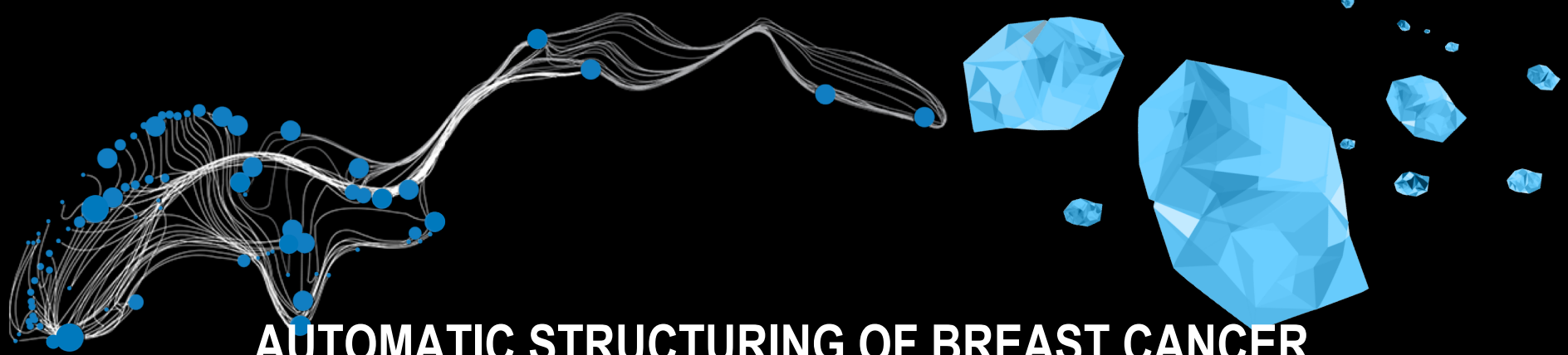

AUTOMATIC STRUCTURING OF BREAST CANCER RADIOLOGY REPORTS FOR QUALITY ASSURANCE

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Masters in Computer Science
DMBIH 2018

