

neo4jsbml: import Systems Biology Markup Language data into the graph database Neo4j

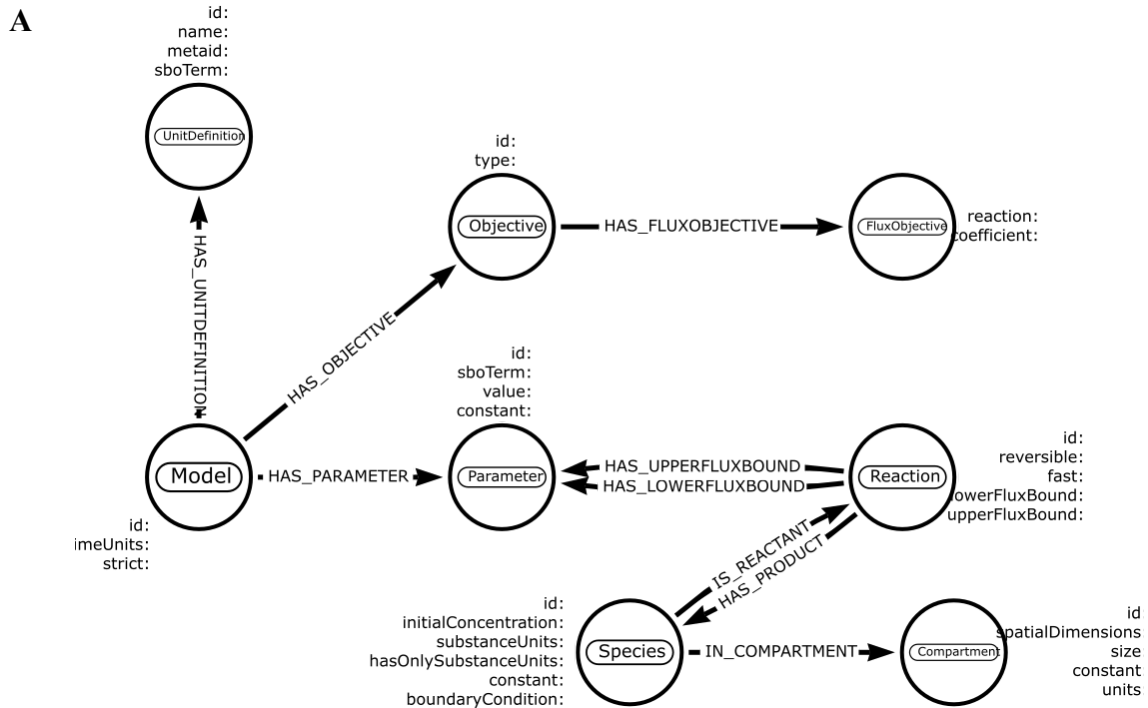
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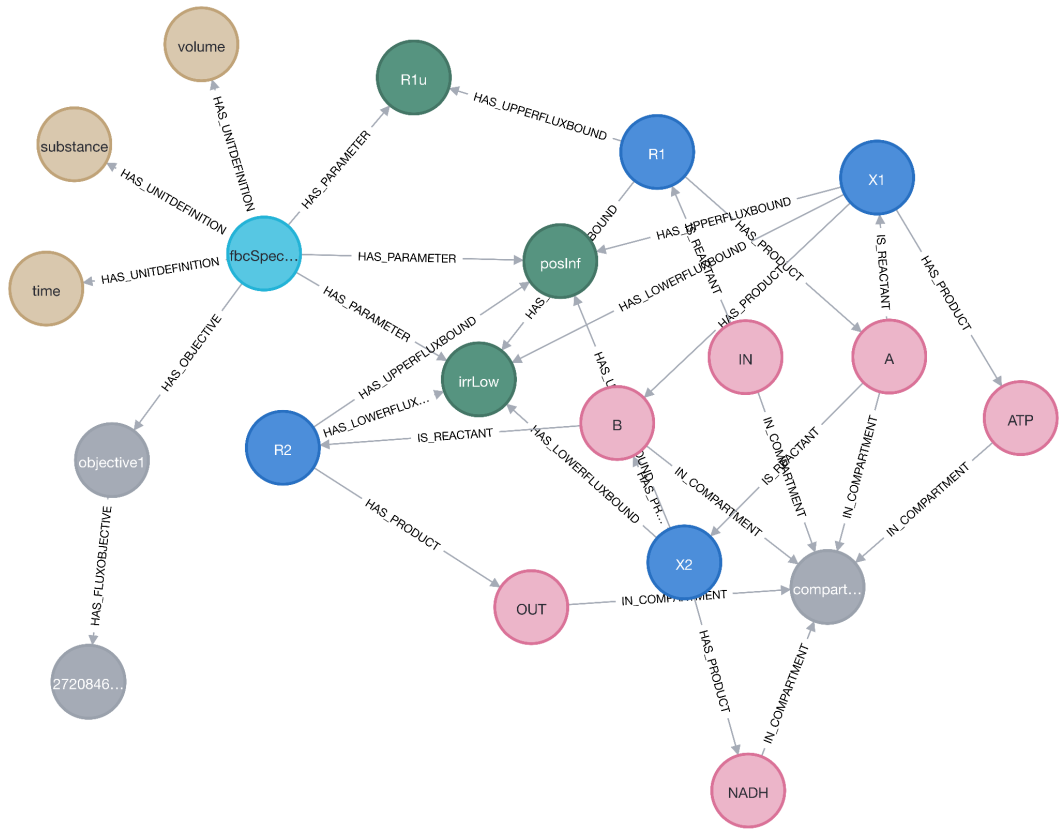
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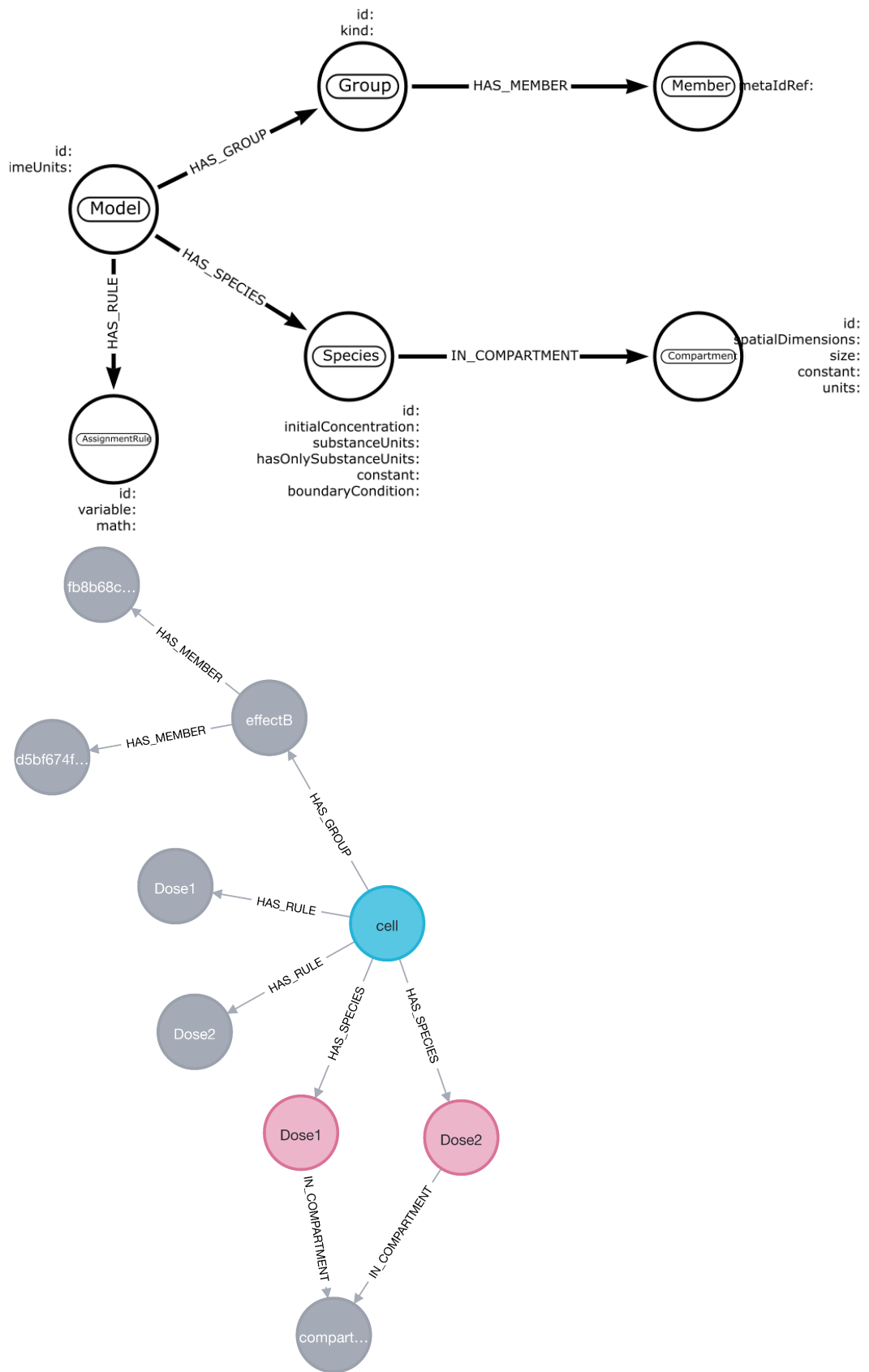
Supplementary Figure S2

