

LexMapr: a rule-based text mining tool for ontology-driven harmonization of short biomedical specimen descriptions

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Introduction

- LexMapr is an **open-source, ontology-driven, rule-based, text-mining** system developed to harmonize pathogen sample metadata, often encoded as inconsistent free text short phrases.
- LexMapr combines basic lexicographic transformation with light Natural Language Processing and other functionality to standardized text to ontology terms.
- LexMapr subsequently performs ontology-driven classification of specimen data using third party classifications, initially with extended Interagency Food Safety Analytics Collaboration (IFSAC+) food categorization schema.
- LexMapr addresses many challenges in processing short textual biomedical data, such as specimen phrases (Figure 1).

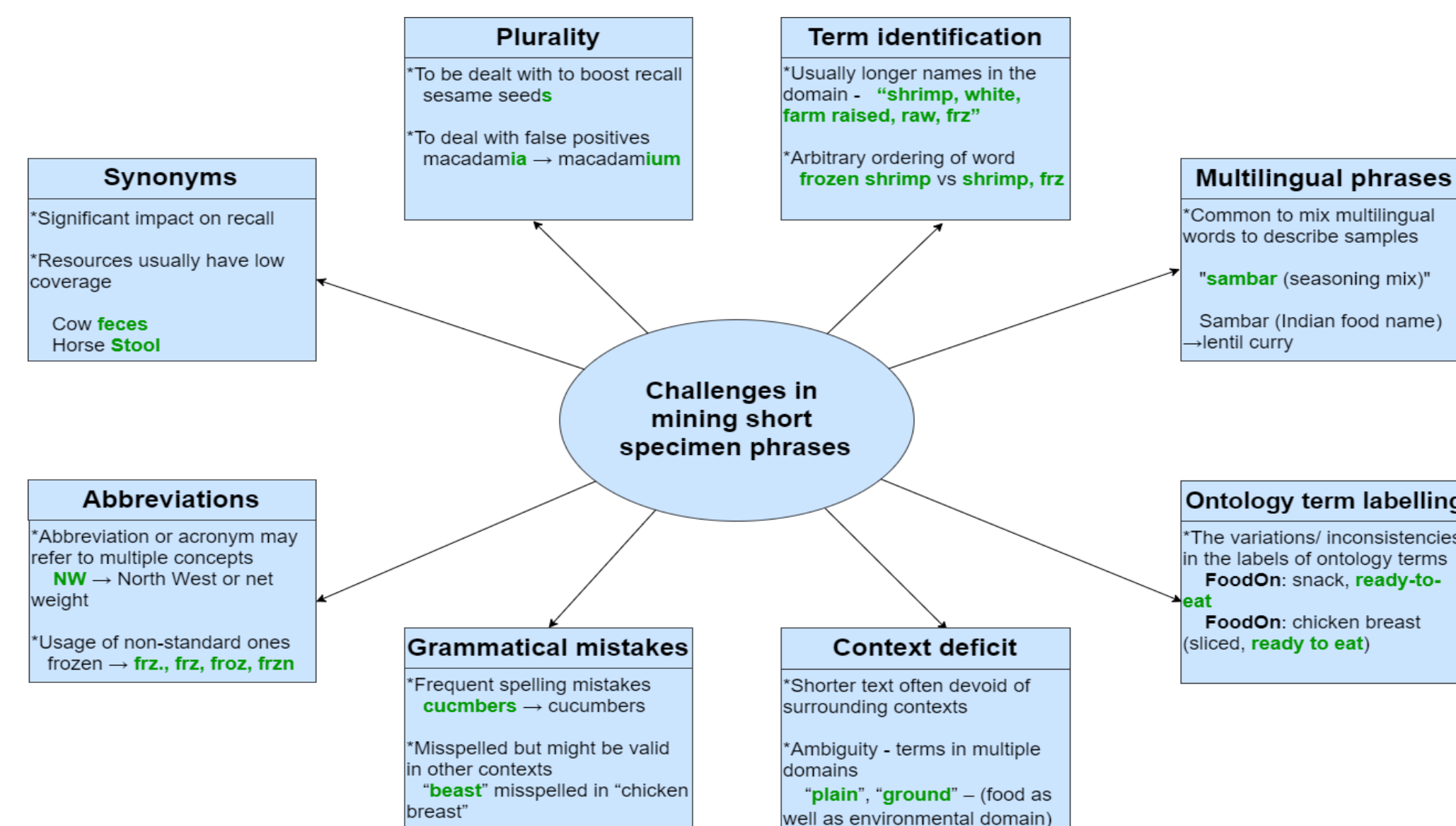


Figure 1: Challenges in mining of short biosample phrases

LexMapr

- LexMapr has been developed as a rule-based system by using different manually developed rules along with a number of lexical resources in the form of locally created lookup tables. LexMapr architecture and pipeline are shown in Figures 2 and 3.

Resources used:

- Ontologies:** FoodOn, GenEpiO, NCBITaxon, Uberon, CHEBI, Unit ontology -have been used for the underlying specimen domain (*users can dynamically select ontologies for other domains).
- Lookup tables:** For Abbreviations (AbbLex), Spelling corrections (ScorLex), Non-English food names (NefLex) and Additional food synonyms (SynLex).
- Dataset for rule development:** EnteroBase dataset that describes foodborne pathogen isolate source descriptions in short textual form (3391 unique sample descriptions extracted from >50000 samples) has been used for mining rules.

LexMapr availability

- LexMapr is an open source tool and the source code (written in Python language) has been made available at <https://github.com/Public-Health-Bioinformatics/LexMapr>
- LexMapr is currently available as a locally installable command-line tool and it has been released on bioconda with the latest version is available at: <https://anaconda.org/bioconda/lexmapr>
- For new users to LexMapr, a tutorial is available at: <https://docs.google.com/presentation/d/1RI1JIqjp8VcFbssd3OyAg3OxbCriKTrg6qxYpu9nYy4/edit#slide=id.p1>
- A user-friendly GUI is under development and will be made available very soon.

