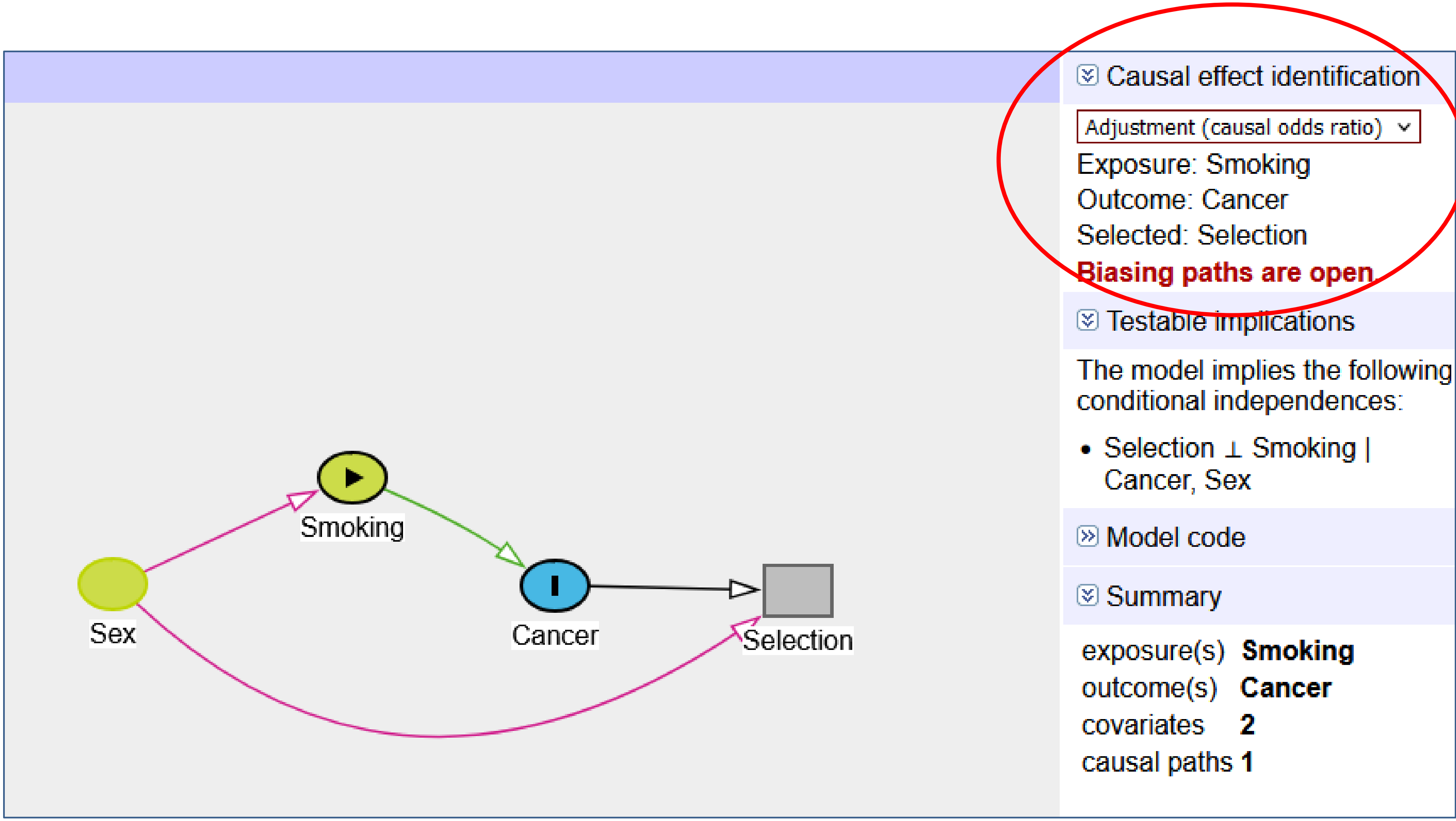
Exemple 5

A case-control study on smoking and lung cancer, matched on sex, with sex a cause of exposure but not of the outcome

