Purpose
With the increasing volume of genomic data, it has become clear that biologists need computational methods for organization and analysis. We are developing a knowledge-based environment for organizing the data into computer-interpretable and human-browsable formats. Our focus is on bridging the gap between high-level physiological processes and molecular-level functions.

Material and Methods
We defined a set of properties that should characterize a biological process model: (1) intuitive, graphical representation, (2) formal semantics that enables verification of the correctness of the model and reasoning about biological processes and the relationships among processes and their participants, (3) modeling the structure, function, and dynamics of a biological system, (4) hierarchical structure to manage the complexity of the representation, and (5) inclusion of a biological ontology.

We assessed eleven models that were developed in the fields of software engineering, business, and biology, with respect to these properties. We found the most appropriate model to be a Workflow model. It supports almost all of the desired properties, except for the inclusion of a biological ontology and reasoning that is dependent on it. The Workflow model maps to Petri Nets, allowing verification of properties such as reachability, boundedness, and soundness.

Results
Our framework for modeling biological processes is based on the Workflow model and incorporates the TAMBIS ontology as a biological controlled vocabulary. We added other elements that are relevant to biological systems: cellular location information for process participants and the types of evidence that support facts in the knowledge base. We augmented the Workflow model with elements taken from Object-Process Methodology, to create a graphical representation of four relationship types that occur between a process and the structural components that participate in it (i.e., catalysts, substrates, products, and inhibitors).

We implemented our framework using the Protégé-2000 tool and tested it by representing Malaria parasites invading host erythrocytes. Using Protégé's axiom language, we composed queries that can aid discovering relationships among processes and structural components. We used reachability analysis to answer queries that relate to dynamic aspects.

Conclusion
We developed a formal yet intuitive knowledge model of biological processes and functions that is graphical, for human comprehension, and machine-interpretable, to allow reasoning. The model enables verification of safety and soundness, and querying information that can assist in discovering relationships among processes and structural components that participate in them.