

# Bayesian Network Decomposition for Modelling Breast Cancer Detection

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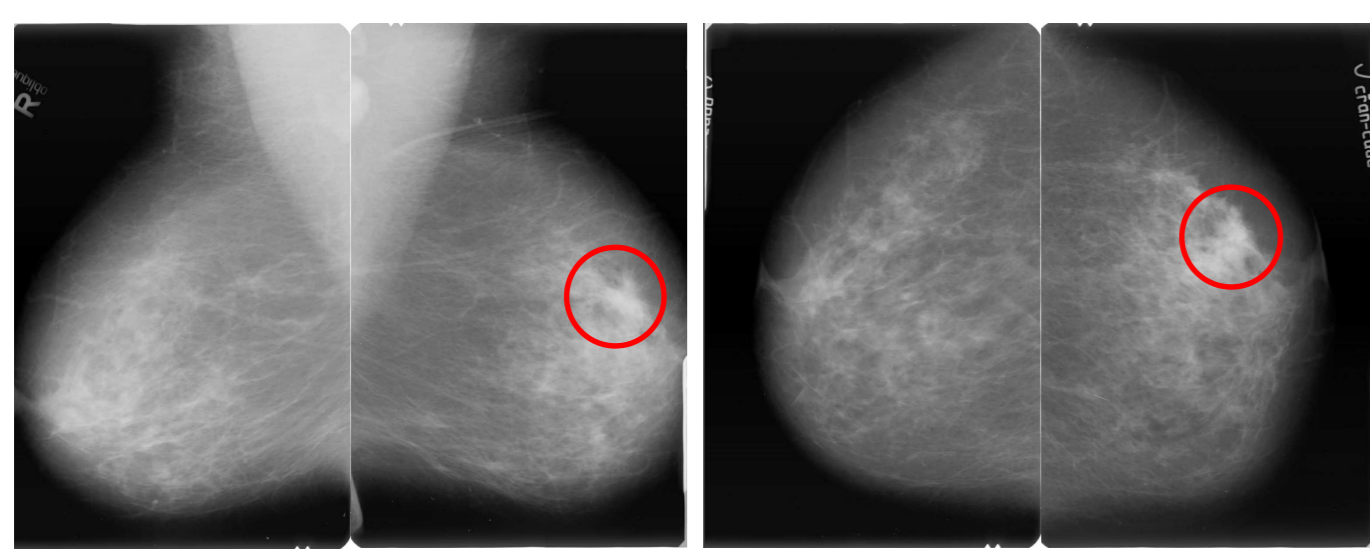
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## Problem definition

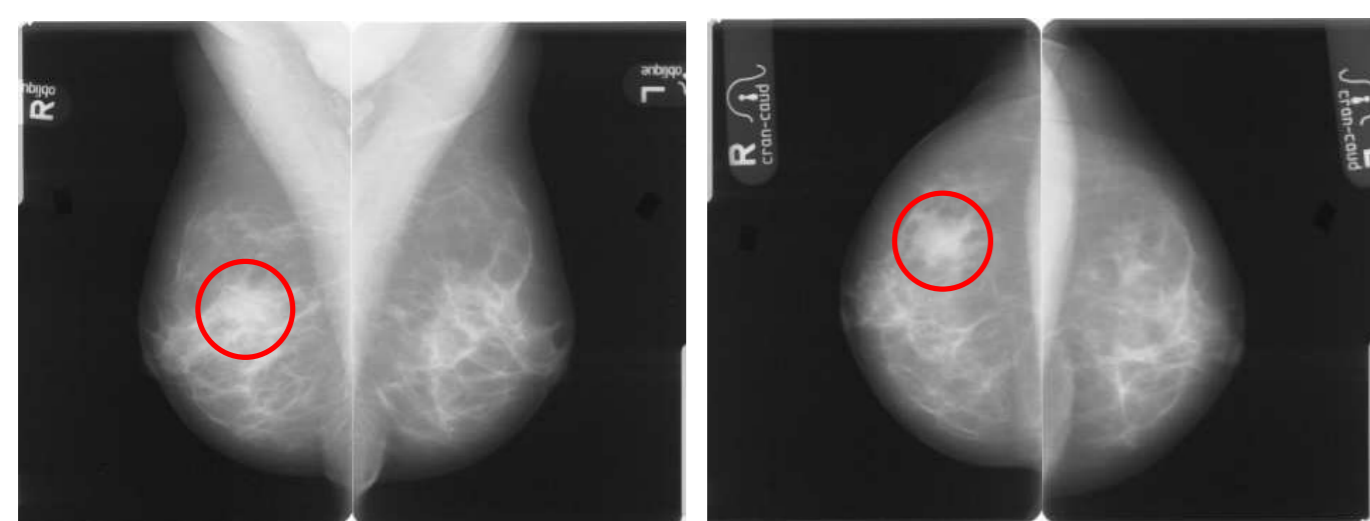
The automated differentiation between benign and malignant abnormalities is a difficult problem due to the inherent uncertainty of the detection of breast cancer using mammograms as obtained in breast-cancer screening. Of particular interest is the distinction of the main breast abnormalities—mass, architectural distortion, and asymmetry—with their level of suspiciousness.