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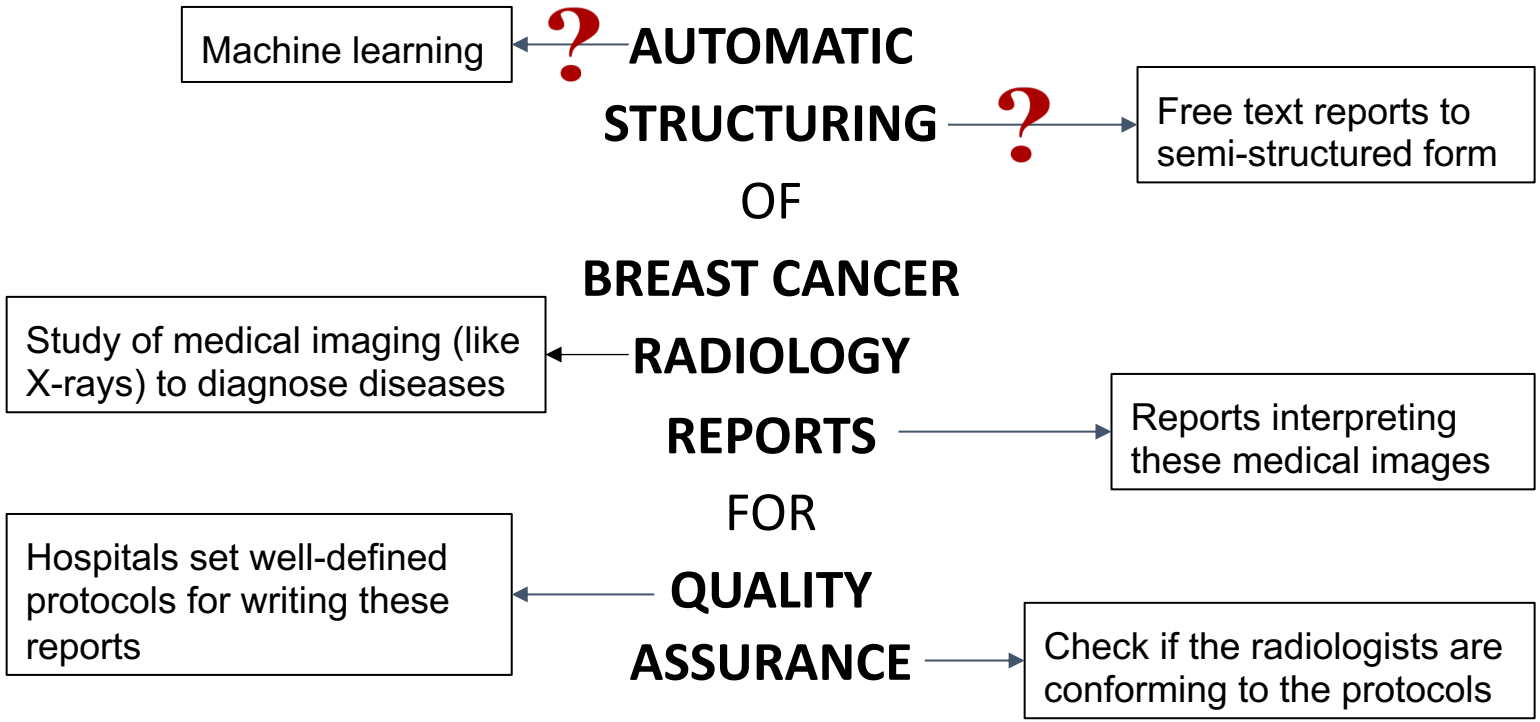
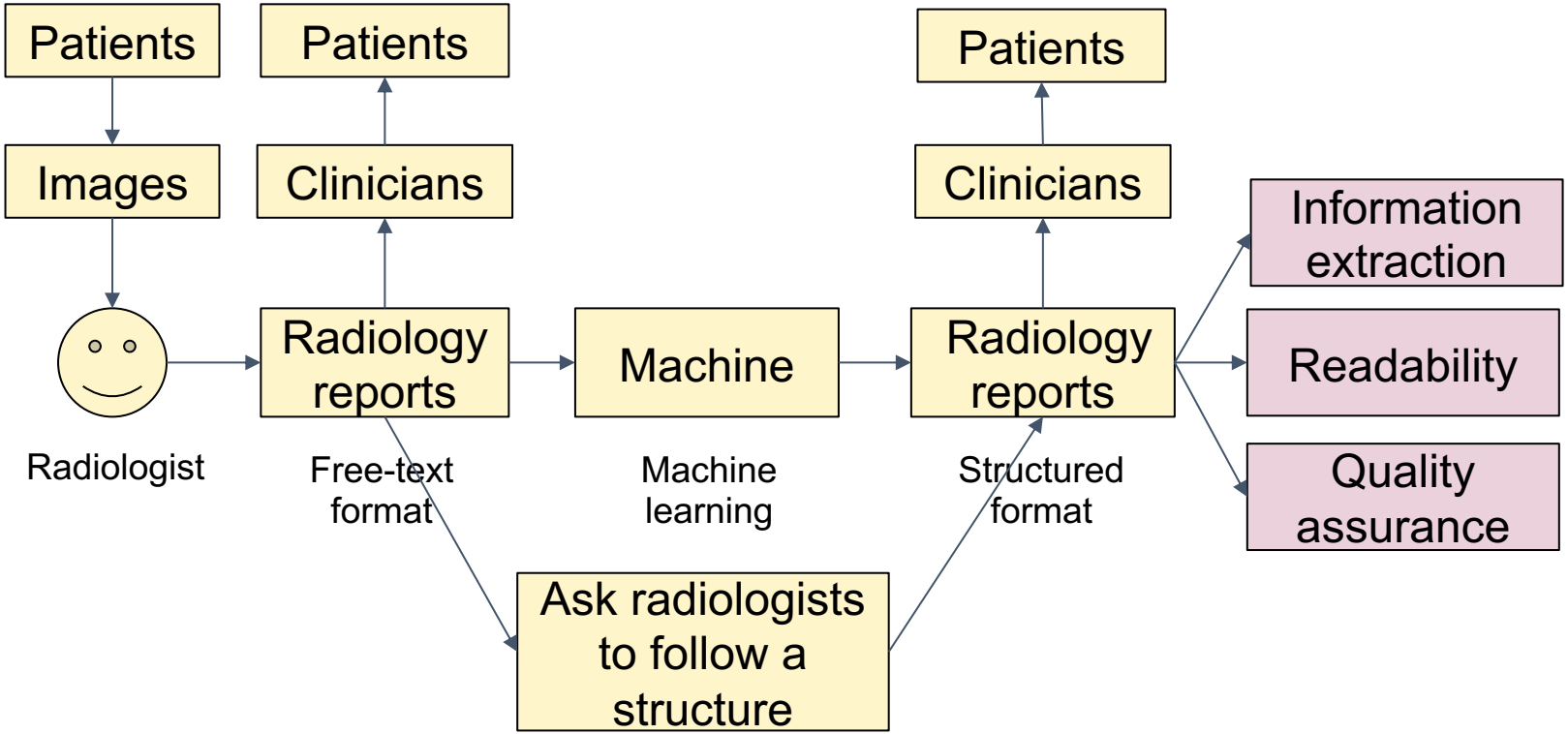
INTRODUCTION



