ModelSEED: Assembling a biological thermodynamic database

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**Abstract**

**Summary:** Computational biology is predicated upon biochemical databases. The Thermodynamics of Enzyme-Catalyzed Reactions database (TECRDB) by NIST is a renowned database of thermodynamic reactions, however, the website has become neglected and consequently the data has become inaccessible to biological modelers. We present work that salvaged, reformatted, and contributed the TECRDB data to the ModelSEED database, where the data will be actively curated and readily accessible to biological modelers. The salvaging, reformatting, and contributing methods were completed through Python scripts, which are provided with the associated documentation in our GitHub repository (<https://github.com/freiburgermsu/Biochemical-databases>).

Systems biology and bioinformatics are test theoretical and experimental biology. Whole cell models (Karr and Goldberg, 2020), for example, critique theoretical schema of interacting biological systems whilst also predicting experimental results by perturbing parameters. These systems-level models are predicated upon biochemical data and databases (Bhat and Balaji, 2020; Zvi *et al.*, 2008; Arakawa *et al.*, 2003). Database are most prevalently online, since the internet reaches a maximum audience and optimally allows real-time updates. Numerous website databases, however, have become neglected as webmasters leave their duties, and consequently many databases have lost usefulness to contemporary modelers.

The TECRDB (Goldberg *et al.*, 2004) is such a database. The TECRDB impressively amalgamates of literature review and database assemblage to create a singular source of biochemical data for 417 enzymatic reactions. The database website, however, has lost critical features that were detailed in the original publication. The website, for example, has disabled the download function, which renders the data practically non-existent for biological modelers who are unlikely to manually transcribe the data. The website has further lost the cited background description of the database, which may allow researchers to understand the data and the associated methods that were used to acquire and\or approximate the data. The symbol key for the sub- and super-scripts, which must adhere to IUPAC and IUBMB standards, are also absent from the database. The querying methods are moreover dissimilar from the published methods, where the current methods are rudimentary. The database furthermore contained 25 broken pages, where the thermodynamic data tables were unpresented.

We recognized the neglected yet valuable data of the TECRDB and elected to refresh the data. This work both reintroduces an important thermodynamics resource to the systems biology community and may ideally inspire bioinformatitians to consider salvaging neglected thermodynamic datasets and contributing the data to a standard resource for the community (Dogucu and Çetinkaya-Rundel, 2020). We used myriad Python scripts, which are published in our GitHub repository (<https://github.com/freiburgermsu/Biochemical-databases>), to web scrape, parse, organize and reformat, and then contribute the TECRDB data to the ModelSEED database, which is an actively curated database of biochemical reactions.

The TECRDB was first web scraped through the BeautifulSoup library of Python. Script iteratively searched the URLs for each functioning database page through the Requests module. The webpages were subsequently parsed the table elements through the <tr> and <th> HTML tags via the BeautifulSoup LXML interpreter, and the acquired data was cleaned of spaces and non-ASCII characters (Massimino, 2016). The data from scraping each webpage were compiled into a single table, where columns of similar data like equilibrium constants were all combined.

The organized TECRDB data was organized and reformatted via the Pandas and JSON modules. The format that is required for ModelSEED contributions was imposed upon every reaction, which required that every compound be identified in the ModelSEED database. The TECRDB reactions were first matched with ModelSEED reactions by matching the chemical equation, where each involved compound in the TECRDB was assigned a ModelSEED ID. The compounds were matched principally by name, although, the myriad common and IUPAC synonyms for every chemical species prevented a broad success with matching solely by the chemical name; thus, the unmatched compounds were identified through a manual investigation of the unmatched compounds in the ModelSEED database. The reactions that failed to matched through the chemical equation per se, which included instances where the constituent compounds were unidentified in the ModelSEED database, were match through the KEGG IDs that the TECRDB ascribed to every one of its reactions.

The aging internet and web-based databases will increasingly require intervention to salvage data. Bioinformatitians must resist the Bystander Effect and proactively rejuvenate old databases by contributing the data into centralized and curated database like ModelSEED, which will be an invaluable resource for biological modelers. The ModelSEED database is eager to receive community contributions of data, for which a step-wise diagram is provided in our GitHub repository.

# **References**

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