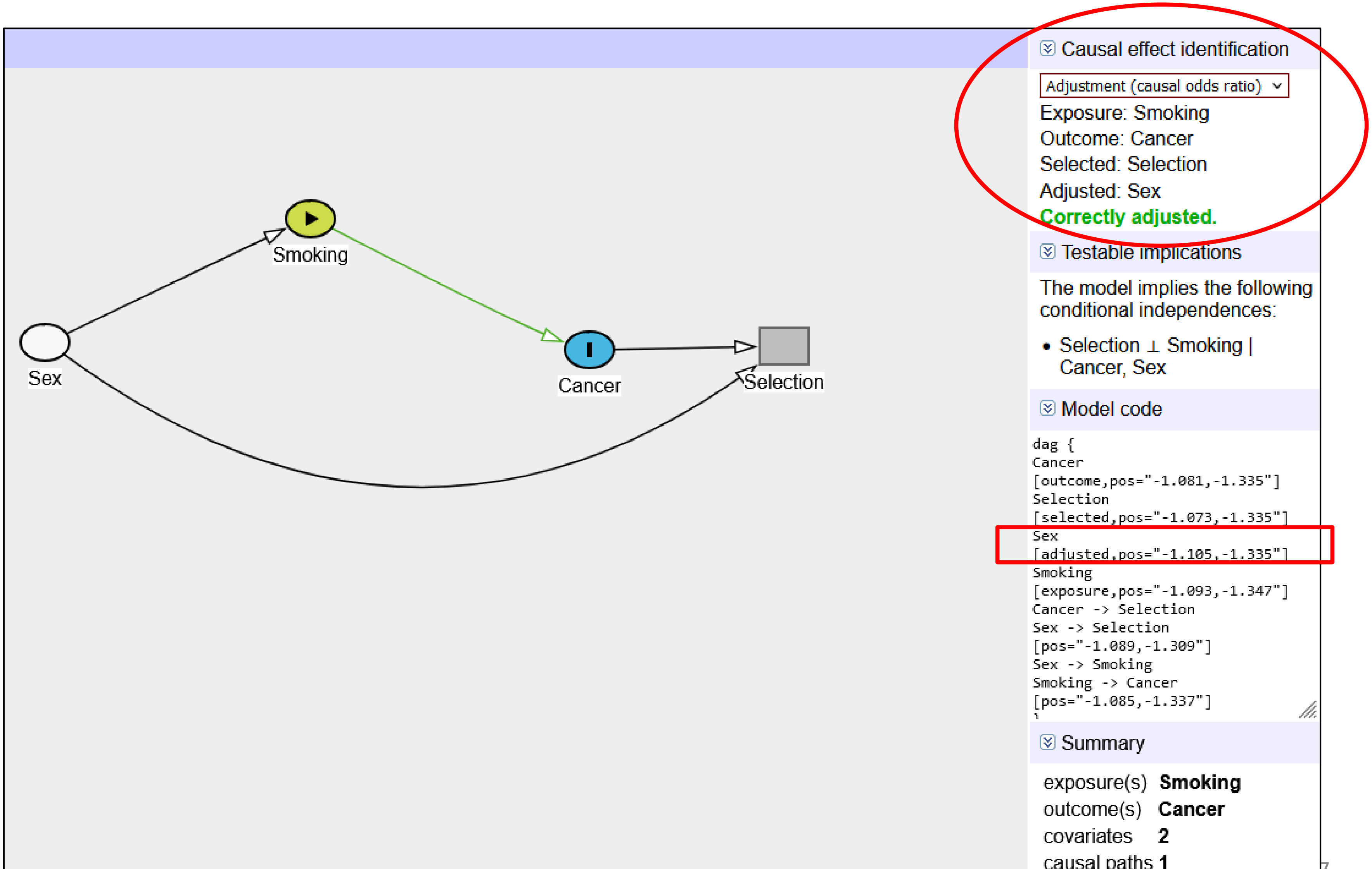



```
dag {
Cancer [outcome,pos="-1.078,-1.344"]
Selection [selected,pos="-1.073,-1.344"]
Sex [pos="-1.085,-1.344"]
Smoking [exposure,pos="-1.083,-1.346"]
Cancer -> Selection
Sex -> Selection [pos="-1.081,-1.341"]
Sex -> Smoking
Smoking -> Cancer [pos="-1.080,-1.345"]}
```