INTRODUCTION

Motivation



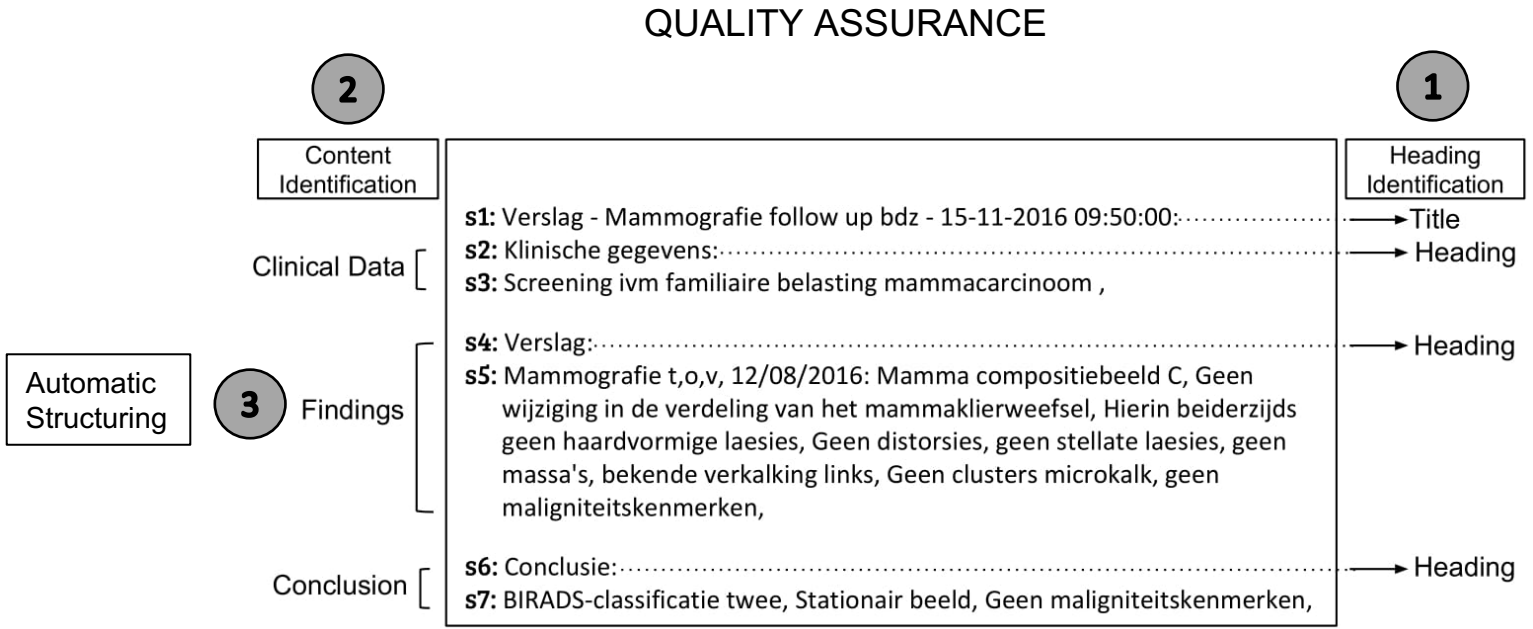
INTRODUCTION
QUALITY ASSURANCE

1. Why important? For correct diagnosis of disease
2. 3%-4% estimated discrepancy rate daily [1]
3. Conformance to rules set by ACR BI-RADS [2]