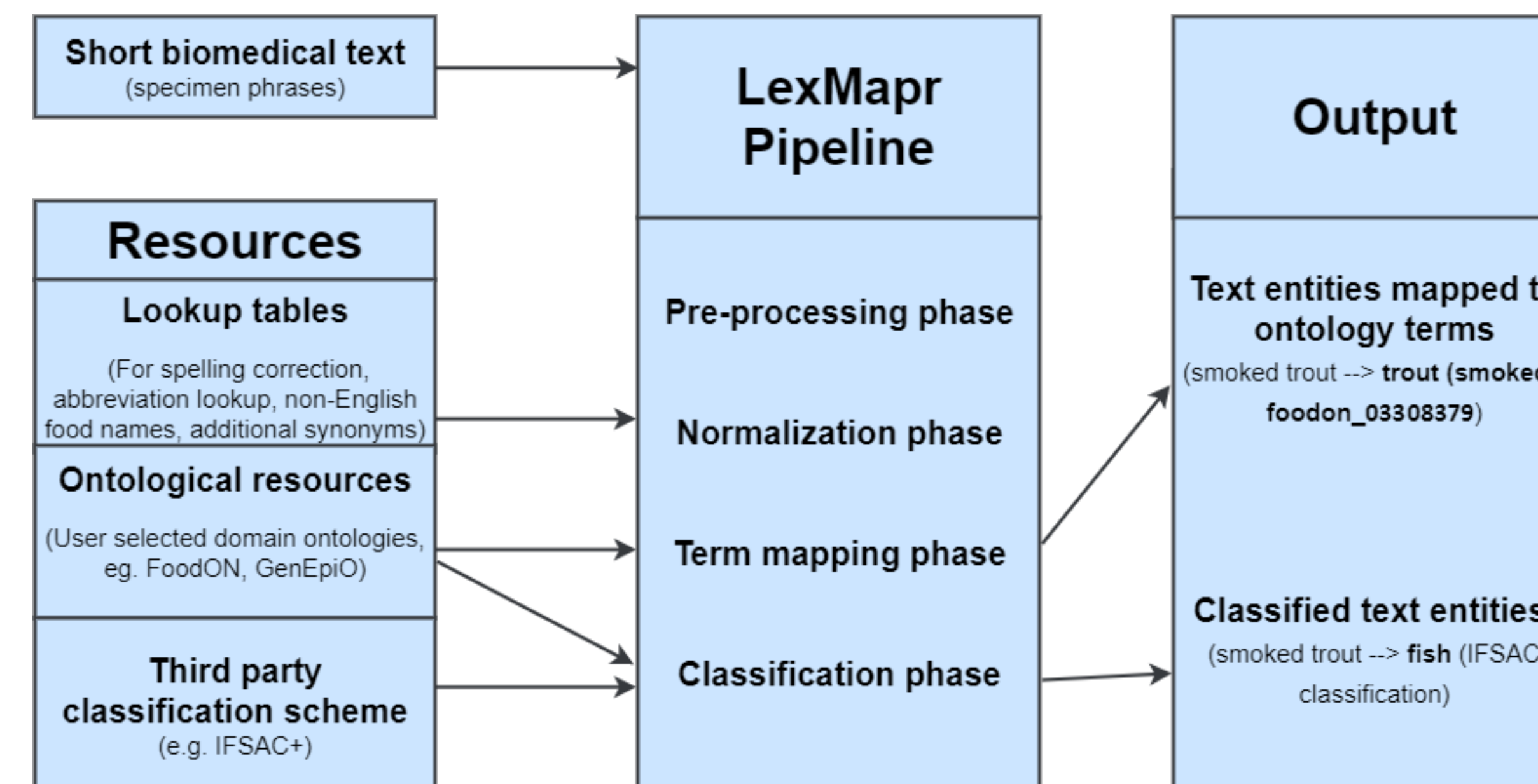


Figure 2: LexMapr architecture

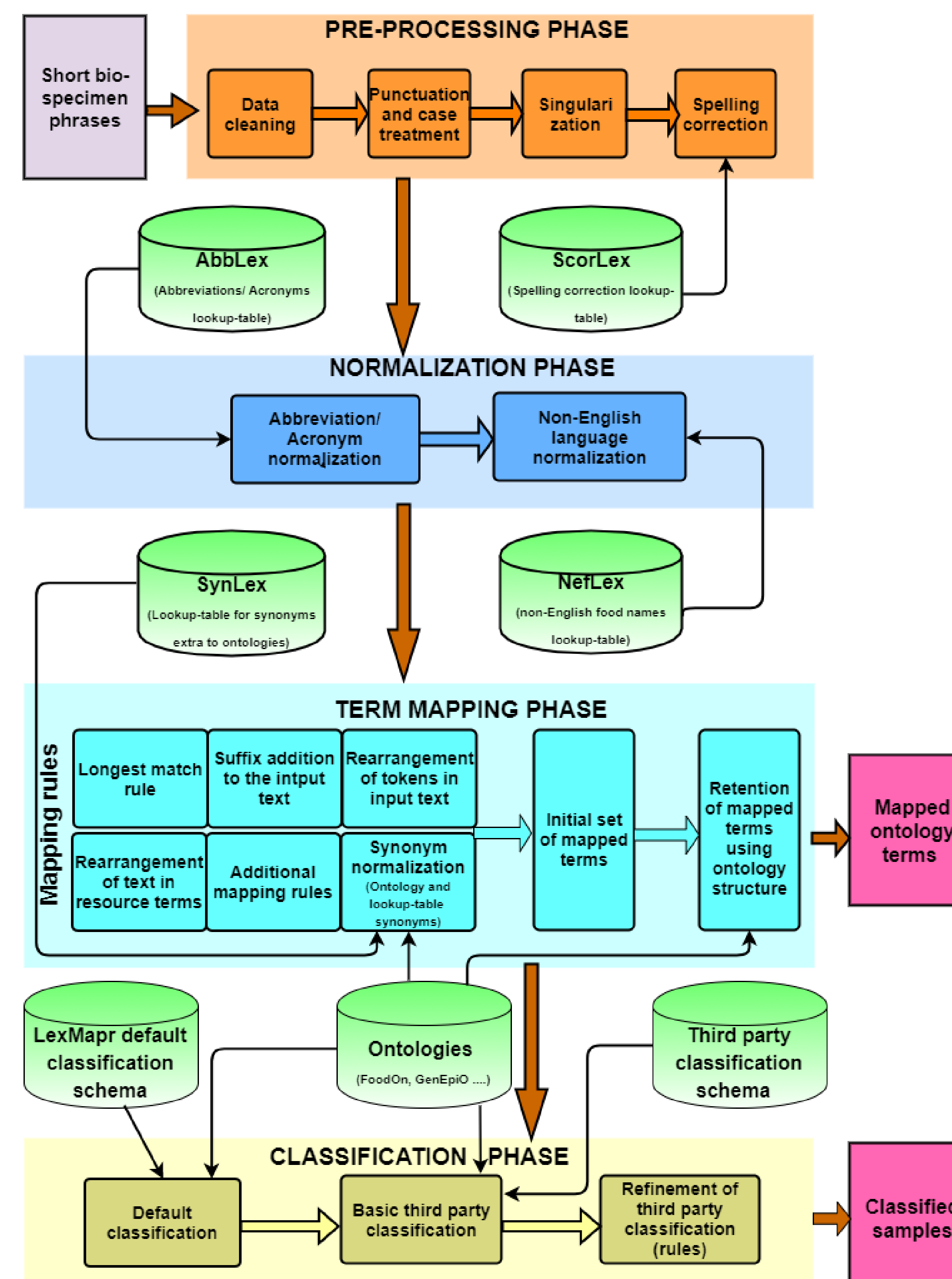


Figure 3: LexMapr pipeline

Results

Table 1: A snapshot of term mapping and classification results

Sample description	Mapped ontology terms	Rule	IFSAC+ Classification
feces-bovine	bovine:foodon_03414374, feces:uberon_0001988	Punctuation Treatment	cow, clinical/research beef
beef, ground	ground beef food product:foodon_00001282		
Rodent (colon)	colon:uberon_0001155, rodentia:ncbitaxon_9989	Synonym Usage	clinical/research dairy
fresh cheese curd	cheese curd:foodon_03310352, food (fresh):foodon_00002457		
Walnuts	walnut:foodon_03316466	Inflection (Plural) Treatment	nuts seeds
sesame seeds	sesame seed:foodon_03310306		
tumeric powder	turmeric food product:foodon_00002323	Spelling Correction Treatment	herbs