### Mammography: MALIGNANT CASE



Medial lateral oblique (MLO) view Cranio-caudal (CC) view

### Mammography: BENIGN CASE



Medial lateral oblique (MLO) view Cranio-caudal (CC) view

## Aims

We propose a novel perspective based on **Bayesian network (BN) decomposition for breast cancer detection**. We consider three methods that allow for different levels of network topological or structural decomposition for tackling classification of breast abnormalities by exploiting the presence of:

- causal independence between breast cancer risk factors,
- contextual independence between mammographic findings and breast abnormalities,
- class information in breast cancer detection domain.

## Bayesian networks

**Causal independence:** multiple causes (parent nodes) lead to a common effect (child node) ([1]).

**Contextual independence:** conditional independence that holds only in certain contexts, i.e., given the assignment of values to certain variables. The so-called *similarity network* proposed in [2] represents contextual independence by splitting up a BN into separate BNs, one for each possible context.

**Language representation:** A general knowledge representation language can be used to specify domain facts and relationships. We concentrate on using a *probabilistic Horn clause-like language* for representing expert knowledge.

## Conclusions

We have examined different techniques for BN decomposition based on the concepts of contextual independence and probabilistic first-order languages for the detection of breast cancer. Several advantages are demonstrated:

- natural and more intuitive representation of breast abnormalities and their features,
- compact representation and efficient manipulation of large conditional probability tables,
- a possible improvement in the knowledge acquisition and representation processes.

## Structure representation of the breast cancer domain

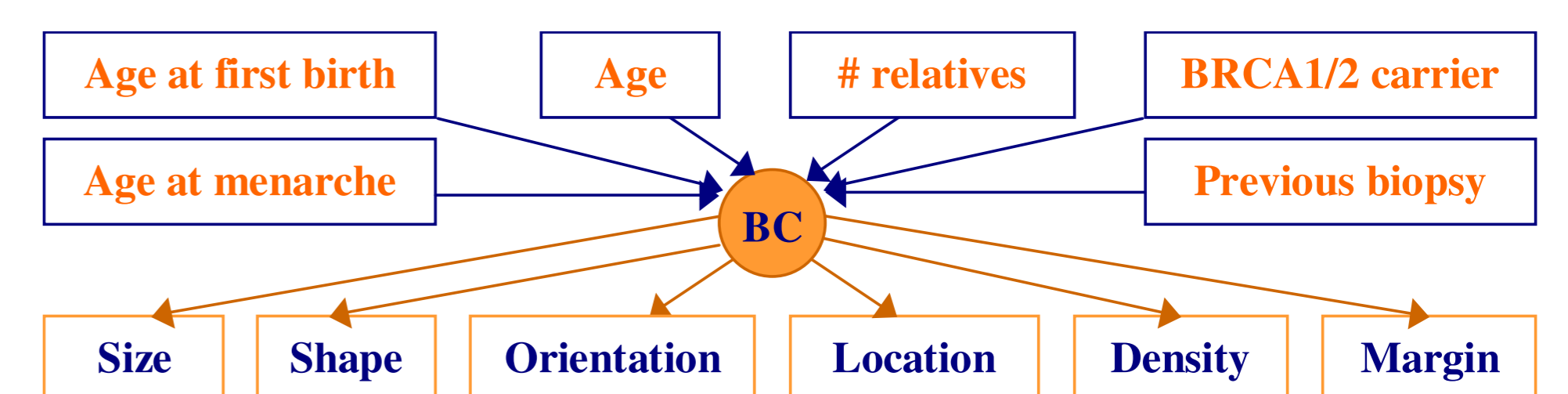
**Problem:** distinction between malignant/benign mass, malignant/benign architectural distortion and focal/benign asymmetry, whose Cartesian product of values represents the class variable *Breast cancer* (BC).

