# Abstract

## Mapping of complex clinical data using the example of microbiological reports in i2b2

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**Previous status:**

i2b2 provides mostly atomic clinical data without complex dependencies for research.Some examples: diagnosis, medical procedures, demographics, simple measurements like blood pressure, respiratory frequency, scores, messurements in blood gas analysis….

Common characteristics is that the informative value has weak interdependencies to each other. Therefore these values may be correlated in any order (evaluation of scientific conclusion will remain unaffected).

**New requirements:**

Having said that there are several clinical data whose expressiveness has strong interdependencies to their descriptive parameters. Some examples: drug administrations or microbiological reports.

Mentioning drugs descriptive parameters are dose equivalent of weight dependent drugs, maximum dose per day, etc.

Similar dependencies exist on microbiological reports. Examining microbiological reports they define danger of a germ mainly using 1.) species, 2.) antibiotic resistance and 3.) location respectively potential transmission route; No 3 can be derived from analyzed material (sputum, blood, smears, …).

**Implementation:**

Due to the fact that the refinement of a medical problem (drilldown) may occur from every mentioned path. Therefore the hierarchical refinement (tree structure) provided by i2b2 doesn't match the requirements well.

The challenge was to provide data using a model which makes it easy for researchers to define the mentioned questions in i2b2. First approach was to use modifiers to add those descriptive parameters to a microbiological report. This approach isn't sufficient because it disables the ability to view parameters at timeline view (particularly with regard to the ability to add other facts from ontology like patient's location).

Having said that we decided to map microbiological reports using the "operational" hierarchy of a report (material -> result / germ -> resistance). To improve handling we added some additional hierarchy levels (material groups, result groups, germs

grouping antibiotics). For performance reasons we didn’t use the well known “like”-operator but a select statement limiting the hierarchy level and use the result for the in-operator.

**Conclusion:**

Both approaches – modifier vs. “operational” hierarchy – leads to handling issues. Both approaches require improvements at code level. The modifier approach seems to be easier to use for researchers. Beside of that it would eliminate the need of the “select for in”-improvement.
It has to be discussed which approach is more reasonable and which code-improvements have to be done.