cantaloupe	cantaloupe fruit food product:foodon_00001288		melon fruit
Frz Catfish	catfish:foodon_03412620, frozen:patato_0001985	Abbreviation normalization	fish crustaceans
Snow Crab, froz	frozen:patato_0001985, snow crab:foodon_03411497		
smoked trout	trout (smoked):foodon_03308379	Permutation of Tokens	fish
haldi	turmeric food product:foodon_00002323	Non English Usage Treatment	herbs
ground beef	ground beef food product:foodon_00001282	Suffix Addition	beef

Evaluation

LexMapr performance has been tested on foodborne pathogen sample data from two different surveillance systems - The US FDA's GenomeTrakr system and The US National Antimicrobial Resistance Monitoring System (NARMS)'s Resistome Tracker platform.

Term mapping evaluation

- Evaluation dataset for term mapping-** 710 testing samples from GenomeTrakr that are completely independent of the previous training or testing samples.

(Previously term coverage assessed at 89% (accuracy 95%) based on strict criteria for >2000 unique samples from Enterobase, GenomeTrakr and BC Public Health Laboratory data).

Table 2: LexMapr term mapping evaluation results based on strict criteria (does not count partial matches)

Measure criteria	No. of specimens	Correct match	Missing match	Pipeline recall	Spurious match	Accuracy (pipeline)	F-Measure (F1)
Strict	710	632	45	93.35	33	95.04	94.18

Classification evaluation

- Evaluation dataset for classification-** 500 unique sample descriptions from NARMS's Resistome Tracker for IFSAC+ classification

Table 3: LexMapr classification evaluation results

No. of specimens	Correct match	Missing match	Pipeline recall	Spurious match	Accuracy (pipeline)	F-Measure (F1)
500	453	13	97.21	34	93.02	95.07

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