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Synthetic biology open language (SBOL) version 3.1.0

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Abstract: Synthetic biology builds upon genetics, molecular biology, and metabolic engineering by applying engineering principles to the design of biological systems. When designing a synthetic system, synthetic biologists need to exchange information about multiple types of molecules, the intended behavior of the system, and actual experimental measurements. The Synthetic Biology Open Language (SBOL) has been developed as a standard to support the specification and exchange of biological design information in synthetic biology, following an open community process involving both bench scientists and scientific modelers and software developers, across academia, industry, and other institutions. This document describes SBOL 3.1.0, which improves on version 3.0.0 by including a number of corrections and clarifications as well as several other updates and enhancements. First, this version includes a complete set of validation rules for checking whether documents are valid SBOL 3. Second, the best practices section has been moved to an online repository that allows for more rapid and interactive of sharing these conventions. Third, it includes updates based upon six community approved enhancement proposals. Two enhancement proposals are related to the representation of an object's namespace. In particular, the Namespace class has been removed and replaced with a namespace property on each class. Another enhancement is the generalization of the CombinatorialDeriviation class to allow direct use of Features and Measures. Next, the Participation class now allow Interactions to be participants to describe higher-order interactions. Another change is the use of Sequence Ontology terms for Feature orientation. Finally, this version of SBOL has generalized from using Unique Reference Identifiers (URIs) to Internationalized Resource Identifiers (IRIs) to support international character sets.

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