Clinical data
Breast composition
Clear description of findings - mass, calcification, asymmetry, architectural distortion, associated feature
Conclusion

DATA SET

A BREAST CANCER RADIOLOGY REPORT



AUTOMATIC STRUCTURING

OVERVIEW

Free-text Format

Mammografie t,o,v, 12/08/2016: Mamma compositiebeeld C, Geen wijziging in de verdeling van het mammaklierweefsel, Hierin beiderzijds geen haardvormige laesies, Geen distorsies, geen stellate laesies, geen massa's, bekende verkalking links, Geen clusters microkalk, geen maligniteitskenmerken,

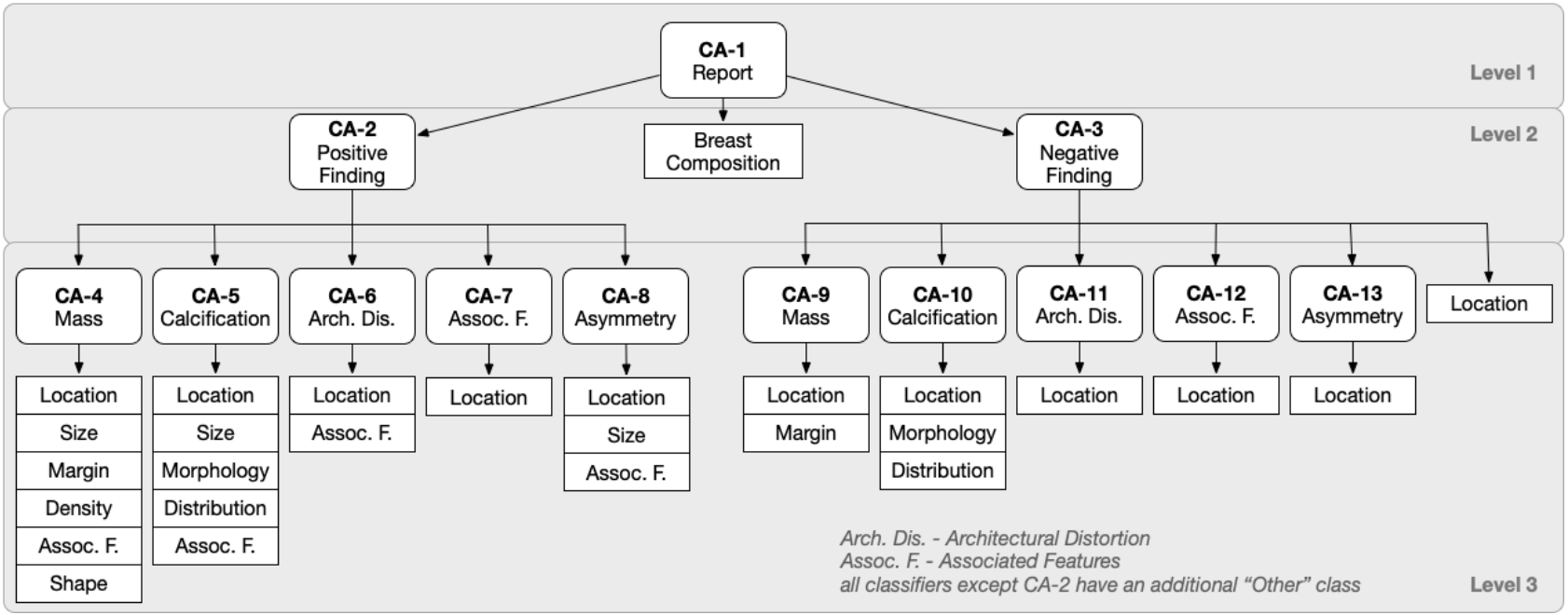
Structured Format

```
<report>
   <O>Mammografie t,o,v, 12/08/2016:</O>
   <breast_composition>Mamma compositiebeeld C,</breast_composition>
   <O>Geen wijziging in de verdeling van het mammaklierweefsel, </O>
   <negative_finding>
      <mass>Hierin
         <location>beiderzijds</location> geen haardvormige laesies,
      </mass>
      <architectural_distortion>Geen distorsies,
      </architectural_distortion>
      <mass> geen
         <margin> stellate</margin>laesies, geen massa's,
      </mass>
   </negative_finding>
   <positive_finding>
      <calcification> bekende verkalking,
         <location>links</location>
      </calcification>
   </positive_finding>
   <negative_finding>
      <calcification>Geen
          <distribution>clusters</distribution>
          <morphology>microkalk,</morphology>
      </calcification>
   </negative_finding>
   <O>geen maligniteitskenmerken,</O>
</report>
```