SBML models were extracted from the SBML specifications, then they were loaded into Neo4j. The Arrows schema used, and all nodes and relationships extracted from Neo4j, were shown for each example. **A.** Model extracted from Chapter 4, Example 1 of the Flux Balance Constraints specification package ¹. **B.** Model extracted from Chapter 5, Example 2 of the Groups specification package ². **C.** Model extracted from Chapter 4, Example 5 of the Layout specification package ³. **D.** Model extracted from Chapter 4, Example 2 of the Qualitative Models specification package ⁴.

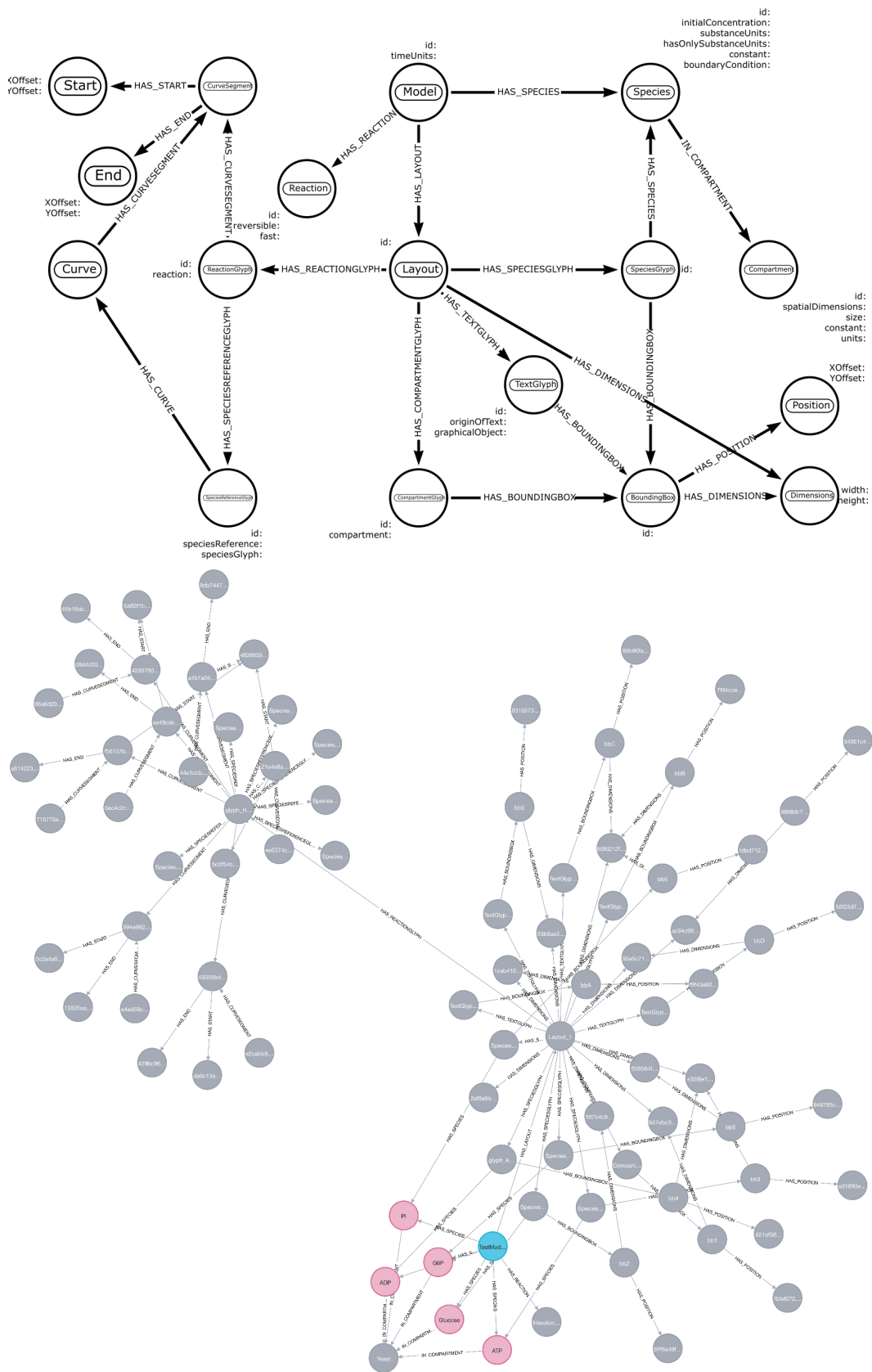




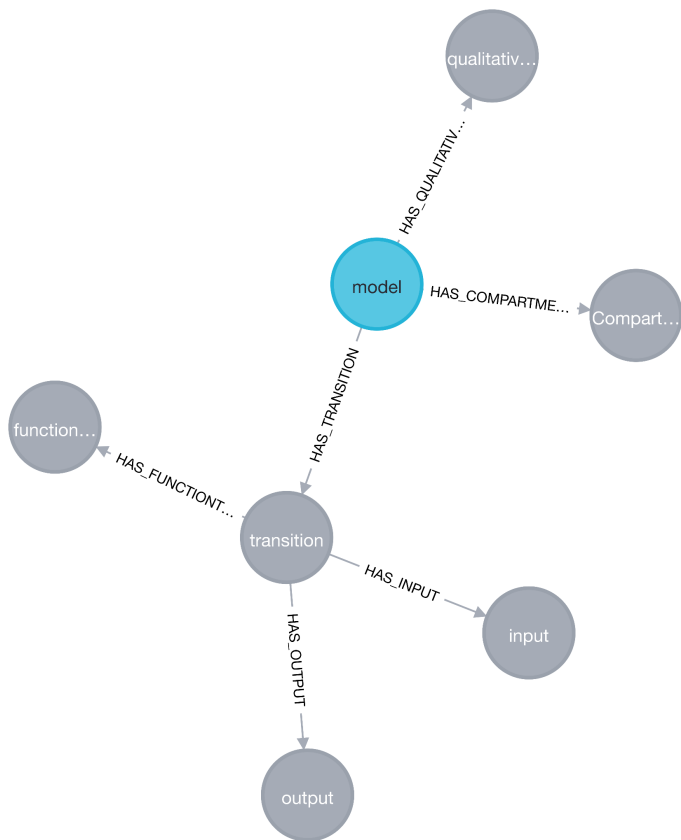
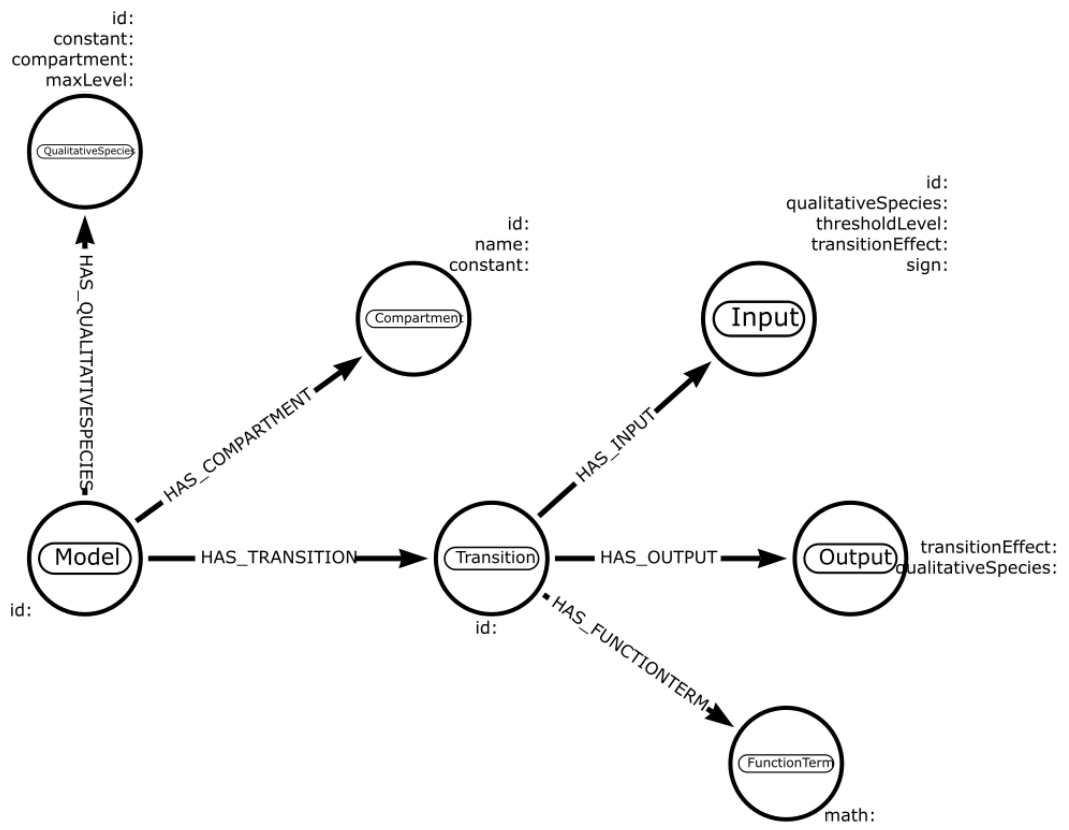
B



C



D



- (1) Olivier, B. G.; Bergmann, F. T. SBML Level 3 Package: Flux Balance Constraints Version 2. *J. Integr. Bioinforma.* **2018**, *15* (1). <https://doi.org/10.1515/jib-2017-0082>.
- (2) Hucka, M.; Smith, L. P. SBML Level 3 Package: Groups, Version 1 Release 1. *J. Integr. Bioinforma.* **2016**, *13* (3). <https://doi.org/10.1515/jib-2016-290>.
- (3) Gauges, R.; Rost, U.; Sahle, S.; Wengler, K.; Bergmann, F. T. The Systems Biology Markup Language (SBML) Level 3 Package: Layout, Version 1 Core. *J. Integr. Bioinforma.* **2015**, *12* (2), 550–602. <https://doi.org/10.1515/jib-2015-267>.
- (4) Chaouiya, C.; Keating, S. M.; Berenguier, D.; Naldi, A.; Thieffry, D.; Iersel, M. P. V.; Le Novère, N.; Helikar, T. SBML Level 3 Package: Qualitative Models, Version 1, Release 1. *J. Integr. Bioinforma.* **2015**, *12* (2), 691–730. <https://doi.org/10.1515/jib-2015-270>.