Look at the results

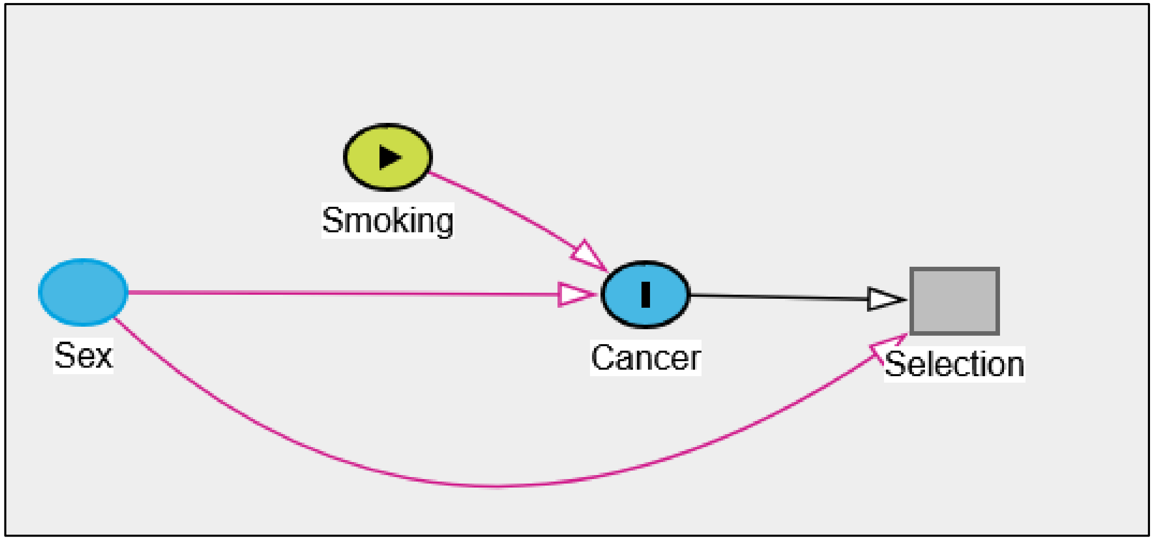


Need to adjust for the matching factor (sex)



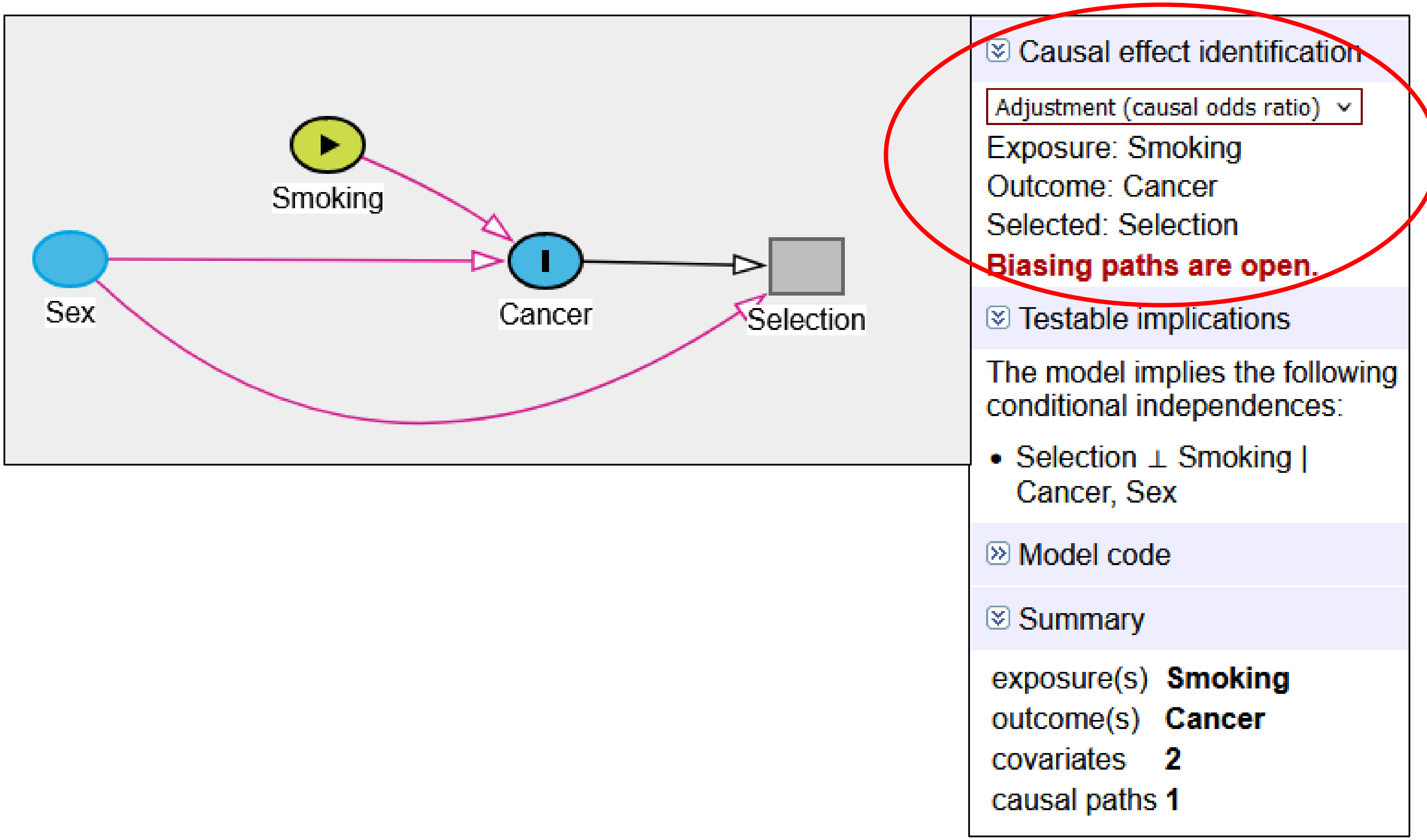
Exemple 6

A case-control study on smoking and lung cancer, matched on sex, with sex a cause of the outcome but not of exposure

