

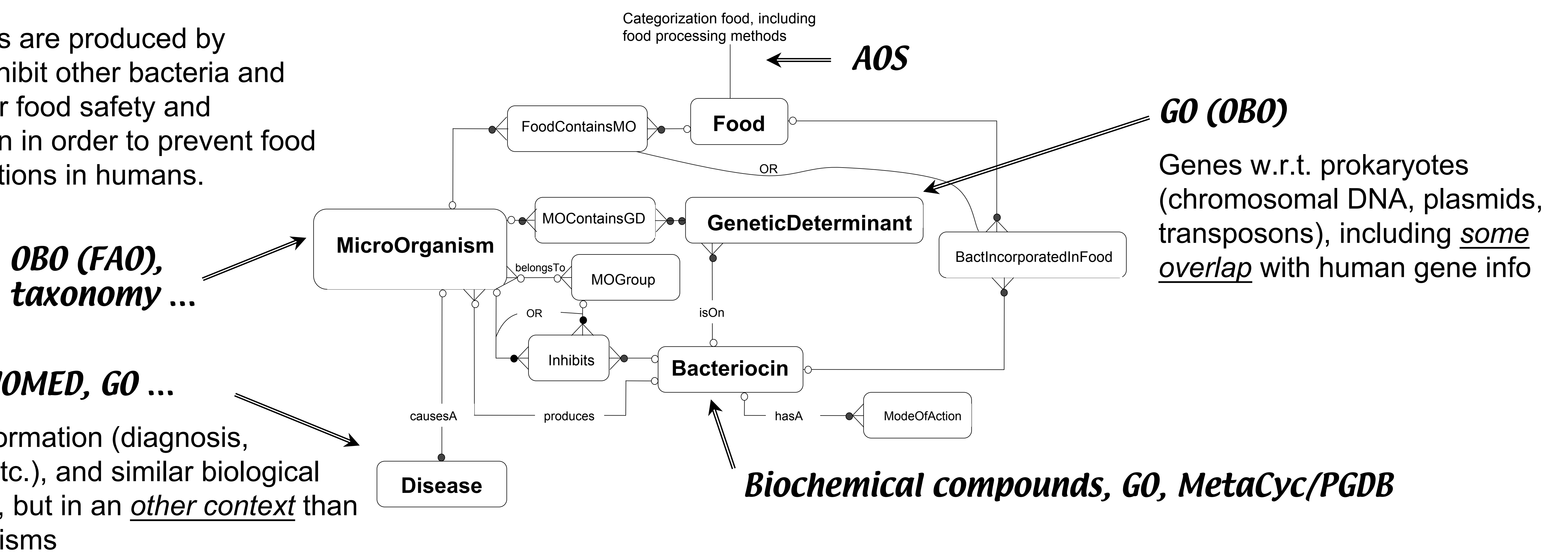
# Ontology integration for applied bioscience

## 1. Semantic integration of disciplines in core and applied sciences

### 1.1 Section of the Bacteriocin model

Conceptual model of the main bacteriocin-related entities, which, if used to develop an ontology, may take advantage of reusing sections of existing ontologies such as the AOS, GO and BiochemicalCompounds, provided ontology ‘integration’ is adequately addressed.

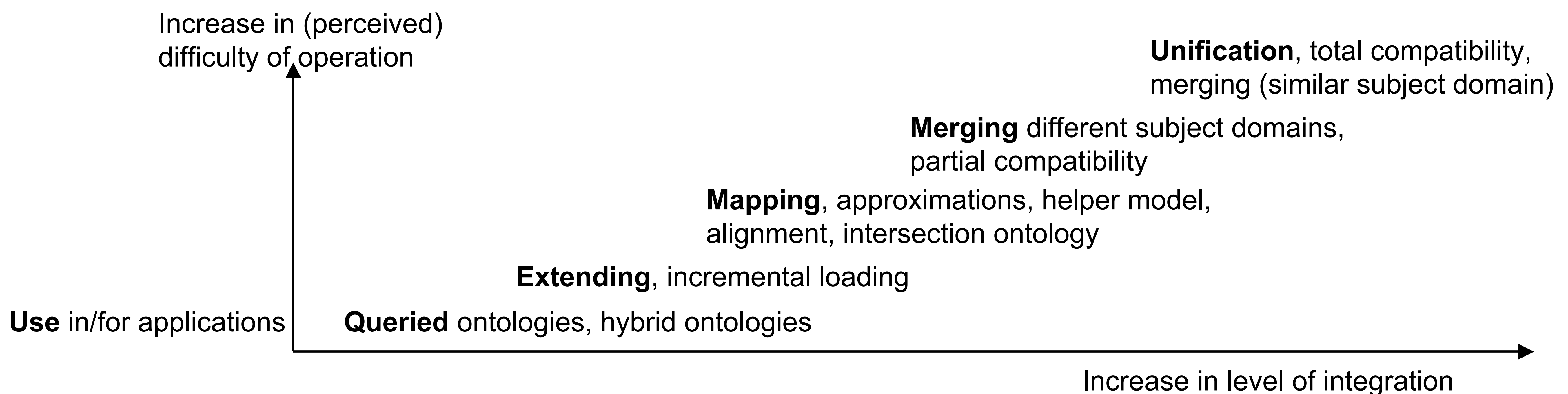
Bacteriocins are produced by bacteria, inhibit other bacteria and are used for food safety and preservation in order to prevent food borne infections in humans.



Biomedical domain links together applied research (biology, biochemistry, genetics), technology (e.g. clinical trials) and practices (e.g. hospital administration), hence requires sections of existing ontologies, where there are seemingly overlapping semantics with relation to concepts and their basic relationships but with *different constraints under different circumstances*: for microbial infectious diseases such as absence / presence nucleus, transcription initiation versus gene expression regulation and, in human body e.g. differences in gene expression and other molecular activity between cells from different tissues.

Ontology ‘integration’ needs to be clarified in order to sensibly integrate ontologies (which & how) and communicate about integration.

### 1.2 Stylized graphical representation of the levels of ontology integration



## 2. Some challenges and options

- Need for an ontology/taxonomy of ontology integration
- “Library” of ontologies and select only relevant sections.
  - What kind of integration for which kind of purpose(s)? Then first all on the formal level, facilitating semi-automatic integration.
  - Save such a ‘situational ontology’ as a conceptual model or new ontology? After multiple occurrences of similar model, develop an ontology design pattern?
- How to address and integrate different “contexts”?
  - Distinct lists of constraints for each context, alike a “GO for prokaryotes” separately from a “GO for humans”, then ‘integrating’ the two? Maintain a separate ‘ontology base’ with basic concepts and ‘simple’ relation without constraints, to add constraints later and separately?
- Modularization, epistemological layering and other ways to abstract away details.
  - Adopt white box/black box scenario as with OO modeling
  - Algorithms for semantic abstractions based on ontological importance
  - Framework/foundational ontologies with ‘leaves’ containing more detail