## Exercise 2 <br> Inclusion Dependencies

- Deadline: Monday, 01.12.14
- The admission to the exam requires all exercises to be solved.
- The exercises should be solved in teams of two students.
- The Metanome project is available at GitHub: https://github.com/HPI-Information-Systems/Metanome
- The datasets and supplemental material can be found at network drive S : $\backslash$ fs $3 \backslash b b s \backslash$ DPDC
- The submission system can be found at:
https://www.dcl.hpi.uni-potsdam.de/submit/
- To solve an exercise, please submit a zip file containing the following items:
- <algorithm_name>.jar: An executable Metanome algorithm.
- <algorithm_name>.zip: The algorithm's source code (maven project).
- <algorithm_name>_docu.pdf: Short documentation of the algorithm.
- <algorithm_name>_pres.pptx/ppt/pdf: Two slides presentation of the algorithm.


## Task 1: Inclusion Dependencies - A discovery algorithm

Write an algorithm that discovers all unary inclusion dependencies on the given datasets. The rules for your implementation are as follows:
a) The algorithm discovers exact results, so no approximate or fuzzy results are allowed.
b) The algorithm is not allowed to use parallelization.
c) The algorithm implements the Metanome interface and is compatible with Metanome.
d) The algorithm takes an arbitrary number of tables as input.
e) The algorithm ignores NULL values.


Abbildung 1: Unary Inclusion Dependencies.

Note that in contrast UCC and FD discovery, IND discovery uses multiple tables. INDs should therefore be discovered within and between tables. You can re-implement an existing algorithm from literature or find your own algorithm. To test and evaluate the algorithm, use the datasets provided on the network share. Your algorithm should at least be able to process the WDC dataset! Before submitting your algorithm, check that it correctly executes within Metanome!

BONUS TASK: If you like to dive deeper, you can try to find n-ary inclusion dependencies as well. Can you think of pruning rules for the n-ary discovery? You can also try parallelization or approximate strategies on your algorithm. If you made changes to your main algorithm, please submit them as a separate algorithm, e.g. <algorithm_name>_nary.jar

## Task 2: Documentation

Write a short (max one A4 page) documentation for your algorithm describing the algorithm that you implemented:
a) Describe the algorithm's basic idea. How does the algorithm cope with the complexity of the given task?
b) If you used an algorithm from literature, provide a reference to the according publication.
c) If you came up with an own approach, provide one or two arguments why it is or could be better than related algorithms.
d) If your algorithm implements an adaption or optimization of existing approaches, describe these briefly.
e) State if your algorithm (jar) should be published as Metanome algorithm providing you as the authors.
f) If you solved a bonus task, please discuss your findings here as well.

In the same document, answer the following questions:
a) How many inclusion dependencies did your algorithm find on the provided datasets?
b) How long did the discovery take on each dataset and what machine did you use?
c) Did you discover any limitations of your approach (e.g. runtime or memory consumption) that made computing a certain dataset impossible?
d) Why is it a good idea to ignore NULL values for IND discovery?

## Task 3: Presentation

Prepare two slides for a short, 5 min presentation of your algorithm in the lecture. One slide about the algorithm and one slide about its performance. Here are some ideas for these slides:
a) Explain the idea of your approach and why you think it works well in comparison to others.
b) How did your algorithm perform on the given datasets?
c) Did you make any interesting observations?
d) What lets your algorithm crash?
e) How hard was it to implement your algorithm?
f) This is also a good time to introduce an optimization or adaption of your algorithm.

Note that each team will present its work once!