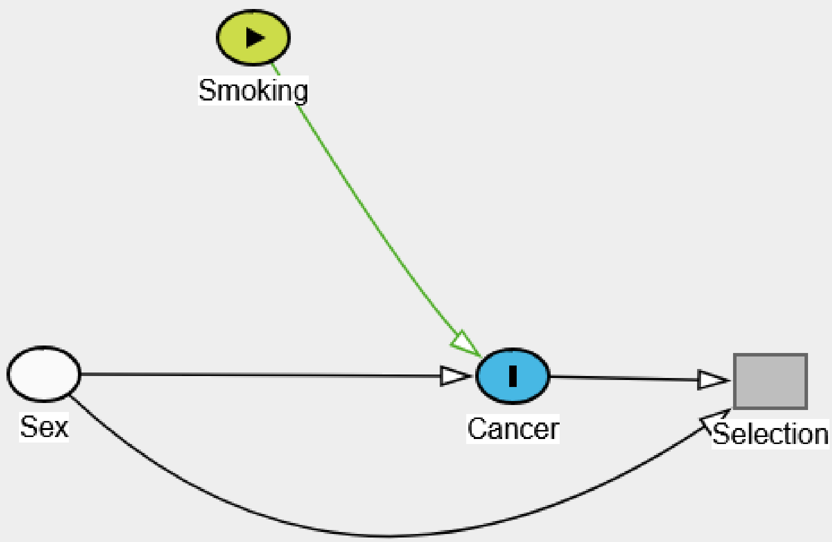



```
dag {
Cancer [outcome,pos="-1.079,-1.343"]
Selection [selected,pos="-1.076,-1.343"]
Sex [pos="-1.085,-1.344"]
Smoking [exposure,pos="-1.082,-1.345"]
Cancer -> Selection
Sex -> Cancer
Sex -> Selection [pos="-1.081,-1.341"]
Smoking -> Cancer [pos="-1.080,-1.344"]}
```

Look at the results



Need to adjust for the matching factor (sex)



Causal effect identification

Adjustment (causal odds ratio)

Exposure: Smoking
Outcome: Cancer
Selected: Selection
Adjusted: Sex
Correctly adjusted.

Testable implications

The model implies the following conditional independences:

- Selection ⊥ Smoking | Cancer, Sex

Model code

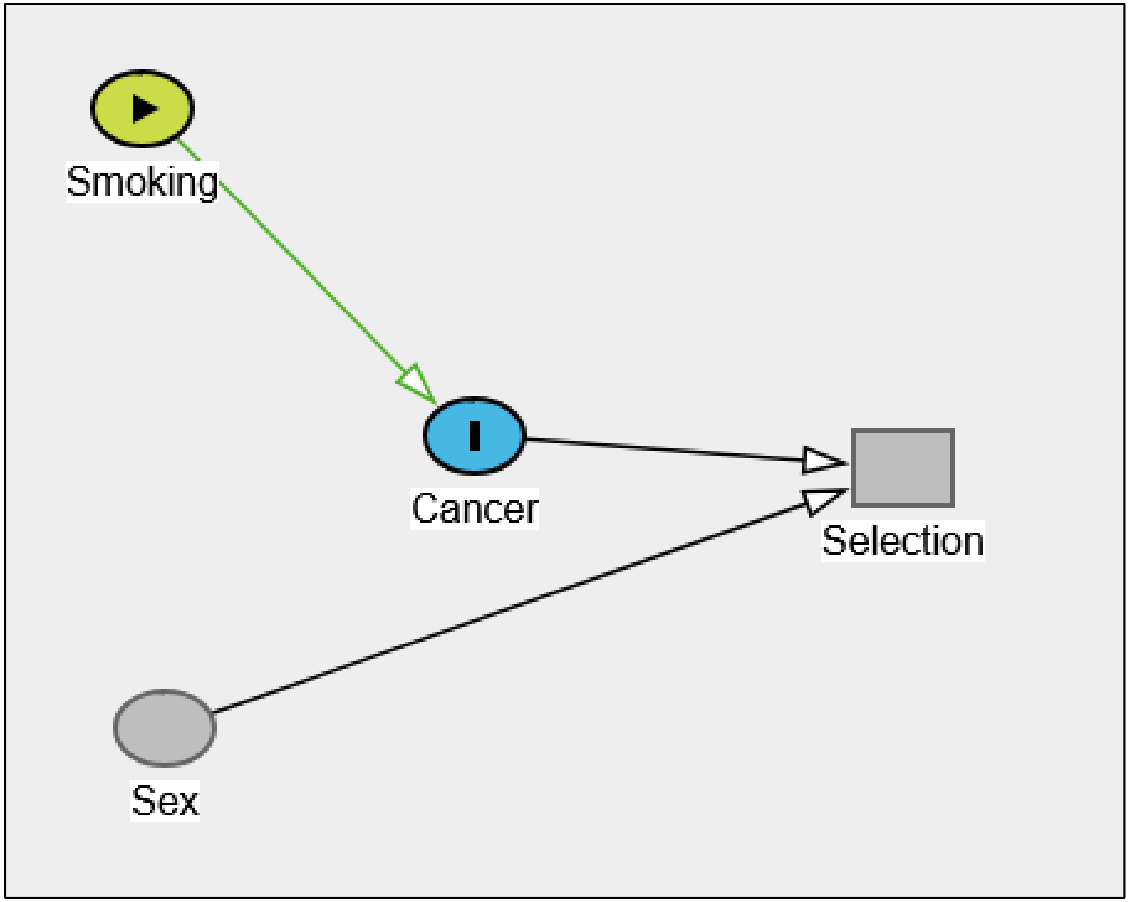
```
dag {
Cancer
[outcome,pos="-1.079,-1.343"]
Selection
[selected,pos="-1.076,-1.343"]
Sex
[adjusted,pos="-1.085,-1.344"]
Smoking
[exposure,pos="-1.082,-1.347"]
Cancer -> Selection
Sex -> Cancer
Sex -> Selection
[pos="-1.081,-1.341"]
Smoking -> Cancer
[pos="-1.080,-1.344"]
```

