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Merging of Biomedical Decision Diagrams

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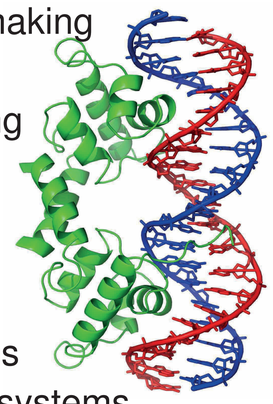
1. Decision Diagrams in Medicine

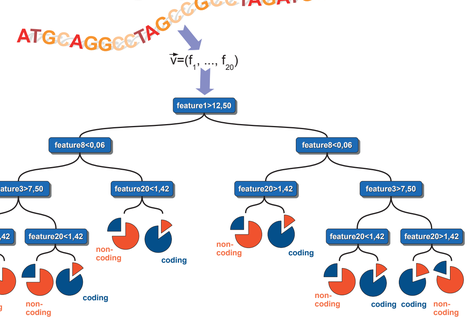
Decision diagrams are a common aid for decision making

- Intuitively understandable
- Not only for professionals in information engineering



Medical Examples

- Staging of tumor diseases
- Severity appraisal in clinical practice
- Therapy selection depending on patient’s conditions
- Multidimensional indices in case-based reasoning systems



Other Life Sciences and Related Fields

- Molecular biology: DNA classification
- Psychology: tests for diagnosis of personality disorders

Even Beyond

- Numerous applications in economy (e.g., liquidity appraisal)

2. Multiple Decision Diagrams

Sometimes we have more than one diagram with similar content.

Reasons

- Different expert opinions
- Different training sets (e.g., due to parallel computing settings where each cell works on a subset of the complete training set)
- Randomized machine-learning algorithms
- Several research groups work on similar projects and come to slightly differing results due to statistical fluctuations

3. Existing Solutions have Drawbacks

Ensemble Learning methods

- The object to classify is put into each of the decision diagrams.
- Afterwards the individual results are united, e.g., by majority voting.

Disadvantages

- Still multiple diagrams: Only the results are merged, but not the diagrams themselves
- No compact representation

Other existing solutions

- Mostly assume that original training data is still available
- Often convert diagrams into sets of rules before merging

4. New Approach

Incorporating of several decision diagrams into a single one

- without referring to original training data
- without translating them into rules

Technology

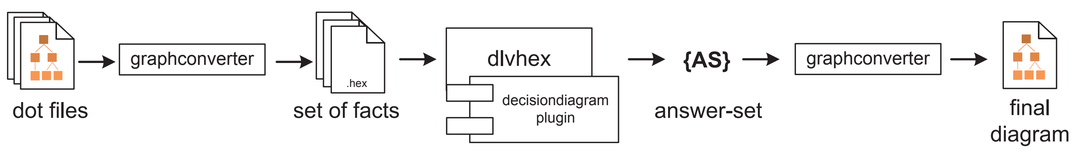
- dlvhex and mergingplugin (a dlvhex extension) [1]
- user-defined operators ensure applicability in many scenarios

Benefits

- Easy to experiment with several merging techniques and make comparisons without repeating manual incorporation.

5. Processing Decision Diagrams with dlvhex

1. Input: Human-readable DOT graphs
2. Automatic translation into a machine-readable set of facts
3. Application of algorithms for decision diagram merging
4. Output as answer set and back-translation into a DOT graph
5. Visualization using the DOT tools



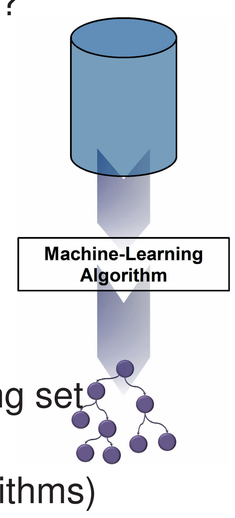
6. Case Study: DNA-Classification

Is a sequence over $\{A, C, G, T\}$ protein-coding or junk?

1. Training

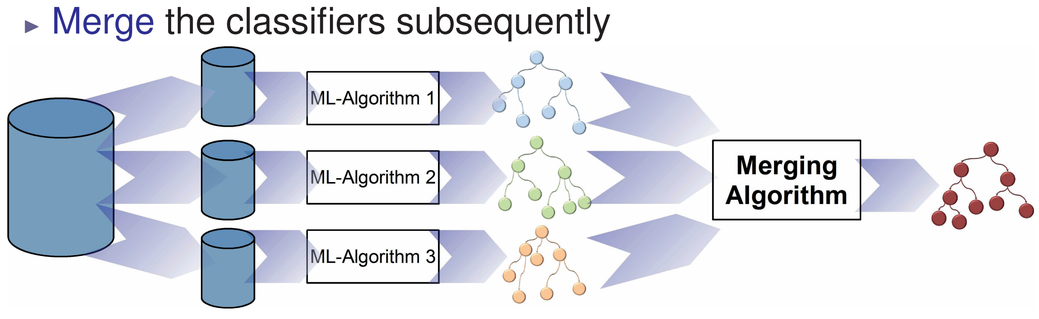
Traditional approach

- Use a large set of annotated sequences
- Compute 20 numeric features for each sequence
- Train a single decision tree over the full training set



Our solution

- Train multiple decision trees on subsets of the training set
- Aim for a diversity among the classifiers (e.g., by randomization or selection of different algorithms)
- Merge the classifiers subsequently



2. Classification: Compute the same features for the query sequence and classify it using the merged decision tree

3. Evaluation: Quality of result depends on settings and algorithms; finding the optimum is supported by our framework.

Interesting observations:

- Potential to increase accuracy
- By combining diagrams from different learning algorithms, number of necessary training samples decreases

These observations could hardly by made without the framework!

7. Further Aspects

- Quality of result depends on: training set, machine-learning algorithms and merging procedure
- But: Our framework perfectly supports the user when experimenting and evaluating results!

Advantages

- Increase of accuracy
- Parallel-computing possible
- Easy to change the training set or the merging procedure

References

- [1] Redl, C. (2010). *Development of a Belief Merging Framework for dlvhex*. Master’s thesis, Vienna University of Technology

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