AUTOMATIC STRUCTURING

THREE LEVEL ANNOTATION SCHEME

Example global class: positive finding/mass/location



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PROBLEM DEFINITION

Sequence labeling problem

Label	PF/C/L	NF/C/O	NF/C/DI	NF/C/MO
Sequence	links	Geen	clusters	microkalk

Conditional Random Field (CRF) is one of the best sequence labeling algorithms

```
<positive_finding>
    <calcification> bekende verkalking,
        <location>links</location>
    </calcification>
</positive_finding>
<negative_finding>
    <calcification>Geen
        <distribution>clusters</distribution>
        <morphology>microkalk,</morphology>
    </calcification>
</negative_finding>
```

AUTOMATIC STRUCTURING

FEATURE EXTRACTION FOR CRF

x_t (t^{th} token in the sequence) → feature vector

List of features used:

1. Word itself	5. Is word a Dutch stop word? (0,1)
2. Word stem	6. Is word in uppercase? (0,1)
3. Suffix for word (last 2 and 3 characters)	7. Is word a punctuation? (0,1)
4. Word starts with capital or not (0,1)	8. Part of speech (POS) of word and POS prefix (first 2 characters)

Feature vectors of the adjacent tokens are also used as features.

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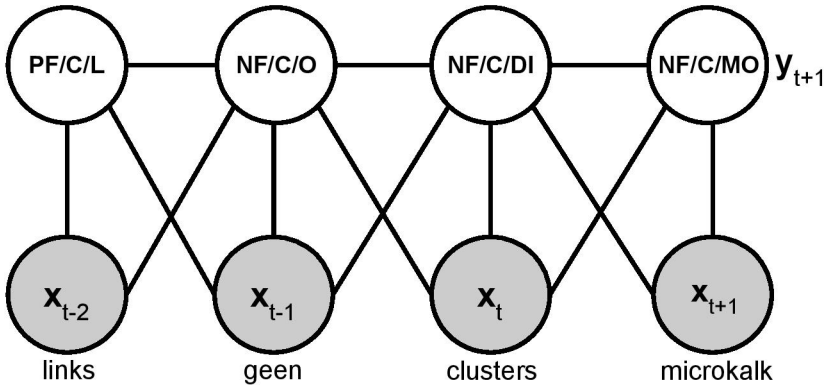
BASELINE MODEL