Summary

exposure(s)	**Smoking**
outcome(s)	**Cancer**
covariates	**2**
causal paths	**1**

Exemple 7

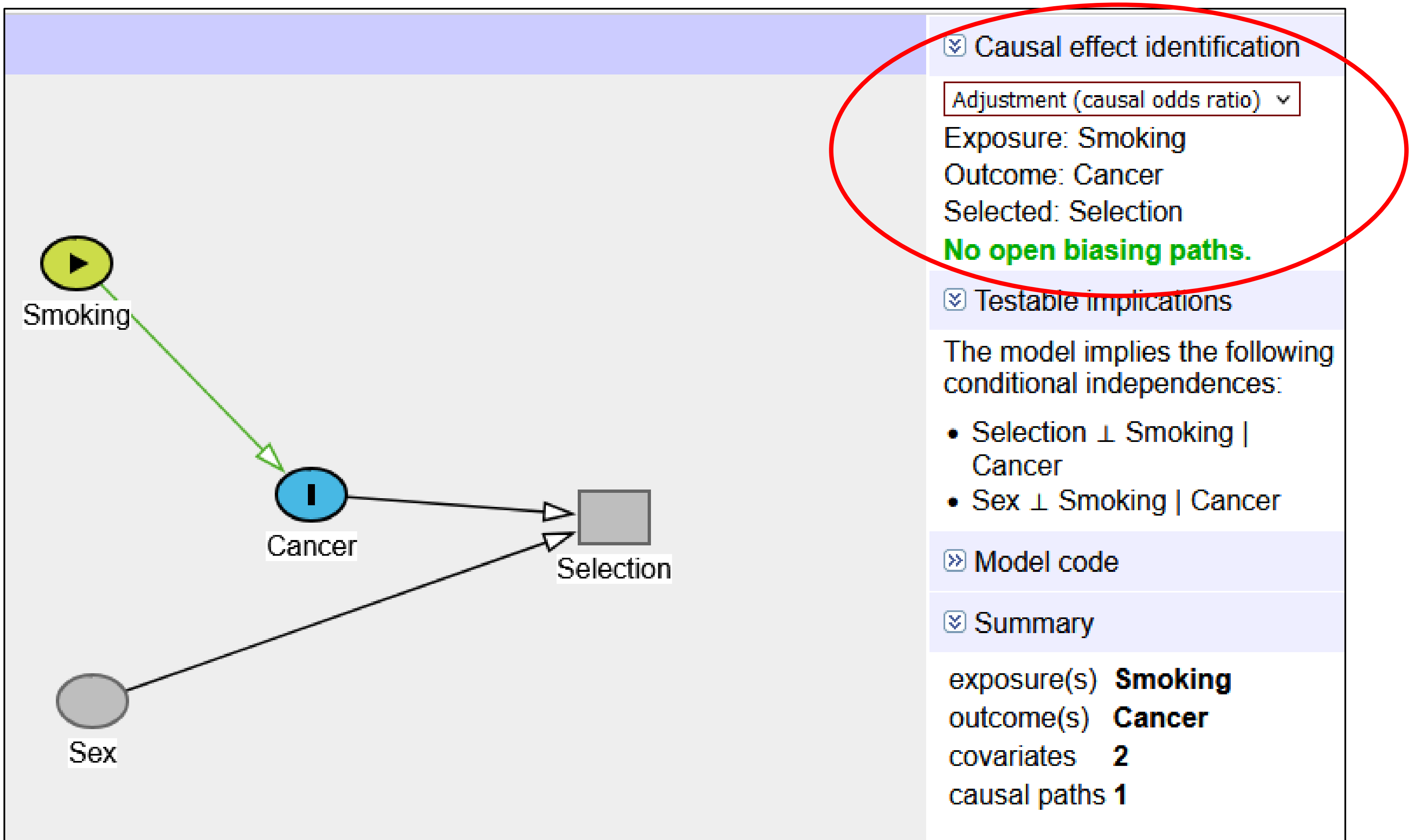
A case-control study on smoking and lung cancer, matched on sex, with sex neither a cause of outcome nor exposure



