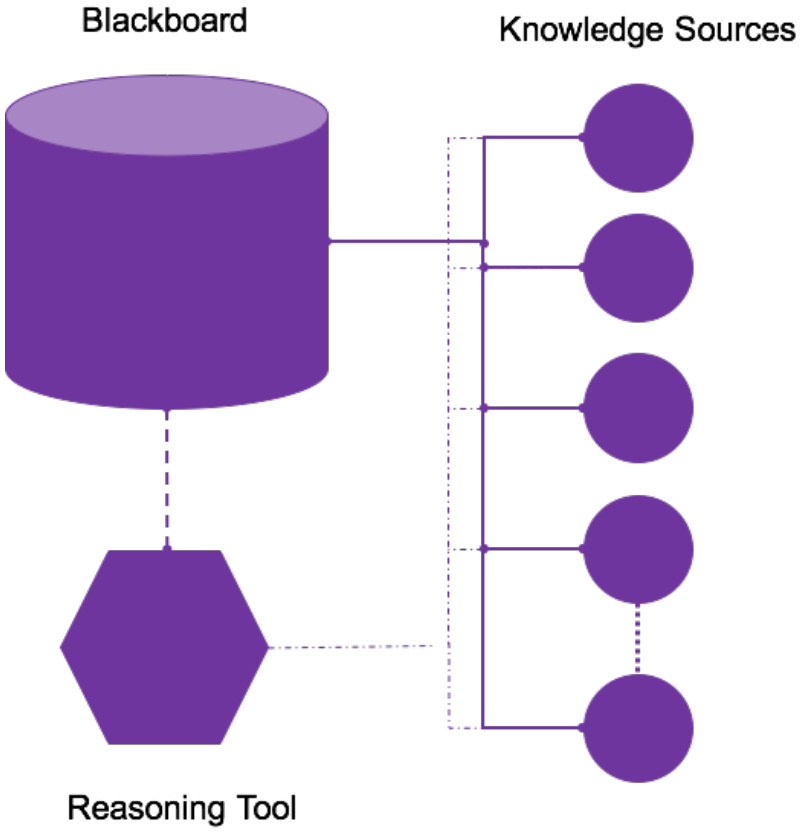
Further Information on Biomedical Data Translator



The general architecture currently employed by the Biomedical Data Translator is based on the Blackboard architecture. This architecture is comprised of three components

- Knowledge Sources (KS) - this component corresponds to specific data or information sources. This can correspond to traditional databases such as Uniprot, ChEMBL or Entrez Gene. But a KS can also be an algorithm that has well defined inputs and outputs. See website for a description of some KS's currently used by the Biomedical Data Translator.
- Blackboard (BB) - this component represents a space within which data queried from KS's is collated. The Biomedical Data Translator project has two BB implementations https://tkbio.ncats.io/ and https://translator.ncats.io/blackboard
- Reasoning tool - this component accepts a query, prioritizes KS's based on relevance to the query, coordinates requests to the KS's and computes on the retrieved data to produce an answer or a dataset that can be used by the user to formulate the answer. Currently, the reasoning tool function of the Translator is addressed by humans, and the actions of the reasoning tool are recorded in a Python Notebook. See here for a series of examples.

The goal of this solicitation is to support the research and development of a reasoning tool prototype to automate Translator operation as far as possible, and if not achievable, identify critical bottlenecks that must be resolved before such a reasoning tool can be implemented.