have been proposed to determine biomedical annotation [16,17], i.e., to link biomedical objects or documents to describing ontology concepts. Such methods produce recommendations that support domain experts in finding correct and complete ontology mappings and annotations.

Usually, ontologies are not static but modified on a regular basis. This process is known as *ontology evolution*. For instance, ontologies need to be changed to incorporate new domain knowledge, remove design errors or to achieve changed requirements. Often ontology development is a collaborative process that is supported by tools such as Protégé [19] or OBO-Edit [20]. In the life sciences, many ontology consortia continuously release new ontology versions. For instance, GO releases a new version every day, while the National Cancer Institute Thesaurus (NCIT) [21] is published on a monthly basis. Fig. 1 exemplarily shows the history of changes between 2015–11 and 2016–04 in GO. Typically, new versions contain improved and extended knowledge such as new concepts (classes), relationships or attributes like synonyms. However, existing knowledge can also be revised or removed, e.g. concepts might be deleted or marked as obsolete. For instance in the shown time period for GO (see Fig. 1), new classes have been added continuously, in 03-2016 some concepts were set to obsolete, and some definitions and class labels have been deleted. To manage the evolution of ontologies it is essential to determine changes, e.g. by analyzing change logs or by computing the difference (Diff) between two given versions of an ontology. Such a Diff is useful to synchronize changes in collaborative ontology development and to adapt dependent applications.

The evolution of ontologies has impact on ontology-based applications. For instance, ontology mappings and annotations can become invalid when the underlying ontologies are changed. This is especially critical in highly volatile domains such as the life sciences. Fig. 2 illustrates two ontologies (O1 and O2) and a mapping between them ($M_{O1,O2}$). In O1, one concept has been removed (red) while two concepts have been added to O2 (green). Another concept in O2 has been revised (blue) e.g., by changing the concept name. These ontology changes have impact on the set of correspondences (dashed lines) and might require changes in the mapping. In the example, one correspondence is associated to a deleted concept, and might therefore be removed. Moreover, the added and revised concept might lead to novel correspondences. Hence, ontology-based mappings can become out-dated as a consequence of ontology evolution. In order to keep mappings up-to-date they need to be migrated to currently valid ontology versions. On the one hand, a manual mapping maintenance can be very time consuming or even infeasible since ontologies and mappings can become very large. On the other hand, automated methods could be simply reapplied on the same data to obtain a valid mapping w.r.t.
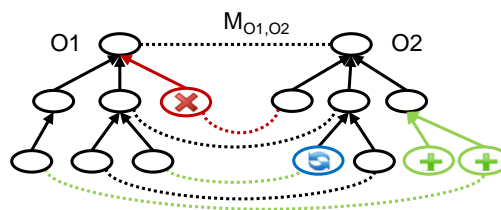

Fig. 2. Example ontology and mapping evolution.

the current ontology version. However, this can lead to a huge loss in quality since existing mappings might have been manually verified and corrected in the meantime. Just recomputing the results would discard this valuable knowledge. Moreover, usually a smaller part of an ontology is changed such that it seems likely to adapt only affected mapping parts. Therefore, it is useful to apply (semi-) automatic adaptation methods to migrate out-dated ontology-based mapping to currently valid ontology versions.

In this review, we will first introduce the problem of ontology and mapping evolution (Section 2) and then give an overview of recently proposed evolution methods for the biomedical domain and discuss open challenges:

- Methods for ontology evolution have been surveyed in several contexts before (e.g. [22–25]). Here we will focus on recent approaches that we see relevant for semi-automatic adaptation of ontology-based mappings and applications in the life sciences. This includes novel directions in ontology change detection and prediction and the visualization of ontology evolution. (Section 3)
- We will then discuss requirements for mapping evolution and provide a comparison and overview on existing (semi-) automatic adaptation strategies for ontology-based mappings. (Section 4)
- We will finally outline open challenges and future directions for the evolution of ontologies and ontology-based mappings and applications (Section 5).

2. Problem formulation

In this section, we will introduce the basic scenario of ontology and mapping evolution along with an illustrating example. An ontology $O = (C,A,R)$ consists of a set of concepts C (or classes) that are connected via a set of relationships R with different semantics such as *is-a* or *part-of*. Often ontologies form so-called Directed Acyclic Graphs.
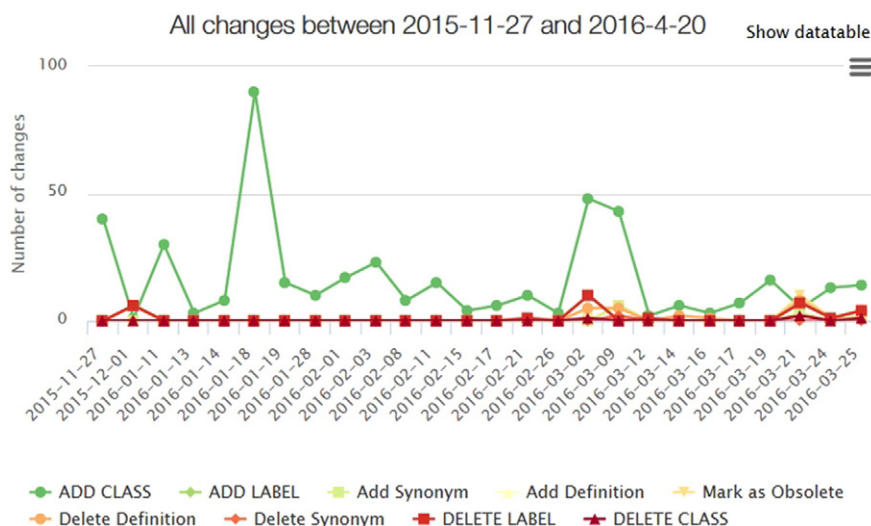

Fig. 1. History of changes in Gene Ontology (generated with ontology lookup service [18]).