1 CRF classifier predicting 34 classes (Each class of the form: level1/level2/level3)

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<positive_finding>
    <calcification> bekende verkalking,
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    </calcification>
</positive_finding>
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    <calcification>Geen
        <distribution>clusters</distribution>
        <morphology>microkalk,</morphology>
    </calcification>
</negative_finding>
```

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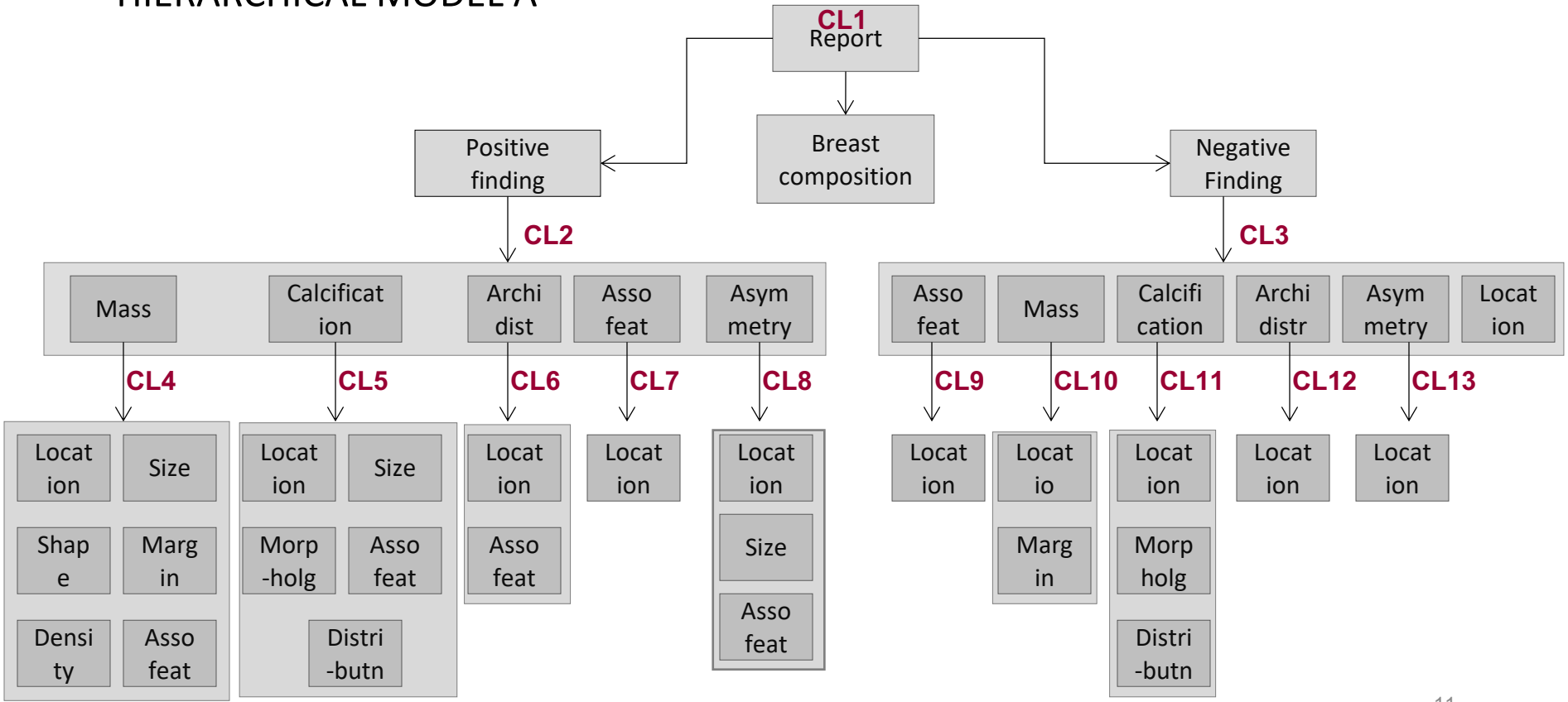
HIERARCHICAL MODEL A



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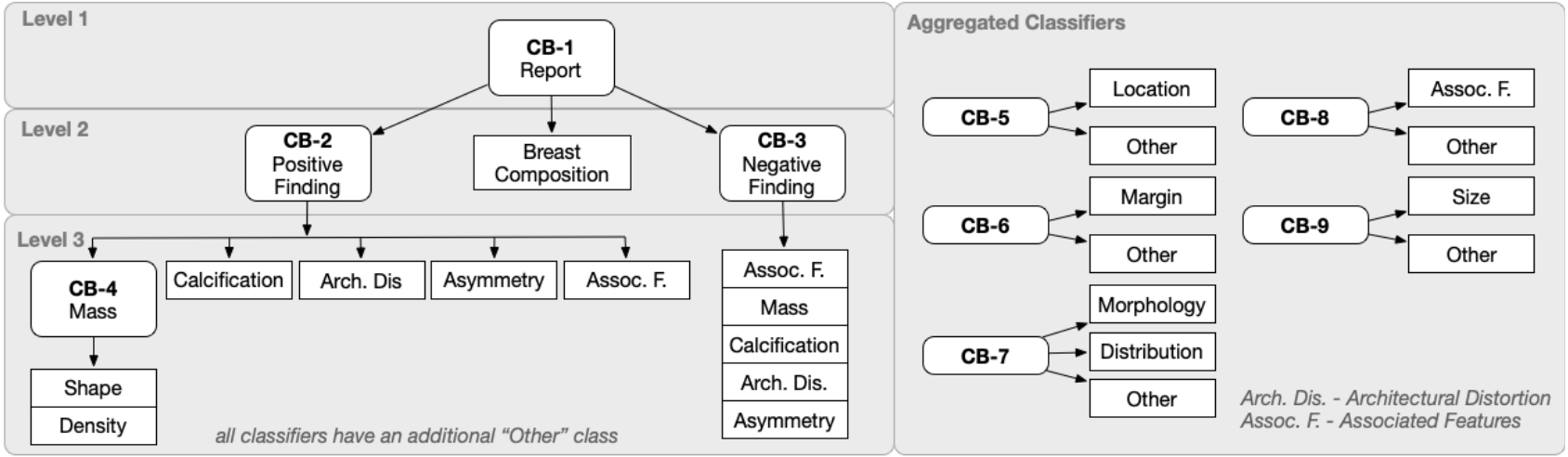
HIERARCHICAL MODEL B



Example: Positive Finding/Assymmetrie/Size is decided by classifier chain CB-1, CB-2, CB-9

RESULTS

HEADING & CONTENT IDENTIFICATION

Heading Identification

Classes	NB	SVM	RF	#Instances (Sentences)
Heading	0.96	0.96	0.88	540
Not Heading	0.98	0.98	0.94	991
