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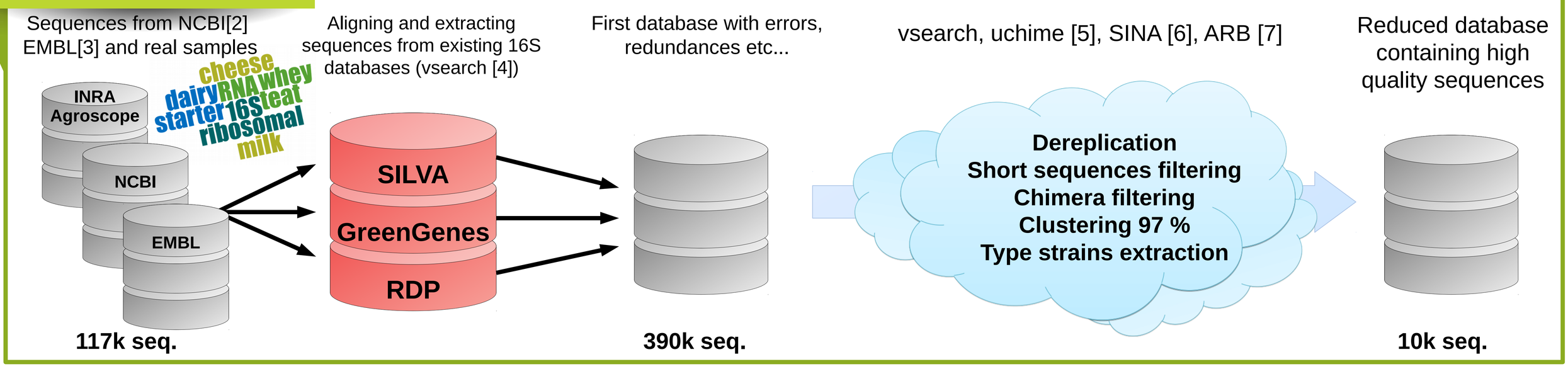
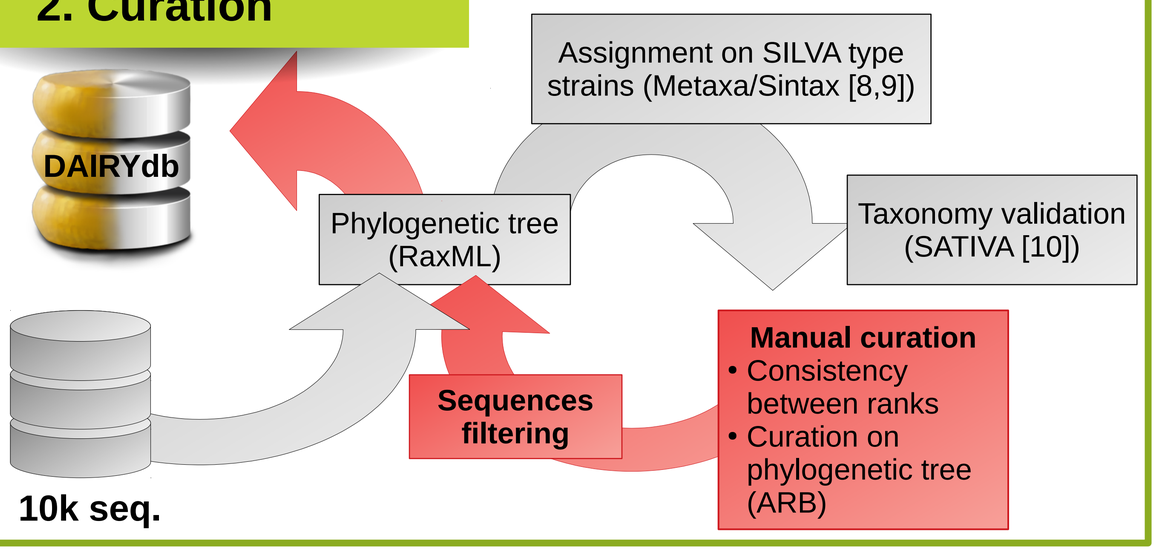
Context