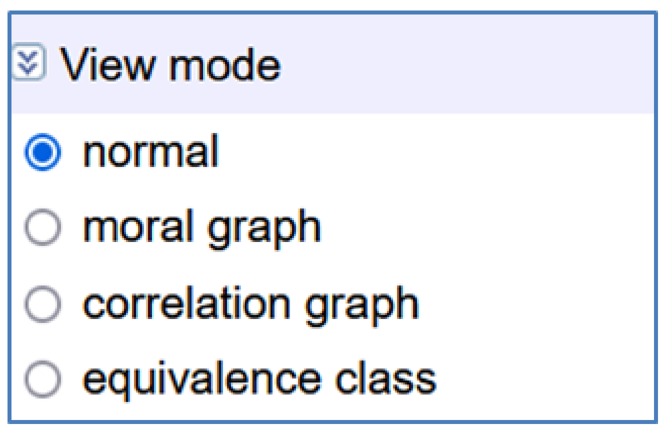

```
dag {
Cancer [outcome,pos="-1.080,-1.344"]
Selection [selected,pos="-1.076,-1.344"]
Sex [pos="-1.083,-1.342"]
Smoking [exposure,pos="-1.083,-1.346"]
Cancer -> Selection
Sex -> Selection
Smoking -> Cancer
}
```

Look at the results

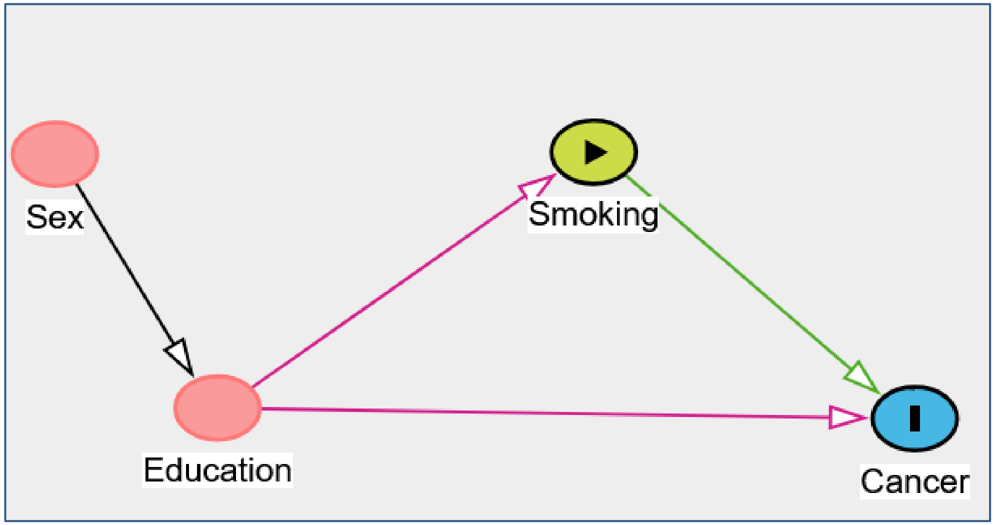
No need to adjust for the matching factor (but to no reason to have matched on it!)