Title	0.97	0.98	0.99	60
Avg (F_1^M)	**0.97**	**0.97**	**0.92**	1591

Content Identification

Classes	NB	SVM	RF	#Instances (Sentences)
Title	0.89	0.99	0.91	60
Clinical Data	0.86	0.94	0.70	405
Findings	0.88	0.94	0.82	678
Conclusion	0.89	0.92	0.92	413
Avg (F_1^M)	**0.88**	**0.94**	**0.81**	1591

RESULTS
AUTOMATIC STRUCTURING

Comparison of all models

Measure	Baseline	Model A	Model B	#Instances (Tokens)
F_1^M	0.71	0.78	0.78	4230

RESULTS
AUTOMATIC STRUCTURING

Global classes performance comparison (F1) for the 3 models

Models	NF/C/DI	NF/C/MO	NF/MS/O	NF/MS/MA	NF/AF/O	BC
Baseline	0.98	0.95	0.93	1.00	0.96	0.89
Model A	0.98	0.91	0.88	0.96	0.96	0.94
Model B	0.99	0.97	0.89	0.97	0.96	0.94
#Instances	54	56	210	35	397	622

Models	PF/C/SI	PF/C/L	PF/MS/L	PF/MS/MA	PF/C/AF	PF/AS/O
Baseline	0.00	0.50	0.30	0.53	0.00	0.00
Model A	0.00	0.44	0.40	0.72	0.18	0.58
Model B	0.22	0.60	0.47	0.70	0.00	0.56
#Instances	14	68	139	59	33	172

RESULTS
AUTOMATIC STRUCTURING

Radiologist annotation