**Risk factors for breast cancer:** *Age, Number of relatives with breast cancer, Age at menarche, Age at first live birth, Previous biopsy, Presence of BRCA1/2 genes*

**Mammographic features of a finding:** *Density, Location, Margin, Orientation, Size, Shape*

All the causal and feature-abnormality relationships are presented by a single BN ([3, 4]).

**Disadvantage:** does not naturally represent the causal and contextual independence present in the domain of breast cancer detection.

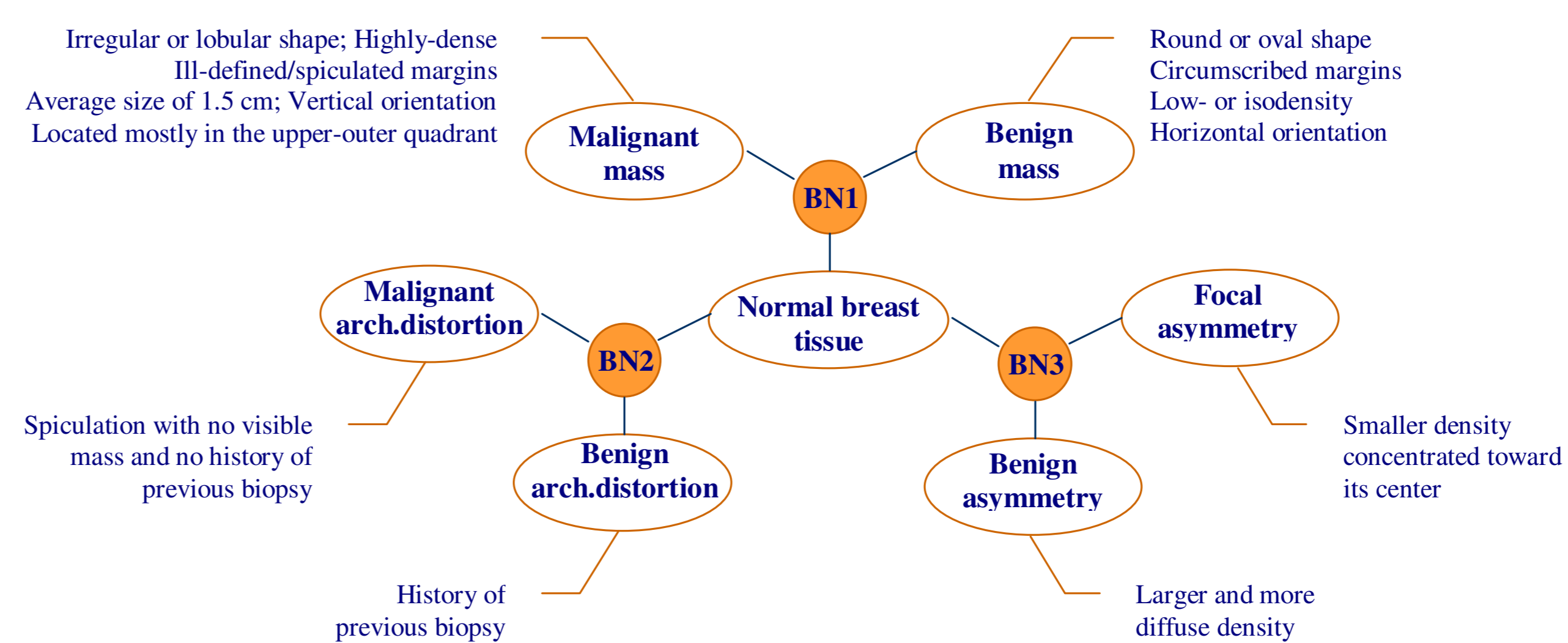


## A decomposable Bayesian network approach

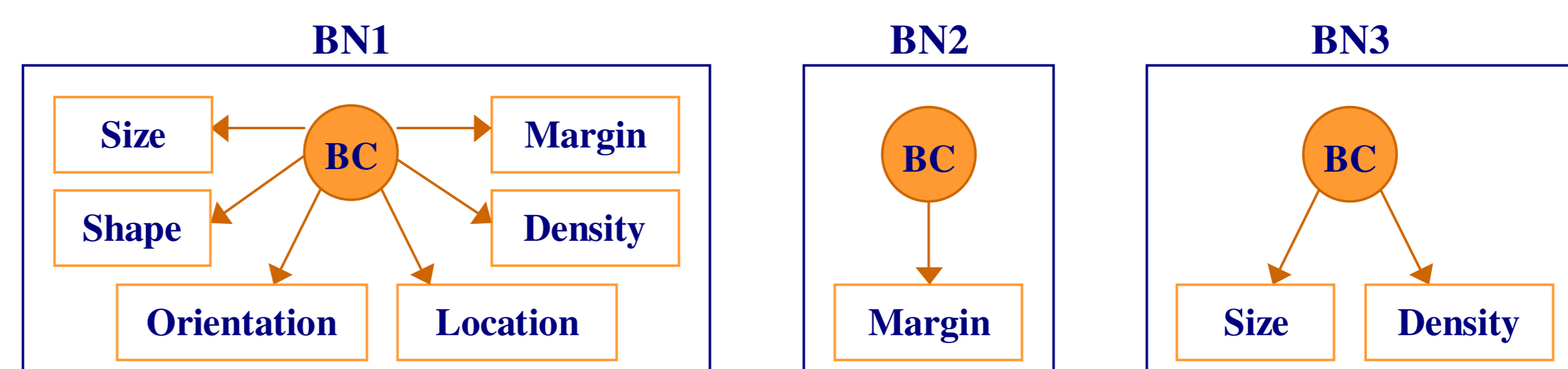
**Causal independence of the risk factors.** A *BRCA1/2 (brca)* carrier establishes a very high probability for developing breast cancer, irrespective of the values of the other factors. If that genetic sign is not present, having a first-degree relative (*nrelat*) determines another probability value. Having neither of those factors, the age and the history of previous biopsy become the factors to pay attention to. Women older than 35 years with known previous biopsy are in a high-risk group compared to women younger than 35. In the latter group, age at menarche (*agemen*) plays an important role as well. This knowledge is represented by:

$$\begin{aligned}
 P(bc(X, present) \mid brca(X, yes)) &= p_1. \\