Taxonomic assignment of amplicon sequence variants (ASV) is a key step in the metabarcoding data analysis for microbial community studies of cheese and dairy products. The taxonomic assignment depends mainly on the quality of the reference database. Current databases such as SILVA, RDP or Greengenes (GG) are complete and produce reliable assignments but do not allow to obtain an accurate taxonomic assignment of ASVs at species rank [1]. These databases also contain partial sequences of 16S rRNA with incomplete or erroneous taxonomy which impacts the assignment accuracy. Only a few percentage of their representative sequences present assignation at species rank.
DAIRYdb is a database built from complete and good quality 16S rRNA sequences from bacteria commonly found in cheese and dairy products. Thanks to the different bioinformatic treatments, we obtained a reduced database containing about 10,000 sequences. This allowed us to manually correct their taxonomy and then increase the assignment accuracy of ASVs from dairy products.

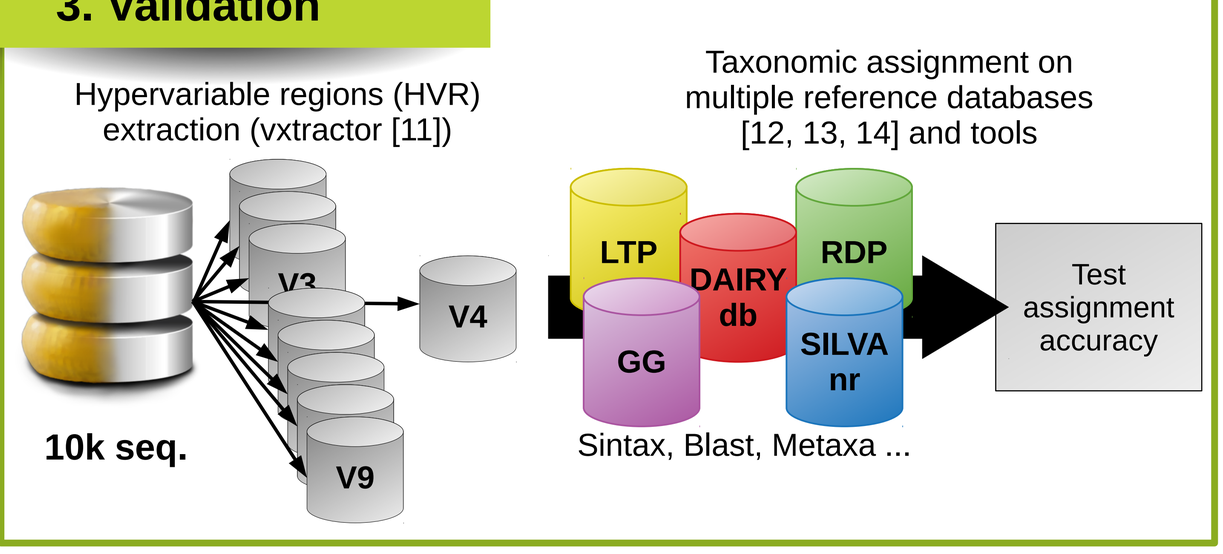
1. Contruction



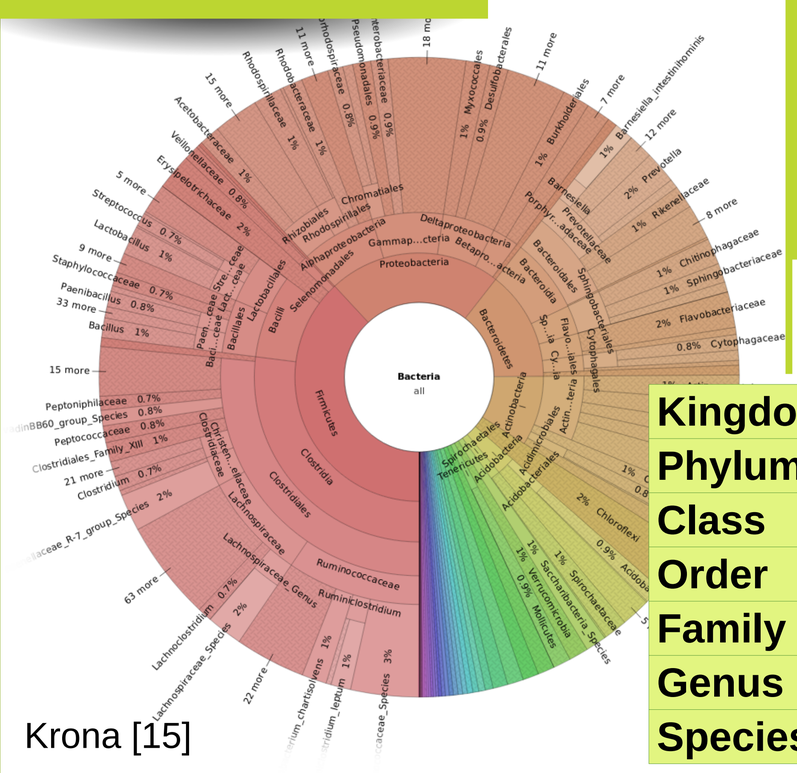
2. Curation



3. Validation



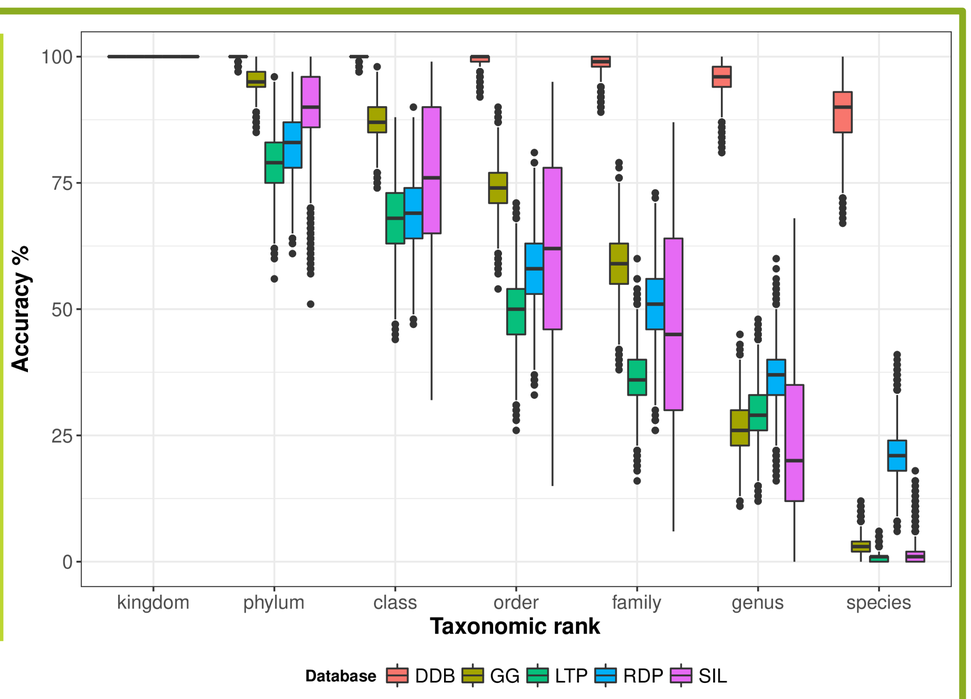
4. Curation



- DAIRYdb is composed of over 10000 sequences
- High diversity
- 38 % Firmicutes, 22 % Proteobacteria, 14 % Bacteroidetes, 9 % Actinobacteria

Kingdom	2
Phylum	46
Class	133
Order	244
Family	462
Genus	1754
Species	4027

- Assignment on each HVR
- DAIRYdb significantly improves taxonomic assignment at each rank.



Sintax assignment accuracy boxplot on every HVR (V1 to V9) tested on 5 different databases.

Conclusions

- DAIRYdb shows better taxonomic assignment accuracy up to species rank than standard databases.
- An environment specific reference database with authoritative full-length 16S sequences covering the diversity of dairy products.
- The reduced number of representative sequences, decreases risk of conflict (high identity and different taxonomy).

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Available on git repository at :
https://forgemia.inra.fr/umrf/dairydb