```
<report>
   <O>Mammografie t,o,v, 12/08/2016:</O>
   <breast_composition>Mamma compositiebeeld C,</breast_composition>
   <O>Geen wijziging in de verdeling van het mammaklierweefsel, </O>
   <negative_finding>
      <mass>Hierin
         <location>beiderzijds</location> geen haardvormige laesies,
      </mass>
      <architectural_distortion>Geen distorsies,
      </architectural_distortion>
      <mass> geen
         <margin> stellate</margin>laesies, geen massa's,
      </mass>
   </negative_finding>
   <positive_finding>
      <calcification> bekende verkalking,
         <location>links</location>
      </calcification>
   </positive_finding>
   <negative_finding>
      <calcification>Geen
          <distribution>clusters</distribution>
          <morphology>microkalk,</morphology>
      </calcification>
   </negative_finding>
   <O>geen maligniteitskenmerken,</O>
</report>
```

Machine annotation

```
<report>
    <O>Mammografie t,o,v , 12/08/2016 :</O>
    <breast_composition>Mamma compositiebeeld C ,</breast_composition>
    <O>Geen wijziging in de verdeling van het mammaklierweefsel ,</O>
    <negative_finding>
       <mass> Hierin
          <location>beiderzijds</location>geen haardvormige laesies ,
       </mass>
       <architectural_distortion>Geen distorsies ,
       </architectural_distortion>
       <mass>geen
          <margin>stellate</margin> laesies , geen massa's ,
          bekende verkalking ,
          <location>links</location>
       </mass>
       <calcification>Geen
          <distribution>clusters</distribution>
          <morphology>microkalk ,</morphology>
       </calcification>
    </negative_finding>
    <O>geen maligniteitskenmerken ,</O>
</report>
```

CONCLUSION

1. This project is a step towards quality assurance. Prototype can be developed for use in clinical trails in hospital.

2. A study showed pre-structuring of reports decreased report accuracy [3]. So, our post-structuring approach can be better.

3. This method can also be used for information extraction from reports. For example: to answer questions like “How many patients have breast cancer in left breast?”

4. A similar study of information extraction from Italian mammography findings was done [4]. Their F1: 0.87 > our model (F1: 0.78). They had labeled reports = 500 and no. of predicted classes = 9. We had not much training data (180) for all the classes and predicted more classes (34).

5. Our models can be extended to reports in different languages and medical conditions.

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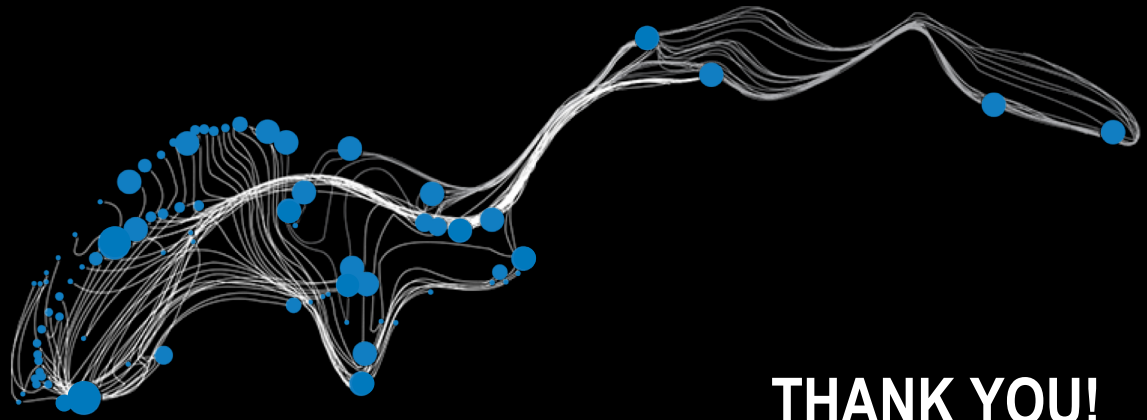
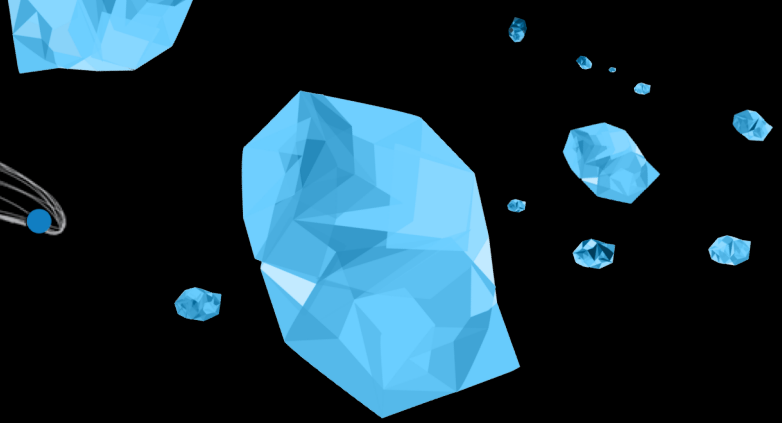
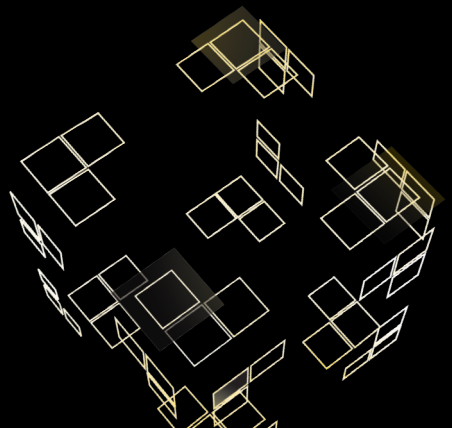
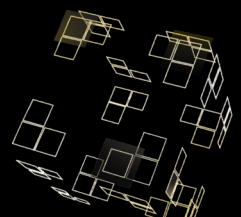


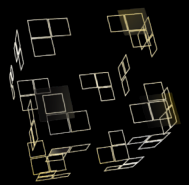


THANK YOU!

Questions?







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