 P(bc(X, present) \mid brca(X, no), nrelat(X, 1)) &= p_2. \\
 P(bc(X, present) \mid brca(X, no), nrelat(X, 0), age(X) > 35, pbiopsy(X, yes)) &= p_3. \\
 P(bc(X, present) \mid brca(X, no) \wedge nrelat(X, 0) \wedge age(X) \leq 35 \wedge agemen(X, < 12)) &= p_4.
 \end{aligned}$$

**Contextual independence on the mammographic findings.** We apply the similarity network method where a connected cover of mutually exclusive class variables is constructed.



The cover contains three triplets corresponding to the distinction between each of the abnormalities with its level of suspiciousness. Each triplet is a local Bayesian network with a given structure.



**Class information.** The presence of a suspicious mass on the MLO view yields a high probability that the same mass is present on the CC view, i.e., based on the class information for one view the belief for the class information on the other view can be updated:

$$\begin{aligned}
 &mass(Mass: Lesion, View: Mammog, Patient: Person, Value) \\
 &val(mass) = \{no, benign, malignant\} \\
 &margin(Mass: Lesion, View: Mammog, Patient: Person, Value) \\
 &val(margin) = \{NA, circumscribed, ill-defined, obscured, spiculated\} \\
 &P(mass(Y, CC, X, malignant) \mid margin(Y, CC, X, spiculated), mass(Y, MLO, X, malignant)) = p.
 \end{aligned}$$

## References

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