View mode of the graph

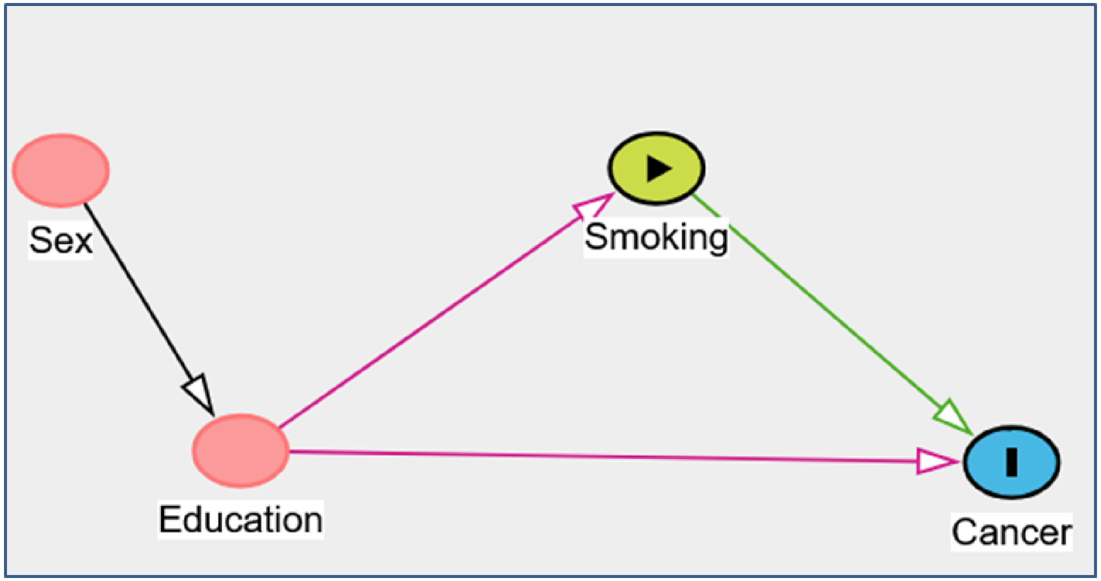


Example 8: Smoking and lung cancer




```
dag {
Cancer [outcome,pos="-0.895,-1.060"]
Education [pos="-1.629,-1.078"]
Sex [pos="-1.800,-1.527"]
Smoking [exposure,pos="-1.233,-1.531"]
Education -> Cancer
Education -> Smoking
Sex -> Education
Smoking -> Cancer
}
```

Look at the results



Causal effect identification

Adjustment (total effect)

Exposure: Smoking

Outcome: Cancer

Biasing paths are open.

Minimal sufficient adjustment sets for estimating the total effect of Smoking on Cancer:

- Education

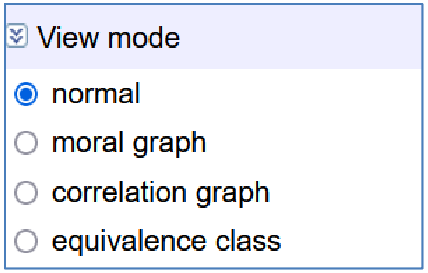
Testable implications

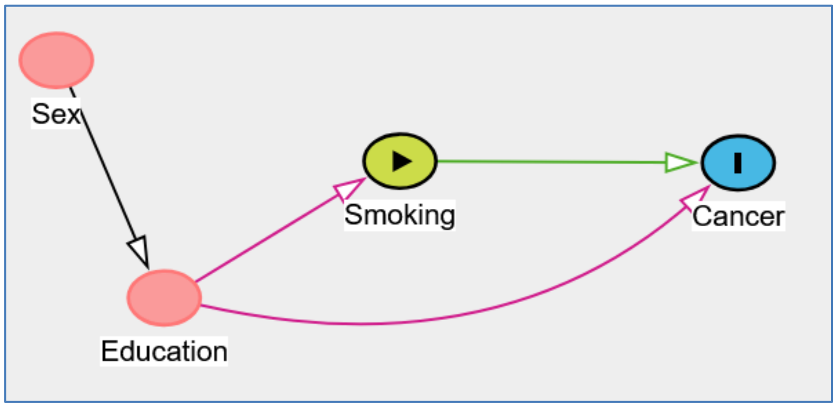
The model implies the following conditional independences:

- Cancer ⊥ Sex | Education
- Smoking ⊥ Sex | Education

Correlation graph

- Not a DAG, but a simple graph with lines instead of arrows.
- Connects each pair of variables that, according to the DAG, could be statistically dependent.
- These pairwise independencies are also listed in the “Testable implications” field

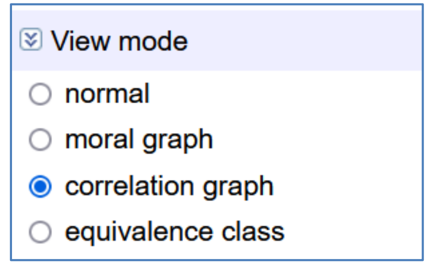


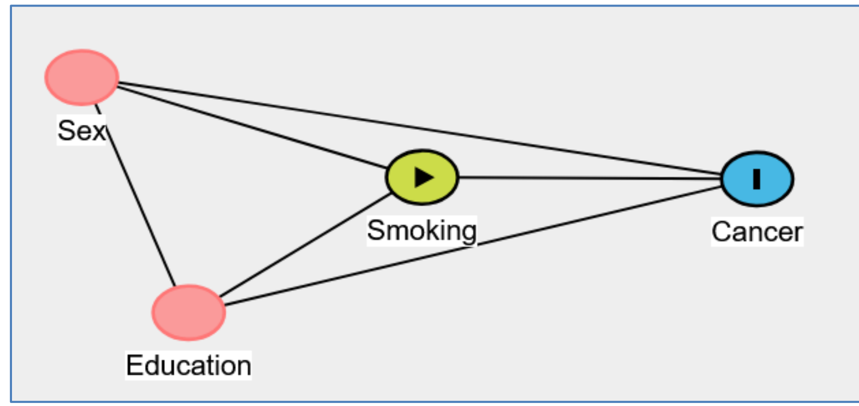


Testable implications

The model implies the following conditional independences:

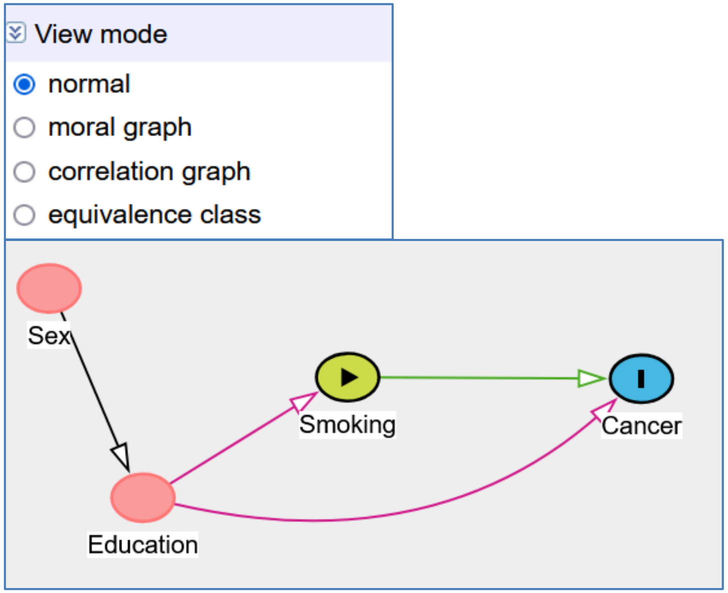
- Cancer ⊥ Sex | Education
- Smoking ⊥ Sex | Education

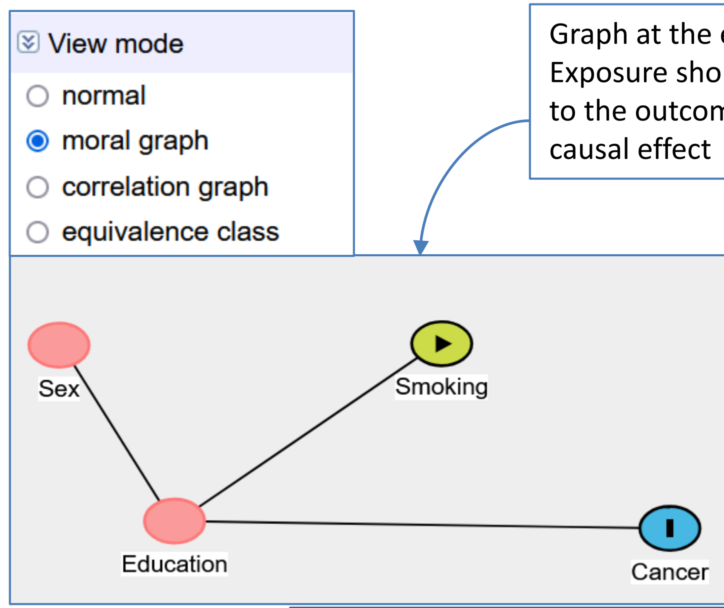




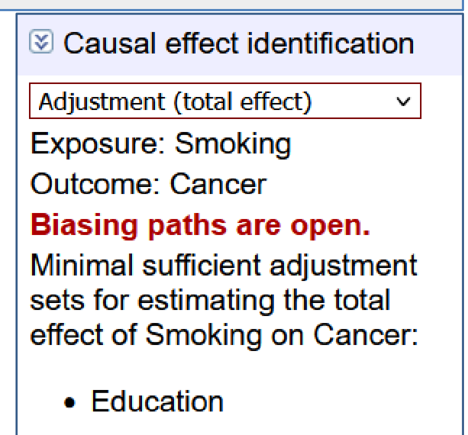
Moral graph

- Undirected graph version of the DAG used by DAGitty to identify minimal sufficient adjustment sets
- Recommended to verify the calculation by hand for complicated DAG





Graph at the end of Step 6. Exposure should be disconnected to the outcome to estimate the causal effect



6-step approach described in
Shrier and Platt. Reducing bias through directed acyclic graphs. *BMC Medical Research Methodology* 2008

DAGitty selected references

- Textor et al. A Graphical Tool for Analyzing Causal Diagrams. *Epidemiology* 2011
- Textor et al. Robust causal inference using DAGs: the R package ‘dagitty’. *Int J Epidemiol* 2016
- Shrier et al. Identifiability of causal effects in test-negative design studies. *Int J Epidemiol* 2023
- Shrier and Platt. Reducing bias through directed acyclic graphs. *BMC Medical Research Methodology* 2008
- Textor. Drawing and Analyzing Causal DAGs with DAGitty. DAGitty user manuel Version July 18,2023. https://www.dagitty.net/manual-3.x.pdf. Consulted on August 18, 2025